Proceedings of the

Fourth York Doctoral Symposium on Computer Science

Department of Computer Science, The University of York, UK
20th October 2011

Editor:
Christopher M. Poskitt

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We are extremely grateful to all of the following institutions for generously sponsoring our symposium this year.

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Preface

The annual York Doctoral Symposiums are aimed at new Computer Science researchers undertaking PhDs or Masters-level degrees. For those who contribute papers, talks, or posters, they provide a means of gaining feedback on early work within a friendly setting and from an audience representing a wide range of research interests. For the students who contribute as Organising and Programme Committee members, they provide a taste of what is involved in putting together a conference. For the attendees, they provide academically stimulating days, a chance to find out what colleagues in other research groups are doing, and last but not least, an excellent social occasion in the evening!

The *Fourth York Doctoral Symposium on Computer Science* (YDS 2011) was held at the University of York, and for the second time, at our new Heslington East campus. Full-length papers were again invited for submission, but for the first time, so were extended abstracts and posters. Most submissions were received from the Department of Computer Science at York, but we were delighted to also receive submissions from York's Department of Electronics, the University of the West of England, University College London, the University of Sunderland, and even the University of Oslo. All papers were reviewed by three members of the Programme Committee (PC) via EasyChair. PC members then met in person to decide on a final programme comprising seven full-length papers and three extended abstracts. Poster authors were invited to produce a short abstract for the proceedings; eight authors chose to submit one, each of which was checked by two PC members. The papers and posters accepted are a good representation of the wide-ranging research undertaken by Computer Scientists.

We were delighted to have two external keynote speakers this year. Professor Alan Winfield (University of the West of England) introduced mobile robots, and discussed a method for artificially evolving a robot to optimise its design. Lidia Oshlyansky (Google, Inc.) spoke about working in industry as a user experience designer, and also discussed the working life and culture of Google. Myself, the PC, and the organisers are all grateful to our keynote speakers for agreeing to speak at YDS 2011.

I would like to convey my thanks to the PC, who undertook the task of reviewing submissions and choosing a programme very thoroughly and professionally. I would also like to thank the Organising Committee members for all of their efforts, too; they are to be credited for a record number of submissions, record sponsorship, excellent coffee breaks and food, and for the fact that all organisational matters were dealt with quickly and effectively.

October 2011 Christopher M. Poskitt

PC Chair, YDS 2011

Organisation

All YDS 2011 Organising and Programme Committee members are from the University of York, UK.

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Part I

Keynote Talks

Let's get Physical: Robot Bodies and how to Evolve them

Alan F. T. Winfield

University of the West of England, Bristol
Alan.Winfield@uwe.ac.uk

Abstract

Robots have bodies, and bodies must obey the laws of physics. The behaviour of a mobile robot is the result of the physical interaction of the robots body and its working environment. In this talk I will introduce mobile robots and show how we design robot bodies. A powerful new approach is called evolutionary robotics. Inspired by Darwinian evolution it is a method for artificially evolving a robot to optimise its design. Illustrated with video clips of robots in action, and some real robots, I will explain how roboticists are evolving strange new robot bodies.

Biography

Alan Winfield is Professor of Electronic Engineering and Director of the Science Communication Unit at the University of the West of England, Bristol. He conducts research in swarm robotics in the Bristol Robotics Laboratory and is especially interested in robots as working models of life, evolution, intelligence and culture. Alan is passionate about communicating science and technology. He holds an EPSRC Senior Media Fellowship with the theme Intelligent Robots in Science and Society, and blogs about robots, open science and related topics at `http://alanwinfield.blogspot.com/`.

Working at Google — Especially in User Experience

Lidia Oshlyansky

Senior User Experience Researcher, Google Inc.
lidiaosh@gmail.com

Abstract

This talk will focus on alternatives to academia, in particular, working in industry (with a focus on industry in the UK). It will explore the types of roles available to engineers, researchers, and "user experience" designers. The focus will primarily be on the user experience roles available, and the challenges faced by those who undertake them within the context of a large company. The talk will also reveal some facts about the working life at Google and the company's culture.

Biography

Lidia began her professional career as a social worker before moving into Computer Science. Here, she moved from database programming and computer architectures to Human Computer Interaction (HCI). Her career in HCI has taken her through various roles and companies. She has worked for dot-com companies (including Orbitz.com and Cars.com), as a consultant in the financial sector, and for an agency (where clients included WWF.org, Royal Mail, and the UK's Department of Health). More recently she has worked as a user researcher for Nokia and now Google. At Google, she has worked as a researcher for AdSense, YouTube, Google Product Search, and also assisted teams investigating emerging markets.

Lidia completed her PhD in HCI in the UK, where she has been working and living for the last eight years.

Part II

Full-Length Papers

3D Texture Analysis using Co-occurrence Matrix Feature for Classification

Shahzad Anwar, Lyndon N. Smith, Melvyn L. Smith

Machine Vision Laboratory, Department of Engineering, Design and Mathematics, University of the West of England, Frenchay campus, Coldharbour Lane, Bristol, BS16 1QY, UK.
shahzad2.anwar@live.uwe.ac.uk

Abstract. This article describes the usefulness of employing co-occurrence matrices (CM) as feature extraction and neural network (NN) for classifying 3D texture. The goal is to extract 3D textural features and analyse them for classification. To accomplish this, this research has adopted Photometric stereo (PS) method for capturing images and a CM based approach for modelling the surface normals and a backpropagation NNs for classification. The PS acquired images were processed, slant and tilt angles were calculated as features. The network trained for 20000 epochs and 10 hidden layer neurons were employed for classification. The system overall performance shows a regression of 0.89, which confirms the suitability of the model. We have examined three different textures as case sample for a three class problem. The respective method demonstrates how images are analysed, processed and characterised and how the NN is applied to this imaging problem.

Keywords: 3D imaging, co-occurrence matrix, neural network

1 Introduction

Texture is a term often referring to properties that represent the surface of an object; it is widely refereed in literature, however, has no precise definition due to its wide variability. Here we describe texture a group of pixels repeating in a pattern (a texture primitive or texture element). Texture classification is to assign texture label to unidentified texture according to the training samples and classification rules. Two main subjects are crucial for texture analysis, the feature extraction and classification. The foremost objective of texture classification is to find the best matched category for a given texture among existing textures. There are numerous approaches in the literature for texture analysis where research community have comprehensively discussed statistical, signal processing and model-based techniques [1-3].

Texture analysis via computer vision is a challenging area, attracting much of the research community. The problems encountered are due to the inherent complexity contained in the images. Neural Networks (a biological nerves system) have proved to be very useful in application to complex image understanding as well as within clinical imaging analysis. During the past decade NN's have become a tool for classification. NN applications in Computer Aided Diagnosing (CAD) corresponds to the foremost application of computational intelligence in medical imaging [4-6]. NN contribution are wide-ranging for all medical problems due to the fact that NN's have the quality of learning from input information and by using an appropriate learning algorithm are capable of adjusting in accordance with the variation in the inputs. NNs have the capability of optimising the input output relation, leading to reliable solutions. The work reported the machine vision laboratory UWE Bristol have appraised NN with great success [7, 8].

Using a computerised model for the detection of melanoma in clinical images, Ding [9] examined skin tilt /skin slant method for feature analysis. Three-layer multilayer perceptron (MLP) NN was employed to classify benign and malignant images. The method use error-back propagation network with two input units corresponding to the skin tilt/skin slant features of each image; with one classifier output (one indicating melanoma and zero benign). Twenty clinical samples (images) were investigated in the experiments.

Many researchers have refereed NNs in literature, incorporating NNs for classification. For instance Cheng [10] suggested NN together with a mathematical model for cluster micro-calcifications with a noisy background. The scheme is based on allowing all mammogram as topographic descriptor where micro-calcification appears as an elevation comprising a regional maximum. Similarly Nagel [11] investigated three methods of feature analysis, rule based, NN and a combined method. The NN scheme employed having three-layer error-back propagation (EBP) network with five input units equivalent to the radiographic description of all micro-calcification and one output unit correspond to the microcalcification. The design was based on two inner layer neurons with a suggestion to increase the hidden neurons for quality performance. This work is based on [12], where CM were incorporated for quantification of the bump map. To implement gradient analysis, the gradient of the bump map was quantised into discrete values. This was achieved by categorising each gradient in terms of its angle from a set vector (slant angle) and the four quadrants of the x/y plane. Four ranges were introduced to quantify the angle, subsequently two four by four matrices were obtained. The CM data was next fed to the NN for classification. There are numerous clinical areas where NNs have successfully been employed [13-16], however, yet to deal with classification needs further research.

To offer helpful insights into our NN techniques for information processing, we organised the article in sections. Section 2 presents materials and methods in understanding the structure followed by a brief description of CM and feature extraction. In section 3, we have presented results followed by discussion. Finally, section 4 concludes the article.

2 Materials and Methods

2.1 Photometric Stereo (PS)

The hypothesis of the PS model is based on 3-light photometric stereo [17] which uses a Lambertian diffuse model to describe the surface reflectance properties by capturing three images, with each under a differently-positioned illumination as illustrated in **Fig. 1**.These three images are necessary to solve the irradiance equation. This is in contrast to conventional photographs which are susceptible to image artefacts such as shadows and highlights. The PS theory is to use a surface reflectance model to recover the surface's physical properties (orientations and reflection). At least three images each captured from a fixed point under different illumination are required for dimensional orientation. The next stage is to compute surface normal vectors which are calculated via solving the irradiance equations, thereby generating 3D surface description.

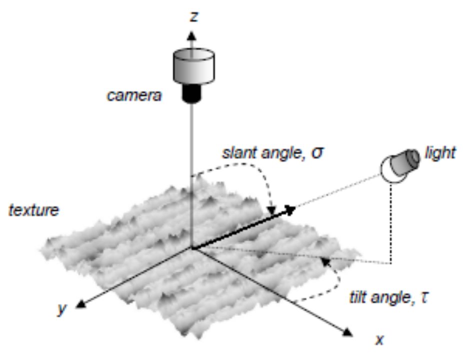

Fig. 1. PS geometry with tilt & slant angle

The light sources are point sources at a distance in different positions. The direction of the light which is a single moveable source is defined by two angles. The slant angle δ is the angle between the illumination vector and the *z*-axis. The tilt angle τ is the angle between the *x*-axis and the projection of the illumination vector onto the *x*-*y* plane. The surface texture to be composed of components each one of which corresponds to a unique image pixel. The orientation of each facet is given by the surface normal *n*. It is also often represented in terms of the surface gradients *p* and *q*. If the texture is described by a height function *z*(*x, y*), then surface gradients are given by:

$$p = {}^{\partial z(x,y)}/_{\partial x} \quad \& \quad q = {}^{\partial z(x,y)}/_{\partial y}\,. \qquad (1)$$

We begin from a hypothetical replica of a solitary neuron followed by introducing a choice of NN to disclose their arrangement, function and training algorithms. Where $X = \{x_i, i = 1,2,3...n\}$ represent the inputs to the neuron and *Y* represents the output. Here each input is multiplied by its weight w_i. This is added to a bias b , associated with each neuron and their sum goes through a transfer function *f*. The connection between the inputs and outputs could be described as follows.

$$Y = f(\sum_{i=1}^{n} w_i x_i + b) \ . \tag{2}$$

In theory, the fundamental structure of a neuron could be modelled as depicted in **Fig. 2**.

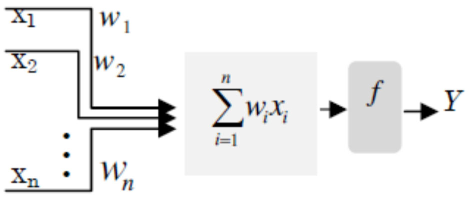

Fig. 2. A representation of perceptron

There are a range of transfer functions available to process the weights. Three basic transfer functions widely adopted for image processing are illustrated in **Fig. 3**. The particular output could be achieved via employing suitable transfer function.

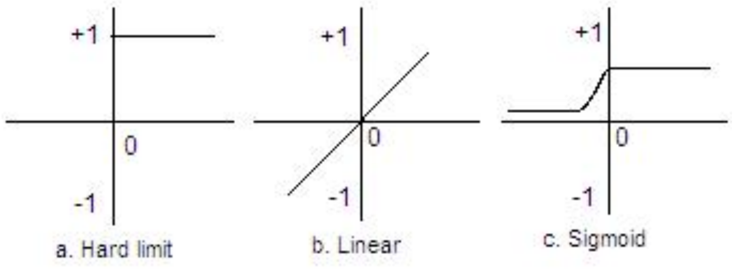

Fig. 3. Three commonly employed transfer functions

A MLP is a particular type of feed-forward network utilising three or more layers with nonlinear transfer functions in the hidden layer neurons. The MLP is able to associate training patterns with outputs for nonlinearly separable data. These networks are predominantly appropriate for applications in image processing where inputs/outputs are numerical and pairs of input/output vectors provide an obvious foundation for training in a supervised manner.

The apparatus has been tested in the Machine Vision Laboratory UWE Bristol on three set of textures. The apparatus is composed of an IEEE 1394 digital camera (PIKE F100B) and a high-resolution compact lens (Schneider, 1.4/23 mm). The Pike F-100B is equipped with Kodak KAI-1020 CCD sensor. At full resolution it runs at 60 fps (Mono8/RAW). The camera's image pre-processing functions include a high signal to noise mode (up to *24 dB* better signal-to-noise ratios). The imaging device works with customised software. In practice, the CCD camera is placed with its axis perpendicular to the object (texture) and takes 3 images each under a different LED illumination. Once the images are captures next step is to model the surface normals (bump map) and extract the features, this was accomplished via employing Co-occurrence Matrix.

2.2 Co-occurrence Matrix (CM)

The image histogram can provide useful information about the pixel distribution however; it may not provide valuable information about texture (the spatial relationships of pixels in an image). Statistical method that does consider the spatial relationship of pixels is co-occurrence matrix (CM). Whilst CMs are a rich representation of an image at the same time they are too bulky. The CM conveys information concerning the simultaneous occurrence of two grey values in a certain relative position. CM texture considers the relation between two pixels at a time called the reference and the neighbour pixel. The neighbour pixel is chosen to be the one to the east (right) of each reference pixel. This could also be expressed as a (1, 0) relation: 1 pixel in the x direction and 0 pixels in the y direction. Now, given that the levels are discrete this function is defined over pairs of discrete values and so it becomes a discrete function which may be represented by a matrix. These elements of CM have been shown to be good textural descriptors [18].

2.3 Feature Selection

In order to implement the model, the surface normal is quantised into discrete values that correspond to grey levels. This was achieved by splitting each gradient in terms of its angle from a set vector and the four quadrants of the Cartesian plane in which it is situated. Each individual vector makes a horizontal angle between 0 to 360^o on the *x-y* plane which is called the *tilt* angle and is denoted by τ. The same vector makes a vertical angle between 0-45^o, called the *slant* angle and is denoted by δ. To quantise the CM data, the slant angle was divided into three 15^o ranges which is shown in **Table 1**a and the *tilt* angle τ into three 120^o angles range which is illustrated in **Table 1**b.

Direction of Vector δ (Slant)	Vector Angle
$0 < \delta \leq 15^o$	1
$15^o < \delta \leq 30^o$	2
$30^o < \delta \leq 45^o$	3

a

Direction of Vector τ (Tilt)	Vector Position
$0 < \tau \leq 120^o$	1
$120^o < \tau \leq 240^o$	2
$240^o < \tau \leq 360^o$	3

b

Table 1. Slant and Tilt angle quantisation

This results in two CMs, which represent the surface gradient at a given location (one for the angle and one for the quadrant location of the gradient vector). A distance (d = 1) and relative angles of 0^o, 45^o, 90^o and 135^o were employed for experiments. Three ranges were employed to quantify the angle so two three by three matrices (i.e. nine coefficients) were obtained for the CM at each region analysed. The size of the CM depends upon the number of levels (corresponding to grey levels in 2D image). The intensity variations which characterise the texture are generally due to some physical variation in the scene. These intensity variations are distributed over a region in texture. This model has the ability to capture features depending on grey level in 3D imaging. The dimension of the texture feature space derived from the CM matrices at different pixel distances and directions was very large. It was observed that the presence of ineffective features often degrades classifier performance especially when the training data set is small. Investigators in CAD research have employed different methods for feature selection. Wu [19] suggested features were based on the difference in the average values of the individual features between the two classes. In addition Lo [16] ranked the importance of each feature based on its effect on the classification accuracy and then eliminated the features at a time; from the least important to the most important to determine the smallest set of features that provided the highest classification accuracy in the data set. The procedure in linear analysis is an established method for the selection of features for classification task. Momentarily, a single feature is added to or removed from a selection of feature set. We employed feed-forward backpropagation NN for feature classification. The classification accuracies of different feature sets were subsequently evaluated via regression analysis.

3 Results and Discussion

In the setup, nodes are organised with in an input layer, an output layer and hidden layers as shown in **Fig. 4**. The learning of the NN is a supervised process where known training set are the input to the NN and the weights are adjusted with an iterative backpropagation procedure in order to accomplish a desired input–output association. To enhance the convergence rate and steadiness a batch processing were implemented where the weight changes obtained from each training set were accumulated and weights were updated after the entire set of training cases. The batch processing method improves the stability with a trade-off in the convergence. The three inputs to the network consist of two inputs from CMs generated and third input indicating the direction and distance of the pixel (as described in section 2.2).

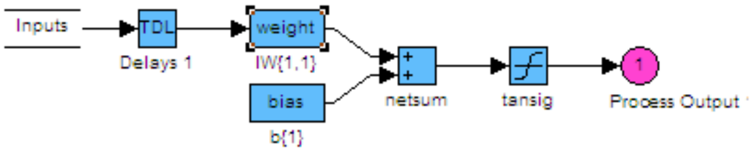

Fig. 4. NN simulink diagram

The weights were introduced in backpropagation where nodes were interconnected via weights and information propagates from input layer to the next through sigmoid transfer function. The preliminary test involves investigating three texture; specifically the oats, stones and pebbles are shown in **Fig. 5**. We investigate these three complex textures as a test case (for study). Typically, coefficients between 600 and 900 CM were used in the training. In practice, the CM coefficients were the input to the neural networks. For a given feature set containing *I* features, an NN (with *I* input nodes, 10 hidden nodes, and output node) was trained.

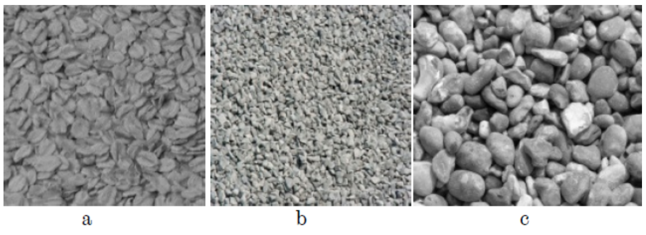

Fig. 5. Test images (a) The oats (b) pebbles & (c) stones

A data set with *N* samples is available for training and testing, m samples to be used for testing the classifier. Hence *(N - m)* will be evaluated with the remaining sample. Initially for each training cycle with (*N* − m) training cases, the NN was trained up to 20000 epochs. The dependence of epochs is shown in **Fig. 6**a. The accuracy, generally increased rapidly for the first few thousand (till 5000) epochs and then stable gradually. Here, when the network was trained for between 7000-13500 epochs the accuracy remained at a steady level of about 0.87. In some cases the accuracy decreased when the network was over-trained for instance more than 18000 epochs. We further evaluate variation in weights initialisation on classification accuracy. Two different random number weights were introduced to generate the initial weight in the network. The differences in accuracy were small and within the range of 0.01. This confirms that the initial weights do not have a strong effect on the convergence of the NN. The accuracy is plotted in for the NN with different numbers of hidden nodes in **Fig. 6**b.

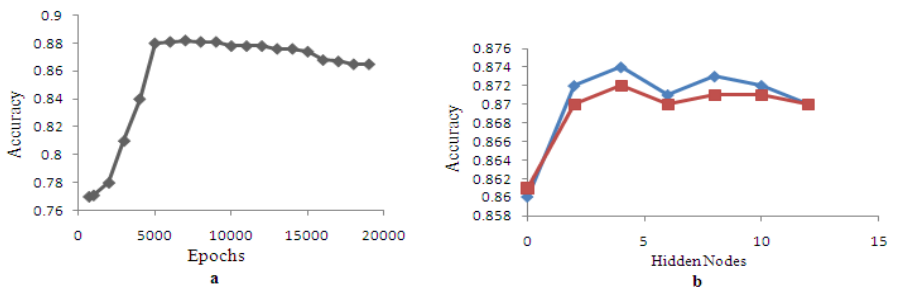

Fig. 6. (a)The dependency of training vs. accuracy (b) Weights initialization effect on accuracy

The network was trained from CM data gathered using 350 random regions and the results are shown in **Fig. 7**. It was observed that the NN in general maps the data well to the class, however; with some mismatches. It is likely that this might be due to the generation of a CM for a region not noticeably different in the data sets. The test image of stones and pebbles may have similar gradients at certain points or stones and oats have coherence in gradients up to certain limits.

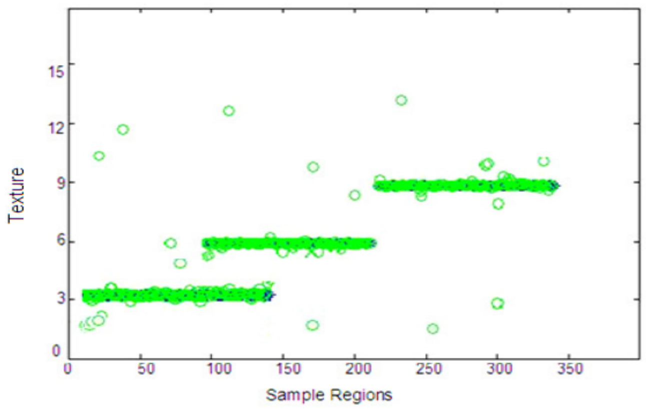

Fig. 7. NN texture prediction (o) & text data (*). (3) Oats, (6) stones and (9) pebbles

The accuracy of the network was assessed through linear regression which performs a linear regression between the network response and the target, and then computes the correlation coefficient (R-value) between the network response and the target. The validation of the performance is depicted in **Fig. 8**, where T indicates texture and A is associated with the accuracy. The regression R=0.89 indicate that the network have modelled maximum of the data.

We have examined the usefulness of employing CM as texture feature in differentiating the classes. The pattern in texture could be analysed via computerised analysis where the differences are not visually apparent. A NN was incorporated as (feature) classifier for the classification task. In the experiments, NN with ten hidden layer neurons provided an optimum performance. The results appear in **Fig. 8**, validate the performance. However, it should be noted that the performance of a classifier depends on the number of training samples relative to the number of parameters to be trained in the classifier. The texture of the human skin varies with the probability of the presence of melanoma. We believe that the model described here, could be implemented in classifying clinical images in analysing the texture of a wound afterwards classifying them in either melanoma or benign.

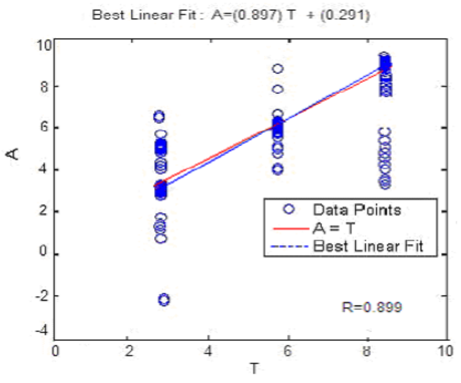

Fig. 8. Regression analysis

4 Conclusions

An approach based on CM to model the surface normals and NN for classification is demonstrated. Three ranges were introduced to quantify the angle, two three by three matrices were obtained and data was subsequently fed to the network for classification. The neurons works in a distributed mode to learn from the inputs harmonise internally and optimise the final output via descriptions extracted from the regions. Therefore a method combining CM and NN has been implemented, and it has been demonstrated to be suitable for analysing and quantifying 3D surface irregularities. This study consequently demonstrates the suitability of computerised classification in image interpretation. Further investigation to determine how well the study could analyse the texture of melanoma (in human skin) is in process. In future, both the feature extraction techniques and the classifier would be improved by optimising various parameters using large data set.

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Confidentiality Annotations for *Circus*

Michael J. Banks and Jeremy L. Jacob

Department of Computer Science, University of York, UK
{Michael.Banks,Jeremy.Jacob}@cs.york.ac.uk

Abstract This paper presents a novel construct for specifying confidentiality properties over *Circus* processes. By extending the semantics of *Circus*, we identify how functionality and secrecy can be united within a single framework. We use this construct to formalise a selection of confidentiality properties over a model of an auction system.
Keywords: information security, information flow, confidentiality, semantics, *Circus*, unifying theories of programming

1 Introduction

Confidentiality mandates that a system does not reveal secret information to low-level (untrusted or unprivileged) users. In this context, secrets may be information about the interactions that other high-level users perform with the system, or sensitive or valuable data stored within a system (such as cryptographic keys or classified documents).

Regulating a low-level user's ability to infer information about a system's behaviour is crucial for safeguarding secrets. If a system S features a behaviour ϕ involving a secret, then it is crucial that a low-level user Low cannot infer (with certainty) that ϕ has taken place, for otherwise Low could deduce the secret.

One approach for protecting the secret is to ensure S features alternative *cover story* behaviours. A cover story behaviour for ϕ must generate the same interaction with Low as does ϕ, but it should not involve the secret element of ϕ. The presence of cover stories for ϕ prevents Low from inferring that S behaved as ϕ — and thereby deducing the secret — because Low cannot rule out the possibility that S behaved as one of the cover stories for ϕ instead.

This paper outlines an integration of confidentiality properties with a formal method for software development. We introduce a notation for specifying these properties and embed this notation into the *Circus* formalism [1]. In essence, *Circus* is a specification language that combines the CSP process algebra and the state-based specification facilities of Z to provide a cohesive platform for modelling systems in terms of their interactions with the external environment. This integration is underpinned by a semantics [2] defined in Hoare and He's *Unifying Theories of Programming* (UTP) [3].

2 A Motivating Example

A *Circus* process interacts with its environment by engaging in events over a set of designated channels. A process declaration features an internal state (hidden from the environment), a state invariant and a collection of named *actions*. *Circus* actions can be grouped into Z schema expressions and guarded commands (representing operations on the state), invocations of other actions (by name) and CSP constructs (modelling interaction with the environment). The behaviour of a *Circus* process is defined by a distinguished nameless main action, which follows the declarations of the other actions.

We introduce *Circus* by way of a small example. Consider a first-price sealed-bid auction contested by Alice and Bob. Each contestant independently submits a secret bid (a natural number) to the auctioneer. Afterwards, the auctioneer declares the winner of the auction as the contestant who made the larger bid (or either contestant, if the bids are equal).

Here is a *Circus* specification of the behaviour of the auctioneer:

$$
\begin{array}{l}
\mathit{BIDDER} ::= \mathit{Alice} \mid \mathit{Bob} \\
\textbf{channel}\ \mathit{bid} : \mathit{BIDDER} \times \mathbb{N}_1 \\
\textbf{channel}\ \mathit{winner} : \mathit{BIDDER} \\
\textbf{process}\ \mathit{Auction} \triangleq \textbf{begin} \\
\quad \textbf{state}\ \mathit{ST} \triangleq [a, b : \mathbb{N}] \\
\quad \mathit{Init} \triangleq [\mathit{ST}' \mid a' = 0 \land b' = 0] \\
\quad \mathit{BidAlice} \triangleq \mathit{bid}?\mathit{Alice}.n \to a := n? \\
\quad \mathit{BidBob} \triangleq \mathit{bid}?\mathit{Bob}.n \to b := n? \\
\quad \mathit{Submit} \triangleq (\mathit{BidAlice} \mathbin{;} \mathit{BidBob}) \sqcap (\mathit{BidBob} \mathbin{;} \mathit{BidAlice}) \\
\quad \mathit{Declare} \triangleq \left(\begin{array}{l} \quad a > b \mathbin{\&} \mathit{winner}!\mathit{Alice} \to \mathit{Stop} \\ \Box\ a < b \mathbin{\&} \mathit{winner}!\mathit{Bob} \to \mathit{Stop} \\ \Box\ a = b \mathbin{\&} \sqcap c : \mathit{BIDDER} \bullet \mathit{winner}!c \to \mathit{Stop} \end{array} \right) \\
\quad \bullet\ \mathit{Init} \mathbin{;} \mathit{Submit} \mathbin{;} \mathit{Declare} \\
\textbf{end}
\end{array}
$$

This process first initialises its state, then accepts bids from Alice and Bob in an arbitrary order, before it announces the winner of the auction and finally halts.

We may expect an auction system to uphold various kinds of security requirements, but the *Auction* process specification tells us nothing about those requirements. Consider three example confidentiality requirements that *Auction* may be expected to fulfil:

C1 Neither Alice nor Bob can deduce if the other's bid exceeds £100.
C2 Neither Alice nor Bob can rule out the possibility that their bids are equal.
C3 Neither Alice nor Bob can learn who placed the first bid.

We assume that Alice can observe her own bid (but not Bob's), Bob can observe his own bid (but not Alice's), and both contestants can observe the *winner* channel. At first glance, we may be tempted to say that the *Auction* process upholds these requirements in all circumstances. But this is not so, if Alice and Bob know the design of the *Auction* process:

– Suppose that Alice places a bid of £200 and Bob is declared the winner of the auction. Alice can then infer that Bob's bid was at least £200, exceeding the threshold of £100 and violating **C1**.

– Likewise, **C2** may be defeated by specific bids from Alice and Bob. We leave the task of determining the values of those bids as an exercise to the reader.[1]

It would be desirable to specify these confidentiality requirements formally, so they can be accommodated as "first-class citizens" within *Circus* developments.

3 Specifying Confidentiality Properties

In a departure from conventional approaches for specifying confidentiality properties, we extend the syntax of *Circus* with a novel specification construct. A *confidentiality annotation*, or *κ-annotation* for short, may be embedded within a *Circus* process, alongside *Circus* actions, as a means of documenting confidentiality requirements. A κ-annotation is written in the form $\langle\, L : \theta \,\rangle$, where:

– L denotes the *window* of Low, being the set of channels over which Low can monitor interactions between the process and its environment; and
– θ encodes a relation between (i) the state variables (including input and output variables) of the process, denoted by v; and (ii) a renaming of those variables, denoted by $\widetilde{v}$. Here, the v variables represent secret states, while the $\widetilde{v}$ variables represent cover story states associated with secret states.

Example 1. Let a be a state variable of type $\mathbb{N}$. The following κ-annotation specifies that states where $a = 0$ are secret to Low, while states where $a > 0$ are cover stories for $a = 0$:

$$\langle\, L : [\, a, \widetilde{a} : \mathbb{N} \mid a = 0 \land \widetilde{a} > 0 \,] \,\rangle$$

By inserting a κ-annotation within a process design, we may specify confidentiality properties over the state of the process. Since the behaviour of a *Circus* is influenced by its state, we can use κ-annotations to express confidentiality properties over the behaviour of processes.

Informally, a κ-annotation $\kappa = \langle\, L : \theta \,\rangle$ requires that, if the process executes κ in a state ψ classed as secret by θ, then it must also be possible for the process to execute κ in *at least one* state marked as a cover story by θ.

3.1 A Lifted Semantics

Building on the UTP theory of reactive designs [3, 4], each *Circus* action A is defined as a predicate of the form $\mathbf{R}(ok \land Pre \Rightarrow ok' \land Post)$, where:

– $\mathbf{R}$ is a *healthiness condition* [3] and ok and ok' are Boolean variables;
– Pre is a precondition over the state variables of the process; and
– $Post$ is a postcondition, codifying a relation between the initial process state (satisfying Pre) and all subsequent states that A may reach. The *trace* of the action, denoted by $tr' - tr$, models the sequence of events that A performs with its environment during its execution.

[1] Hint: since bids are of type $\mathbb{N}_1$, they must have a minimum value.

In order to give a semantics to κ-annotations, we need first to *lift* the semantics of *Circus* actions. This lifting is *conservative*, in the sense that a *Circus* specification without κ-annotations has exactly the same meaning in the lifted semantics as it does in the original *Circus* semantics.

Given an action A — where A does not contain a κ-annotation — we define:

$$\mathbf{U}\,(A) \triangleq A \wedge A[\widetilde{x}, \widetilde{x'}/x, x'] \tag{1}$$

where x denotes the state (variables) when A commences, x' denotes the state that A reaches, and $A[\widetilde{x}, \widetilde{x'}/x, x']$ denotes A with a renamed state space.

The lifted action $\mathbf{U}\,(A)$ behaves as A, but each behaviour of A is related to every behaviour of A encoded over a renaming $(\widetilde{x}, \widetilde{x'})$ of A's observational variables. We call the latter behaviours the *fog* of A. Their purpose is to track what Low can infer about the process state at each step in its execution.

In the worst case, Low may possess complete knowledge of a process's design; therefore, Low may infer all process behaviours that are consistent with its interaction with the process. We model Low's inability to distinguish two behaviours of an action by defining a predicate $\mathcal{I}_L$, where $\mathcal{L}$ denotes Low's window set:

$$\mathcal{I}_L = \left(\begin{array}{c} ok = \widetilde{ok} \wedge ok' = \widetilde{ok'} \wedge wait = \widetilde{wait} \wedge wait' = \widetilde{wait'} \\ \wedge\ (tr' - tr) \upharpoonright \mathcal{L} = (\widetilde{tr'} - \widetilde{tr}) \upharpoonright \mathcal{L} \end{array} \right) \tag{2}$$

This predicate maps a behaviour to a fog behaviour if their respective traces — when projected through $\mathcal{L}$ — yield the same observation to Low. Hence, $\mathcal{I}_L$ restricts the fog associated with each behaviour ϕ of a lifted action to only those fog behaviours that are Low-indistinguishable to ϕ.

3.2 Defining κ-annotations

We now proceed to define κ-annotations within the lifted semantics:

$$\mathbf{U}\,(\langle\, L : \theta \,\rangle) \triangleq \mathbf{U}\,(Skip) \wedge \mathbf{R}\left(ok \wedge (\exists\, \widetilde{v} \bullet \theta) \;\Rightarrow\; ok' \wedge \theta \wedge \neg\, \widetilde{wait} \right) \tag{3}$$

The predicate $(\exists\, \widetilde{v} \bullet \theta)$ encodes all states classed as secret by θ.

From the perspective of functionality alone, a κ-annotation behaves as *Skip*: it waits until its predecessor action has finished and then terminates instantaneously, leaving the process trace and state unchanged.

Operationally, if a κ-annotation $\langle\, L : \theta \,\rangle$ is invoked in a state ψ marked as secret by θ, then the fog states associated with ψ are pruned to only those states prescribed as cover stories for ψ by θ. This pruning commits the process design to providing at least one alternative behaviour that passes through the κ-annotation in a cover story state. This commitment is broken if none of the cover story states prescribed by θ are present in the fog associated with the secret state when the κ-annotation is invoked.

This commitment is enforced by the lifted semantics, which ensures that pruning the fog states distributes through the actions of the process. Hence, the commitment may be broken after the κ-annotation is invoked, should the process's subsequent behaviour reveal a secret to Low.

The next two examples illustrate the effects of κ-annotations on processes.

Example 2. What is the effect of inserting the κ-annotation from Example 1 immediately after an assignment $a := 1$? We find that:

$$\mathbf{U}\,(a := 1\,;\langle\, L : [\, a, \widetilde{a} : \mathbb{N} \mid a = 0 \wedge \widetilde{a} > 0\,]\,\rangle) \;=\; \mathbf{U}\,(a := 1)$$

This result is precisely what we should expect: the secret state $a = 0$ cannot be reached by executing $a := 1$, so this κ-annotation is innocuous and can be removed without changing the meaning of the specification. (A proof of this result is given in the Appendix.)

Example 3. Following Example 2, it is natural to ask: what is the effect of inserting the κ-annotation from Example 1 immediately after an assignment $a := 0$? Again, we proceed by calculation, this time in the presence of $\mathcal{I}_L$:

$$\mathbf{U}\,(a := 0\,;\langle\, L : [\, a, \widetilde{a} : \mathbb{N} \mid a = 0 \wedge \widetilde{a} > 0\,]\,\rangle) \wedge \mathcal{I}_L \;=\; \mathbf{U}\,(\mathbf{R}(\neg\, ok)) \wedge \mathcal{I}_L$$

This result deserves an explanation! The commitment made by the κ-annotation is broken: the cover story $a = 1$ state demanded for $a = 0$ cannot be reached by executing $a := 0$. Hence, the process cannot satisfy the confidentiality property imposed on it by the κ-annotation.

The specification $\mathbf{R}(\neg\, ok)$ is the *reactive design miracle*: it is a process which does the impossible (postcondition **false**) if started in any state (precondition **true**).[2] Miraculous processes satisfy *every* specification, which means they are *infeasible*: they cannot be implemented.

In the presence of $\mathcal{I}_L$, a broken commitment manifests as a process exhibiting miraculous behaviour in states with the fog shrunk to empty. Execution from such a state, if it were possible, would potentially reveal a secret to Low, since Low would be able to rule out all the cover stories associated with that state at that point in the process's execution. Hence, our lifted semantics exhibits a remarkable property: *insecure processes are infeasible processes.*

Example 2 and Example 3 represent two extremes of a scale of the effects of κ-annotations. The interplay between *Circus* actions and κ-annotations is often more subtle. This subtlety enables us to express diverse confidentiality requirements over processes, which we demonstrate in the next section.

[2] For an introduction to miraculous specifications, the reader is directed to Morgan [5]. The term "miracle" is due to Dijkstra [6], whose semantics of weakest preconditions legislated against it (by the "Law of the Excluded Miracle"). Nevertheless, miracles are a useful concept in specification languages; for instance, Woodcock [7] has proposed some applications for the reactive design miracle in *Circus*-like languages.

4 Formalising the Example

We claim that κ-annotations are capable of expressing a wide range of confidentiality requirements over the state and behaviour of *Circus* processes. We offer evidence for this claim by formalising the confidentiality requirements listed in Section 2 as κ-annotations over the *Auction* process. Of course, these requirements could be expressed using κ-annotations in many different ways, depending on how their descriptions are interpreted.

First, we instantiate the Low observer as being either Alice or Bob. We specify Alice and Bob's window sets as follows:

$$\mathcal{A} \triangleq \{(bid, (Alice, n)) \mid n \in \mathbb{N}_1\} \cup \{(winner, c) \mid c \in BIDDER\}$$
$$\mathcal{B} \triangleq \{(bid, (Bob, n)) \mid n \in \mathbb{N}_1\} \cup \{(winner, c) \mid c \in BIDDER\}$$

and associate the windows $\mathcal{A}$ and $\mathcal{B}$ with the labels A and B respectively. Next, we revise the *Auction* process to capture **C1**, **C2** and **C3** using κ-annotations. Consider the following declarations, which we substitute into the body of *Auction*:

$$\begin{aligned}
&C1A \triangleq \langle\, A : [\, b, \widetilde{b} : \mathbb{N} \mid b > 100 \land \widetilde{b} \leq 100 \,]\,\rangle \\
&C1B \triangleq \langle\, B : [\, a, \widetilde{a} : \mathbb{N} \mid a > 100 \land \widetilde{a} \leq 100 \,]\,\rangle \\
&C2 \triangleq \langle\, A, B : [\, a, b, \widetilde{a}, \widetilde{b} : \mathbb{N} \mid a = b \land \widetilde{a} \neq \widetilde{b} \,]\,\rangle \\
&C3 \triangleq \langle\, A, B : [\, f, \widetilde{f} : BIDDER \mid f \neq \widetilde{f} \,]\,\rangle \\
&BidAlice \triangleq bid?Alice.n \rightarrow a := n? \,;\, C1B \\
&BidBob \triangleq bid?Bob.n \rightarrow b := n? \,;\, C1A \\
&Submit \triangleq \mathbf{var}\, f \,;\, \begin{pmatrix} BidAlice \,;\, BidBob \,;\, f := Alice \\ \sqcap\, BidBob \,;\, BidAlice \,;\, f := Bob \end{pmatrix} ;\, C2 \,;\, C3 \,;\, \mathbf{end}\, f
\end{aligned}$$

The κ-annotations attached to the *BidAlice* and *BidBob* actions capture **C1**. The κ-annotation declared as $C2A$ specifies that, if Alice's bid exceeds £100, then it must not be possible for Bob to rule out all values of Alice's bid that do not exceed £100. This κ-annotation makes the process behave miraculously in circumstances where its normal behaviour would violate **C1** by leaking information to Bob enabling him to rule out all those values. The κ-annotation $C2B$ specifies the complementary constraint on Alice's inferences about Bob's bid.

We express **C2** by extending *Submit*. Once both bids are made, $C2$ mandates that, if the bid values (recorded in a and b) are equal, then the constraint $\widetilde{a} \neq \widetilde{b}$ is imposed on the fog variables. Again, doing this has the potential to induce miraculous behaviour in certain circumstances. The system developers would need to consult with the customer to resolve this clash between functionality and confidentiality.

To express **C3**, we introduce a local variable f into *Submit* in order to record which contestant bids first. The κ-annotation $C3$ specifies that Bob bidding first serves as a cover story for Alice bidding first ($f = Alice \land \widetilde{f} = Bob$), and vice versa ($f = Bob \land \widetilde{f} = Alice$). The behaviour of *Auction* reveals no information about which contestant bids first, so $C3$ induces no miraculous behaviour. However, $C3$ cannot be removed from the specification without changing its meaning in the lifted semantics.

5 Confidentiality-Preserving Refinement

Refinement is the act of improving a system design, by adding details describing how aspects of the system are to be implemented by a programmer [5]. Refinement of a *Circus* process entails the reduction of non-determinism (removal of possible behaviours) from the process specification [1, 2].

Developing systems to satisfy confidentiality properties is problematic, not least because standard notions of refinement are not guaranteed to preserve these properties in system designs [8, 9]. In our terminology, this is because a refinement T of a process S may lack cover story behaviours present in S while retaining secret behaviours of S; hence, Low may be able to infer secret information about the behaviour of T that it could not infer about S.

This so-called "refinement paradox" is resolved by our lifted semantics: if cover stories that are needed to satisfy a κ-annotation are refined away from the process, then the κ-annotation will induce miraculous (i.e. unimplementable) behaviour into the resulting process. Therefore, *insecure refinements are infeasible refinements*, as they lead to miraculous processes that cannot be implemented.

Example 4. Suppose *Submit* is refined so that *Alice* invariably bids first:

$$Submit \triangleq \textsf{\textbf{var}}\, f\, ; BidAlice\, ; BidBob\, ; f := Alice\, ; C2\, ; C3\, ; \textsf{\textbf{end}}\, f$$

Both Alice and Bob can now deduce that, if they have placed a bid, then Alice must have bid first. Hence, this refinement violates **C3**. But $C3$ now becomes miraculous, as the cover story $\widetilde{f} = Bob$ it demands for $f = Alice$ is absent.

6 Related Work

In previous work [10], we have described a framework for encoding confidentiality properties in the UTP. This framework is generic and can be applied across the range of specification and programming languages that have a UTP semantics. This paper has presented an approach for specialising that framework to *Circus*.

Our notion of cover stories is inspired by Mantel's *Modular Framework for Information Flow Properties* (MAKS) [11], where a library of "basic security properties" are encoded as closure conditions over a system's behaviour set.

The idea of embedding κ-annotations within *Circus* processes has its roots in an earlier YDS paper by the authors [12]. In that paper, a syntactic approach for rewriting a CSP process to uphold a confidentiality property is presented. The approach described in this paper involves more detailed manipulation of syntax and semantics, but its foundations are arguably more solid and it incorporates a notion of confidentiality-preserving refinement.

The lifted *Circus* semantics described in this paper has much in common with Morgan's *shadow semantics* [13, 14], which extends the refinement calculus for sequential programs [5] to prevent refinement from revealing more information about high-level state to Low. In contrast, we have introduced an explicit construct to allow specification of exactly which properties of the state or behaviour of processes are secret, which is arguably a more flexible (albeit more involved) philosophy for integrating confidentiality into formal methods. In addition, by virtue of the UTP semantics of *Circus*, our approach is also applicable to a wider domain of programs than sequential programs.

An alternative approach for formulating confidentiality properties over *Circus* processes is described in another paper by the authors [15]. In that paper, confidentiality properties are not embedded into a *Circus* specification directly, but are instead specified separately over the actions that a process performs. To reconcile these separate specifications, that approach necessitates an extension of the *Circus* semantics that is considerably more complicated than the lifting procedure described in Section 3. The aforementioned paper also describes a method for verifying that a process satisfies its confidentiality properties, by breaking that requirement into a set of proof obligations over localised regions of the process. A similar method can be applied to distribute κ-annotations through a process, justified by laws that follow directly from the lifted semantics.

The authors offer a more thorough account of related work elsewhere [10, 15].

7 Conclusion

In this paper, we have presented an approach for specifying confidentiality properties in *Circus*. The novelty of this work is a single semantic framework welding functionality and confidentiality together. As we have demonstrated in Section 4, this framework is sufficiently expressive to capture a wide range of confidentiality requirements over *Circus* processes.

There is much work needed to make the framework appropriate for use in industrial software development. We are currently evaluating its suitability by applying it to a number of case study developments in *Circus*. There are other topics worthy of investigation, such as identifying a semantics for declassifying secret information once that information need no longer be kept confidential. Furthermore, we conjecture the framework can be adapted to variants of *Circus* that incorporate timing or probabilistic behaviour in their semantic models.

Mechanisms for automatically analysing whether a process satisfies its κ-annotations are a prerequisite for supporting the framework with effective tools. We have not investigated such mechanisms in depth, but we believe that model checking techniques would be a fruitful line of inquiry, based on existing work in the field [16–18]. However, it would be necessary to revise the semantics of κ-annotations in order to work with existing model checkers, which is likely to be a challenging task.

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Appendix

There are laws for lifting the *Circus* operators, but we omit them here for brevity. Rather, we identify just one law concerned with the sequential composition of *Circus* actions and κ-annotations in the lifted semantics:

$$\mathbf{U}\,(A\,;\langle\, L : \theta\,\rangle) = \mathbf{U}\,(A) \land \mathbf{R}\begin{pmatrix} ok \land (\exists\, \widetilde{v} \bullet \theta)[v'/v] \land \neg\, wait' \\ \Rightarrow ok' \land \theta[v', \widetilde{v'}/v, \widetilde{v}] \land \neg\, \widetilde{wait'} \end{pmatrix} \tag{4}$$

The result given in Example 2 is derived as follows:

$\mathbf{U}\,(a := 1\,;\langle\, L : [\, a, \widetilde{a} : \mathbb{N} \mid a = 0 \land \widetilde{a} > 0\,]\,\rangle)$
$\Leftrightarrow \{$ law of sequential composition (Equation 4) $\}$
$\mathbf{U}\,(a := 1) \land \mathbf{R}\left(ok \land a' = 0 \land \neg\, wait' \Rightarrow ok' \land a' = 0 \land \widetilde{a'} > 0 \land \neg\, \widetilde{wait'}\right)$
$\Leftrightarrow \{$ semantics of assignment and $\mathcal{I}_L$ $\}$
$\mathbf{U}\,(a := 1) \land \mathbf{R}\left(ok \land a' = 0 \Rightarrow ok' \land a' = 0 \land \widetilde{a'} > 0\right)$
$\Leftrightarrow \{$ contradiction: $\mathbf{U}\,(a := 1)$ demands $a' = 1$ $\}$
$\mathbf{U}\,(a := 1) \land \mathbf{R}\left(\mathbf{false} \Rightarrow ok' \land a' = 0 \land \widetilde{a'} > 0\right)$
$\Leftrightarrow \{$ propositional calculus $\}$
$\mathbf{U}\,(a := 1) \land \mathbf{U}\,(\mathbf{R}(\mathbf{true}))$
$\Leftrightarrow \{$ property of $\mathbf{R}$ and $\mathbf{U}$ $\}$
$\mathbf{U}\,(a := 1)$

The result given in Example 3 is derived as follows:

$\mathbf{U}\,(a := 0\,;\langle\, L : [\, a, \widetilde{a} : \mathbb{N} \mid a = 0 \land \widetilde{a} > 0\,]\,\rangle) \land \mathcal{I}_L$
$\Leftrightarrow \{$ law of sequential composition $\}$
$\mathbf{U}\,(a := 0) \land \mathbf{R}\left(ok \land a' = 0 \land \neg\, wait' \Rightarrow ok' \land a' = 0 \land \widetilde{a'} > 0 \land \neg\, \widetilde{wait'}\right) \land \mathcal{I}_L$
$\Leftrightarrow \{$ semantics of assignment and $\mathcal{I}_L$ $\}$
$\mathbf{U}\,(a := 0) \land \mathbf{R}\left(ok \Rightarrow ok' \land a' = 0 \land \widetilde{a'} > 0\right) \land \mathcal{I}_L$
$\Leftrightarrow \left\{\right.$ contradiction: $\mathbf{U}\,(a := 0)$ demands $\widetilde{a'} = 0$ $\left.\right\}$
$\mathbf{U}\,(a := 0) \land \mathbf{R}\,(ok \Rightarrow \mathbf{false}) \land \mathcal{I}_L$
$\Leftrightarrow \{$ propositional calculus $\}$
$\mathbf{U}\,(a := 0) \land \mathbf{R}\,(\neg\, ok) \land \mathcal{I}_L$
$\Leftrightarrow \{$ definition of $\mathcal{I}_L$ $\}$
$\mathbf{U}\,(\mathbf{R}(\neg\, ok)) \land \mathcal{I}_L$

Dependency Patterns and Timing for Grid Workloads

Andrew Burkimsher

Department of Computer Science, University of York

Abstract

This paper presents a set of patterns of dependencies for grid computing workloads abstracted from an industrial case study. In addition, algorithms are presented that generate task execution times and arrival times to match desired statistical properties. This is as a part of the research performed by the author on the creation of a simulation environment with which to compare and evaluate the performance of different schedulers on a grid system. The ultimate aim of this research is to improve throughput and reduce response times of work submitted to a grid using improved scheduling algorithms.

1 Introduction

Computing power has become ever cheaper over the past half-century following an observed pattern known as Moore's Law [14]. However, many kinds of academic and industrial endeavour benefit from as much computing power as possible. In recent years, increases in computing power have been gained through increasing parallelism [5].

Where there is sufficient demand for compute power, datacentres have been created to house these parallel computing nodes [13]. Unfortunately, datacenters are limited in size by the availability of electrical power and cooling in a single location [15]. Therefore, networks of geographically distributed datacenters have been created in order to provide the computing capacity required [11]. These networks are known as *grids*. In the model considered by this paper, many workloads may execute concurrently on a grid. In order to ensure good performance of a grid, the work done must be carefully scheduled.

It has been shown that finding an optimal schedule is NP-complete in the general case [9]. Therefore in any system of realistic scale, heuristic scheduling policies have to be used. Where dependencies are present in the workload, some 'simple' scheduling policies such as *First In First Out* (FIFO) exhibit undesirable emergent effects known as 'anomalies' [10, 17]. [10] showed that reducing the number of dependencies, reducing task execution time and increasing the number of processors can all lead to an increase in total workload execution time when using a FIFO scheduler. [17]showed that network delays can mean that executing a workload on a multiprocessor would take longer than on a uniprocessor.

A wide variety of scheduling heuristics have been proposed [2]. The ultimate aim of this research is to develop a framework with which to simulate grids in order to compare the performance of schedulers. The simulation will be composed of three fundamental models: an application model, a platform model and a scheduling model. In this structure, the grid hardware is represented by the platform model. The workload executed by the grid is represented by the application model. The scheduling algorithm is captured in the scheduling model.

This paper is about the creation of workloads as part of the application model. Pertinent literature will be summarised. The DAG shape patterns used in taskset generation, along with algorithms to generate them will be presented. Algorithms to generate workloads where both jobs and task execution times follow desired statistical distributions will be proposed. Finally, algorithms will be proposed to adjust the arrival rate of the work in reference to the ability of a grid to service the work (stability ratio), while keeping the workload otherwise equal. Limitations of the work along with future research directions will be noted.

2 Literature Review

To utilise the computational power afforded by grids, the work must be parallelised. Some kinds of computational work scale naturally to being run in a highly parallel way. However, real-world grid workloads are not like this. They tend to have sections that can be parallelised but others that must run in sequence.

Some nomenclature will now be introduced, following the scheme of [4]. Independent packages of work are known as *jobs*. Within a job, the sections of work are known as *tasks*. Each task runs on a single processor and consumes some input and produces some output. Where one task's input includes another task's output, a *dependency* is defined.

There has been much study of the scheduling of dependent task sets in the literature; notable examples include [10, 12, 16]. The general notion of dependencies in the literature is to consider the dependencies to be representable by a Directed Acyclic Graph (DAG) structure. The acyclic nature of the dependencies means that the computation time of each workload is bounded. The nodes in a DAG represent tasks and edges represent dependencies between tasks.

Although many authors have mentioned the use of a DAG structure for workloads [12], there is scant mention in the literature of the actual structure of these DAGs and how to generate them [7]. This paper will elaborate several classes of DAG structure in Section 3. These structures are abstractions of patterns observed in an industrial case study.

The dependency structure alone, however, does not define a grid workload as the execution times of tasks must also be defined. When generating large numbers of workloads to use in the comparison of schedulers, it is important that the workloads generated have certain statistical properties, so that they form a fair comparison [7]. Algorithms to generate workloads with appropriate statistical distributions of both job and task execution times will be described in Section 4.

3 DAG shape classes

The exact parameters of real-world workloads are unlikely to be known in advance. Therefore, a successful grid scheduling policy should be able to perform well across a wide range of workloads. To evaluate schedulers, therefore, a wide range of workloads must be generated. However, the workloads generated should also contain a fair representation on the kinds of workload likely to be encountered by the scheduler in production use.

The workload DAG patterns presented in this section were developed from an industrial case study. The industrial case study was of a production system that takes CAD models and performs computational fluid dynamic calculations with them in order to produce predictions of aerodynamic characteristics. Workflows are specified in advance, and these workflow task graphs can be inspected. After inspection, general patterns were observed by the author and are presented below. To the best of the author's knowledge, all the patterns except the linear chains pattern are novel and have not been previously described in the literature. Pseudocode algorithms for generating these DAG shapes are also specified.

3.1 Linear Dependencies

The most basic DAG dependency pattern is that of linear dependencies. This is when there is a single chain of purely sequential tasks with dependencies between them, as shown in Figure 1a. However, this pattern could well be considered unrealistic for a grid workload. This is because grids tend to perform best on parallel workloads, so it is highly unlikely that a substantial part of any real grid workload would be composed of linear dependent chains of work. Nevertheless, if it were, an appropriate scheduling policy could be a pipeline arrangement. The pseudocode to set up dependencies like this is shown in Algorithm 4.1.

3.2 Probabilistic dependencies

Sometimes it is desired to have a certain proportion of the possible dependencies present in a workload. If it is desired that these dependencies are randomly sampled from the set of possible dependencies, the probabilistic dependencies method can be used. The pseudocode algorithm for this is shown in Algorithm 4.2. Two sample task graphs are shown in Figure 1d.

This algorithm has the advantage that the shape of the dependency graph can vary significantly, and given enough samples should provide a wide variety of shapes with which to exercise a scheduler. However, there is a strong likelihood when low probabilities are used that the dependency graph for each job can have disconnected sections. By the definition given earlier, disjoint dependency graphs should really be represented as separate jobs.

Although the job could be split into two separate jobs, or have the disjoint sections connected with additional dependencies, this may interfere with the statistical properties desired in the workload. It could be possible to simply discard jobs that where the graph has disjoint parts. However, as the probability is decreased then an increasing number of jobs may be discarded, to the point where it may become impractical to generate workloads this way because too many jobs are being discarded. As the probability is increased, this method approximates the linear dependencies model (if transitive dependencies are removed). For all these reasons, this method is only really suited to probability values in the middle of the probability range.

3.3 Independent Chains

Many workloads are parallelised by applying the same sequence of operations to different chunks of data. Each chain is one following the linear dependencies pattern. This is inspired by the MIMD (Multiple Instruction Multiple Data) parallelism pattern. As observed in an industrial case study, these chains need to be spawned by an initial setup task. Their results are then collected up by a final task. A diagram showing this arrangement is shown in Figure 1b. Pseudocode for generating such a configuration is shown in Algorithm 4.3.

3.4 Diamond

The diamond pattern as shown in Figure 1c is similar to the independent chains model, but where the spawn-out of independent chains does not take place all at once, but requires several stages to perform. It could also be considered like a complete binary tree branching out to the maximum width, and then condensing down again to collect up the data. Pseudocode for defining these dependencies is given in Algorithm 4.4.

3.5 Dependencies over blocks

A single generation of the independent chains or diamond pattern can be considered as a *block*. A block is a subset of the tasks in a job with a single starting and a single finishing task. Workloads can be composed of dependencies between blocks. The existing patterns shown can then be extended to also cover blocks. The first and last tasks of each block are given the incoming and outgoing dependencies of the whole block. These blocks then become building blocks for more complex DAGs. Where a compositional approach is used with blocks, it becomes possible to represent arbitrary DAGs.

A prevalent shape of workload observed in the industrial case study was that of linear chains of blocks, where the blocks followed the independent chains pattern (Figure 1e). This is observed where each stage of the workload can be parallelised, but the data between each stage may need to be collated and transmitted before the next stage of execution can commence. These patterns can be particularly challenging to schedule efficiently because of the multiple bottlenecks between the blocks. However, they are important to study when comparing schedulers, because they represent a significant fraction of the workload observed on some industrial grids.

Algorithm 4.1 Pseudocode for the Linear Dependencies pattern

```
n = number of tasks
task[1].dependencies = {}
for taskid in [2 to n]
        task[taskid].dependencies = {task[taskid-1]}
```

Algorithm 4.2 Pseudocode for the Probabilistic Dependencies pattern

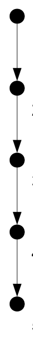
```
n = number_of_tasks
p = dependency_probability
for taskid in 1..n:
        for possible_dep_id in taskid..n:
                if p <= random():
                        tasks[taskid].dependencies.add(
                                 tasks[possible_dep_id])
```

Algorithm 4.3 Pseudocode for the Independent Chains pattern

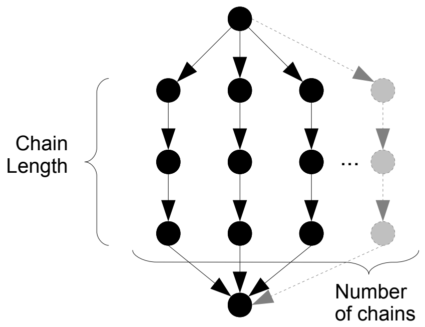
```
all_tasks = empty list of tasks
task_inner_matrix = 2-d matrix of tasks of shape
                        (num_chains by chain_length)
for x in 1..num_chains:
        for y in 2..chain_length:
                task_inner_matrix[x][y].dependencies.add(
                        task_inner_matrix[x][y-1])
                all_tasks.add(task_inner_matrix[x][y])
for x in 1..num_chains:
        task_inner_matrix[x][1].dependencies.add(initial_task)
        final_task.dependencies.add(
                task_inner_matrix[x][chain_length])
all_tasks.add(initial_task)
all_tasks.add(final_task)
return all_tasks
```

Algorithm 4.4 Pseudocode for the Diamond pattern

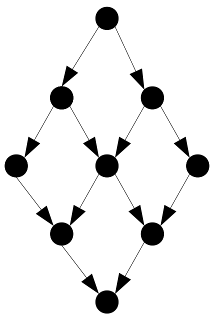
```
d = diamond_edge_length
task_matrix = 2-d matrix of tasks with dimensions d * d
for x in 1..d:
        for y in 1..d:
                if x > 1:
                        task_matrix[x][y].dependencies.add(
                                        task_matrix[x-1][y])
                if y > 1:
                        task_matrix[x][y].dependencies.add(
                                        task_matrix[x][y-1])
```



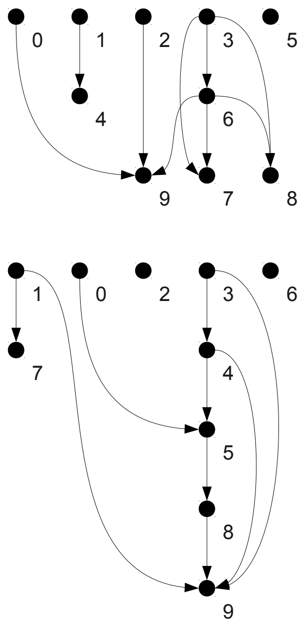
(a) Linear Dependencies



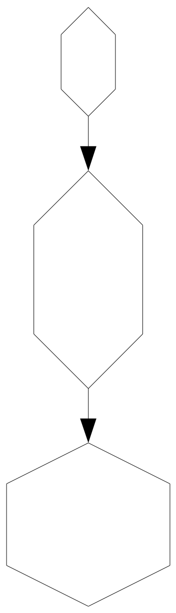
(b) Independent Chains



(c) Diamond



(d) Probabilistic Dependencies ($T = 10, P = 0.3$)



(e) Chain of Blocks

Figure 1: Dependency DAG shapes

4 Execution Times and Stability

Section 3 describes the shape of the DAG of a workload's dependencies. However, the execution times of each task within the workload must also be specified, as must the arrival time of each job. The scheduler must know this information in order to be able to make appropriate scheduling decisions. This section will firstly describe ways of generating workloads with task and job execution times that conform to a desired statistical distribution. Secondly, an algorithm is described to set the arrival time for each job to ensure a given stability ratio.

4.1 Distribution of Execution Times

According to the model defined above, each task has a specified execution time. These task execution times need to be generated in such a way that the workload has statistically robust properties [8].

The simplest method of assigning execution times to all the tasks in the workload is simply to generate a random number in a given range for each task. However, this means that where jobs are composed of a similar number of tasks, they will also have a similar total execution time [1].

When generating many workloads that are comparable, it is highly desirable to be able to create them with the same total workload sum of execution times. In order to create job execution times that all sum to a given value, the UUnifast algorithm as originally described by [1] is appropriate. In the UUnifast algorithm, $n-1$ execution times are sampled from a logarithmic distribution. The final value is then the difference between the sum of all previous values and the target value.

In the industrial case study it was observed that job execution times followed a logarithmic distribution, whereas task execution times followed a normal distribution. Yet in order to satisfy the job execution time distribution, the execution time of the tasks in a job must sum to a particular value. This distribution is created using a similar approach to UUnifast where $n - 1$ values are sampled, but from a normal instead of a logarithmic distribution. The last task execution time value is calculated, as before, to achieve the specified job execution time.

4.2 Stability

Stability can be measured by the percentage rate at which work is arriving into a grid compared to the maximum rate that the grid can process this work. The arrival rate is said to be stable if the arrival rate is less than the maximum processing rate (<100%), and unstable if the arrival rate is faster than the rate at which work can be processed (>100%) [3].

Grids are virtually always run at close to 100% stability ratio. Because the procurement and operational cost of a grid is very high, the operator is highly unlikely to over-buy resources for a grid. In addition, many computational loads can occupy as much computing power as is available. In many industrial grids, the stability ratio fluctuates around 100%. There may even be extended periods where the rate is over 100%, and the extra work must be queued. Therefore, it is necessary to be able to compare schedulers over a range of stability ratios.

A stability ratio for a workload can only ever be defined with relation to a platform, yet it is desirable to be able to adjust the stability ratio independently of the workload and platform. This can be achieved by adjusting the arrival times of jobs. The algorithm for calculating the arrival times of each job for a given platform and workload is given in Algorithm 4.5.

Algorithm 4.5 Pseudocode to define job arrival time with varying stability ratio

```
n = number of processors in system
jobcount = number of jobs in workload
sumj(i) = the sum of all task execution times in job i
p = desired stability ratio as percentage
start(i) = set the start time of job i

start(1) = 0
for j in 2 .. jobcount:
        singleprocworktime = sumj(j - 1) / n
        decimalp = p / 100
        start(j) = start(j-1) + (singleprocworktime / decimalp)
```

An alternative method for generating a workload is by specifying a duration of time for which the specified platform would be at 100% utilisation. The time slots on each processor are then divided up using the UUnifast-Discard algorithm, as presented by [6]. Each time slice on each processor then corresponds to a task. Each task is then randomly assigned a job to belong to. To vary the stability ratio for this method, the requested and actual finish time of the whole workload can be adjusted accordingly.

5 Conclusion

A summary of the issues surrounding Grid Scheduling were described, along with the background that motivates the work of this paper. Classes of Directed Acyclic Graph shapes and patterns that could be useful for evaluating the performance of schedulers were described, and algorithms for generating these patterns were shown. Algorithms for creating workloads with realistic distributions of task and job execution times were presented. The issue of stability was described, as were two methods of creating workloads with a given stability level for given platforms.

Several areas of future extensions to this work are possible. There may be more possible patterns of DAG that could be deduced from further case studies.

Other workloads may demonstrate distributions of job and task execution times other than logarithmic and normal, respectively.

The performance of the implementation of these algorithms should be evaluated. The algorithms presented here for generating workloads can struggle with a high rate of discarding when certain parameters are set to extremes. Investigation into algorithms that still produce tasks and jobs with the desired distributions but eliminate or minimise the discard rate would also be valuable to increase the efficiency of workload generation. From a scheduling aspect, determining which schedulers are best suited to working with each kind of task graph shape is an ongoing topic of research.

The work presented in this paper is intended to demonstrate the algorithms used in the creation of an application model. This application model, when combined with a future platform model, will be used to compare different scheduling policies as to their effectiveness on a variety of grid workloads.

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Interactive cookbooks : how recipe format affects the cooking experience

Lucy Buykx

Department of Computer Science
University of York, UK

Abstract. Interactive cookbooks have been developed to assist novice cooks follow recipes. Where printed recipes usually contain several paragraphs of textual instruction, interactive cookbook recipes are presented in step-by-step format, with clearly written steps, and accompanied by photographs and videos to illustrate ingredients and cooking techniques. Few studies have evaluated the relative benefits to the cook of step-by-step format, good writing and multimedia individually or in combination. This study compared the time taken to complete and user ratings of recipes presented in three different textual formats: original published format, simple step-by-step format and edited step-by-step format. Initial results indicate that transformation of a recipe to step-by-step format and including ingredient quantities improves ease of use ratings and may increase mean time efficiency.

Keywords: Human-computer interaction, interactive cookbooks, recipes

1 Introduction

Several interactive cookbook systems have been developed to assist cooks to use recipes in the kitchen. CounterActive [1] projected the recipe onto the worksurface one step at a time and enhanced the recipe with videos and images. The Augmented Reality Kitchen [2] built on CounterActive, projecting recipe instructions where they anticipated the cook's attention would be and highlighting the location of utensils as they were needed. With the Happy Cooking system Hamada et al [3] presented recipes as a series of simple steps to help cooks prepare multiple dishes to all be ready to go to the table at the same time. The Personal Chef system [4] presented recipes in step-by-step format with illustrations of all the utensils and ingredients needed and videos of all the techniques taken from two angles. These enhancements were designed to increase the confidence of cooks preparing more complex dishes.

The researchers did not describe the transformation processes they used for recipes for their interactive cookbooks but from screen shots we can see several transformations at play. They (a) performed task analysis on the recipe procedure to create a step-by-step process, (b) wrote clear text to describe the task(s) within each step, (c) added photographs of ingredients and utensils and (d) added video to illustrate task(s) within each step. Little user research was reported with these studies so it is not clear what problems, encountered by cooks, these interactive cookbooks sought to resolve. Further, the measures of success are unclear because researchers did not report evaluations of their interactive cookbook against control recipes.

The transformation process described above depended on human expertise so was time consuming and resource heavy. Such media rich and well presented recipes can be found from professional publishing houses but many of the recipes available online on websites such as allrecipes.com and cookpad.com are written and published from members of the public. They vary in accuracy, structure, clarity of instruction and completeness. It is the nature of recipes to contain instructions on many levels of abstraction [5], and anaphora [6] that may further catch the unwary. Within a recipe, day to day words may convey a different meaning so a recipe "simply cannot be understood unless one is of the subculture who knows how to cook." [7]. Further complications arise when recipes are read outside their country of origin; measures (e.g. cups and pints), processed ingredients (e.g. flour), brand names and even the meaning of cooking techniques (e.g. grilling) vary between countries.

The sheer volume of recipes available online presents an opportunity for automated transformation. Attempts thus far to automate the process of recipe task analysis [3] and adding multimedia video clips [8][9] have shown limited technical success and little user evaluation has been reported. A clear understanding of the problems experienced by cooks and an evaluation of how recipe transformations affect the cook will contribute to the development of automated algorithms for recipe transformation and to the development of interactive cookbooks.

This study focuses on textual and structural aspects of recipe transformation performed through (a) task analysis to create a step-by-step recipe and (b) writing of clear task instructions for each step. Sixteen cooks prepared three recipes presented on a commercial recipe application on the Apple iPad [10]. The simple experimental design enabled evaluation of the contribution of textual alterations to a recipe in isolation from multimedia enhancements. Observations of the participant cooks provided a body of data of how cooks interact with recipes, in context, while they are cooking. If the textual alterations to the recipe do benefit the cook and make it easier to understand and follow the recipe this will reduce the overall time it takes to prepare the dish and increase the post task ease of use score.

2 Method

2.1 Participants

16 participants (mean=20.0 years, std dev=1.6, male=8, female=8) were recruited through University of York online notice boards and student newsletters. They were randomly allocated an ID within one of six experimental groups.

2.2 Experiment design

The study used a within-subjects repeated measures design. Recipe format was the single independent variable (IV) with three levels: Control, Simple step-by-step and Edited step-by-step. Table 1 shows the Key lime pie recipe in each condition.

In the control condition, the recipe was presented as the original text from the cookbook. This original recipe was analysed by the author and another HCI expert to create the simple step-by-step format. Each analyst broke the text into individual steps suitable for an automated cookbook to provide step-by-step instructions to a cook. The only text amends were to grammatically complete a sentence. The inter-analyst agreement was 86% for all three recipes.

The edited step-by-step format was based on the simple step-by-step format with further editing:

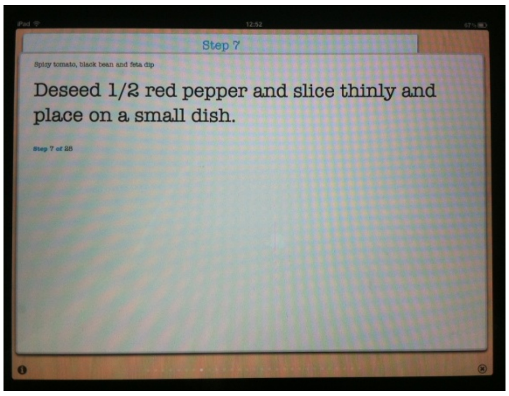
1. preparation instructions were moved from the ingredient list to the method
2. The quantity needed of an ingredient was included when the ingredient was first introduced in the recipe method
3. The order of recipe steps was reviewed and revised for optimal flow e.g. placing the instruction to pre-heat the oven to the start of the instructions so it would be at the correct temperature when the Key lime pie was ready to go in the oven

2.3 Measures

Two measures are reported in this paper: overall time to complete the recipe and post task questionnaire ratings.

2.4 Materials

A paper copy of each recipe was handed to the cook to read as part of the briefing session and left on the kitchen table for referral if needed. During the cooking sessions, recipes were presented to the cooks on the Apple iPad. The iPad was supported in a fixed position on the kitchen work surface. One video camera captured the iPad screen, another captured the activity of the cook. Morae v3.1 was used to record the sessions.


iPad 12:52 67%

Step 7

Spicy tomato, black bean and feta dip

Deseed 1/2 red pepper and slice thinly and place on a small dish.

Step 7 of 28

Figure 1 shows how the recipe was presented using “Cook’s View” mode of MacGourmet for iPad [11]. In this mode the application presents each recipe step in large text on a separate screen. The cook swipes the iPad screen to move between recipe steps.

All the recipe ingredients were provided for the participant cooks. Lime zest and breadcrumbs were

Control format	Simple step-by-step format	Edited step-by-step format
1. Crush the biscuits by putting them in a plastic bag and pounding them with a rolling pin until powdery. Transfer them to a bowl and add the melted butter. Stir well, then place in the base of a small pie tin and pat into place. 2. Put the condensed milk and eggs in a bowl and stir with a fork, gradually adding the lime and lemon juice. The mixture will begin to thicken. Add half the lime zest and pour the mixture on top of the ginger crust. Sprinkle the remaining zest on top. Place in an oven preheated to 180°C/Gas Mark 4 and cook for 10 minutes only. Don't be fooled by the look of the pie into thinking you need to cook it for longer. It is meant to be custard-like. It is not a baked cheesecake, although it does look and taste a bit like one. Once cooled, place in the fridge where it will continue to set. Serve with icecream or whipped cream.	1. Crush the biscuits by putting them in a plastic bag and pounding them with a rolling pin until powdery. 2. Transfer them to a bowl. 3. Add the melted butter. 4. Stir well. 5. Place in the base of a small pie tin and pat into place. 6. Put the condensed milk and eggs in a bowl and stir with a fork. 7. Gradually add the lime and lemon juice. The mixture will begin to thicken. 8. Add half the lime zest. 9. Pour the mixture on top of the ginger crust. 10. Sprinkle the remaining zest on top. 11. Place in an oven preheated to 180°C/Gas Mark 4. 12. Cook for 10 minutes only. Don't be fooled by the look of the pie into thinking you need to cook it for longer. It is meant to be custard-like. It is not a baked cheesecake, although it does look and taste a bit like one. …	1. Preheat the oven to 180°C/Gas Mark 4. 2. Zest the lime and set aside. 3. Crush 125g biscuits by putting them in a plastic bag and pounding them with a rolling pin until powdery. Transfer them to a bowl. 4. Melt 65g butter. 5. Add the butter to the biscuit crumbs, and stir well. 6. Grease a small pie tin. 7. Put the biscuit mixture into the small pie tin and pat into shape so it covers the base. 8. Put 200ml condensed milk and 1 egg in a bowl and stir with a fork. 9. Gradually add 60ml lime and 1 tablespoon lemon juice, and continue stirring. The mixture will begin to thicken. 10. Add half the lime zest to the condensed milk mixture and mix well. 11. Pour the mixture on top of the ginger crust. 12. Sprinkle the remaining zest on top. 13. Put the pie in the oven and cook for 10 minutes only. Don't be fooled by the look of the pie into thinking you need to cook it for longer. It is meant to be custard-like. It is not a baked cheesecake, although it does look and taste a bit like one. …

Table 1: Key lime pie recipe as presented in experimental conditions

prepared in advance to reduce session times. Participants took the finished dishes away with them.

After each recipe was prepared, the cooks were asked to complete a post-task questionnaire. They were asked to rate two statements: “Were the instructions clear?” and “Were the instructions easy to follow?” on a scale of 1 to 5 where 1 was “very unclear/hard” and 5 was “very clear/easy”. A free form text box was provided for additional comments about the recipe and cooking experience.

2.5 Protocol

Each cook prepared three dishes in this order: Key lime pie, Chicken burger, Tomato dip. The author set up the iPad for each dish to display the recipe using the “Cook’s Mode” of MacGourmet. At the end of each dish the cook completed a questionnaire about the recipe.

3 Early results

3.1 Current state of the study

The study is in progress. Results from 16 of the planned 24 participants are reported.

Table 2: Number of cooks who have taken part, by recipe and condition

Condition	*Tomato dip*	*Chicken burgers*	*Key lime pie*
Control	6	4	6
Simple step-by-step	5	7	4
Edited step-by-step	5	5	6

Table 2 shows the numbers of cooks preparing each recipe by condition to date. When the study is complete, 8 cooks will have prepared each recipe in each condition.

3.2 Post task questionnaire

After each recipe cooks were asked to complete a short questionnaire.

Table 3: Were the instructions clear?

Condition	*Tomato dip*	*Chicken burgers*	*Key lime pie*
Control	3.67	4.00	4.33
Simple step-by-step	4.20	4.00	4.75
Edited step-by-step	4.40	4.40	4.83

Table 3 shows the cooks' rating of the clarity of instruction by recipe and condition. Cooks were asked to score the recipe on a scale of 1-5 where 1 was "very unclear" and 5 was "very clear".

Table 4: Were the instructions easy to follow?

Condition	*Tomato dip*	*Chicken burgers*	*Key lime pie*
Control	3.80	3.75	4.17
Simple step-by-step	3.80	3.86	5.00
Edited step-by-step	4.60	4.20	4.67

Table 4 shows the cooks' rating of the ease of use of the instructions by recipe and condition. Cooks were asked to score the recipe on a scale of 1-5 where 1 was "very hard" and 5 was "very easy".

3.3 Time to complete the recipe

Table 5: Mean time to complete recipe, mm:ss (SD)

Condition	*Tomato dip*	*Chicken burger*	*Key Lime pie*
Control	44:05 (6.6)	36:06 (6.6)	32:16 (6.6)
Simple step-by-step	46:04 (14.5)	26:01 (3.5)	26:35 (4.0)
Edited step-by-step	47:09 (10.5)	24:01 (4.9)	26:11 (5.3)

Table 5 shows the total time taken by cooks to complete each recipe. The tomato dip was marked as complete when the dip was placed in a flameproof dish. The chicken burgers were marked as complete when they were placed in the fridge to chill. The key lime pie was marked as complete when it was placed in the oven.

4 Discussion

Initial results indicate that the clarity of instructions in the recipe and the ease of use vary between conditions. Table 3 shows that cooks rated "were the instructions clear?" highest for all recipes in edited step-by-step format and lowest for recipes in control condition, the original published format. Table 4 shows that cooks rated "were the instructions easy to follow?" highest for chicken burger and tomato dip recipes in edited step-by-step format and lowest for all recipes in the control format. The study is in progress so no statistical analysis has yet been performed on the cook's scores, but these initial results indicate that transforming an original recipe into step-by-step format followed by careful editing improves the clarity and ease of use of the recipe.

The mean time taken to complete recipes is reported in Table 5. Initial results suggest that cooks may be more time efficient using the edited step-by-step format however in this study the effect is overwhelmed because the variation between cooks is greater than variation between recipe formats.

Observations of the cooks activity and comments made during the cooking provide additional insight into the benefits and problems of recipe presentation.

The simple and edited step-by-step formats were preferred over lengthy paragraphs presented in recipes in the control condition. Of this condition cooks said:

"There was a lot of information on a single slide which I had to read multiple times." (Cook 10)

"The vast amount of text cluttered the screen and made it seem more complex than it actually was." (Cook 23)

However the fine grain step-by-step nature frustrates some cooks who prefer to scan ahead and plan their next actions. Further analysis of the activity path will provide insight into how cooks interact with sequential recipe steps, whether and by how much they prefer to look ahead.

The tomato dip recipe will provide interesting case study for activity path analysis. It requires 3 stages of cooking, with new ingredients added at each stage. In the control condition, all the preparation was indicated in the ingredients section and the cooks could chose when to prepare the ingredients. In the control condition, cooks were observed to prepare only the two ingredients needed for the first stage of cooking (red pepper and onion) before setting it to cook for 8 minutes. While the pepper and onion were cooking they prepared the rest of the ingredients. In the edited step-by-step condition of this recipe, the ingredient preparation was described in early recipe steps before instructions to start cooking. Cooks who followed steps in sequential order were not free to optimise the recipe and in this case the edited step-by-step format was less time efficient than an ad-hoc optimisation of the original recipe.

Time efficiency optimisation was performed for recipes presented using Happy Cooking [3]. The researchers reported some cooks were unhappy performing certain tasks in parallel and planned to review their algorithm. Further analysis of the activity paths and comments from cooks in this study will provide insight into optimisation strategies that can be incorporated into future interactive cookbook designs.

The most common frustration mentioned by cooks was that, for recipes in the control and simple step-by-step conditions, quantities of ingredients were only available on the ingredient page. This forced the cooks to scroll back to the ingredients list every time a new ingredient was introduced to the recipe. This is the common format of recipes in cookbooks and websites and is recommended as best practice for printed recipes [12] and it persists in recipes imported to commercial recipe applications such as MacGourmet used in this study. These initial results suggest this simple transformation may be one of the most important to cooks for future researchers to address.

4.1 Summary

Initial results indicate that cooks prefer recipes to be decomposed into smaller individual steps with the quantity of ingredients included in the step. These results support the form of transformations performed on recipes by earlier researchers and when all results have been analysed, will provide rich and detailed data from which to improve transformation algorithms and the designs of interactive cookbooks.

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Locality in Co-optimisation Problems

Tom Seaton, Tim Clarke

Univeristy of York, YO10 5DD, UK

Abstract Test-based co-optimisation is a challenging problem in the field of evolutionary computation. We analyse the effect of genotype-to-phenotype locality in the application of coevolutionary algorithms (CoEA) to test-based problems. A normalised definition for locality is established in terms of metric spaces and preliminary results presented on a standard benchmark. Strong correlation is observed between mapping locality and expected performance. The implications for further work on representations and coevolutionary search are discussed.

1 Introduction

A commonly encountered problem in engineering is the aim of optimising a solution against a large collection of tests. For example, the design of a novel system component may require tests in many different environmental contexts, typically too many to allow for an exhaustive set of trials. Co-optimisation [7] is an extension of the mathematical concept of optimisation to *interactive* problem domains, where no objective function describing solution quality is available.

Coevolutionary algorithms (CoEA) are a popular heuristic search technique in Evolutionary Computation (EC) which have been successfully applied to a range of co-optimisation problems [5, 8, 9]. This paper examines the effect of a particular property of CoEA, solution *locality*, on performance of CoEA on competitive, test-based problems. Locality in EC is an attribute of the mapping function which links the syntactic and semantic values of solutions, referred to as the *genotype to phenotype map.* Locality has been shown experimentally to be beneficial for classes of EC problem and is a widely applied heuristic in the design of evolutionary algorithms [10, 11, 13]. Recently, concepts of how to formally measure complex maps have been gaining greater attention [4].

The structure of this paper is as follows. Section 2 introduces basic EC terminology and the genotype to phenotype map. We then briefly summarise necessary background on co-optimisation, test-based problems and coevolutionary algorithms. Section 3 states formal definitions of locality and refines an appropriate measure. Section 4 details our inital experimental approach, including a benchmark problem and preliminary results. Section 5 concludes with a discussion of the significance of locality in coevolutionary algorithm design.

2 Background and Definitions

2.1 Terms in Evolutionary Computation

In the field of Evolutionary Computation (EC), the biological term *genotype* refers to a collection of primitive data. The *genotype representation* is the abstract data structure in which this is stored for computation (such as a tree). A *phenotype* is the decoded expression of a genotype. For example, in the context of a genetic algorithm, the genotype is typically a fixed length binary string and the phenotype the problem specific interpretation, such as a set of parameters. A *population* is a collection of (not necessarily distinct) genotypes. Phenotypes are determined from genotypes by a surjective function or *genotype to phenotype map*. In general, the genotype to phenotype map is non-injective, that is there may be many genotypes which map to the same phenotype.

2.2 Co-optimisation, Test-based Problems and Pareto-Optimality

In a classical optimisation problem, the goal is to maximise or minimise a function which applies over a set of potential solutions. *Co-optimisation* addresses the case where no explicit objective function is available. Informally, co-optimisation problems arise when it is not possible to directly evaluate an individual element of the solution space. This situation is referred to as an interactive problem domain, a term developed in Popovici et. al. [7],

Definition 1. ***(Popovici. et. al. 2009)*** *An interactive problem domain consists of one or more functions, of the form* $f : X_1 \times X_2 \times ... \times X_n \rightarrow R$*. The sets* X_i *are* domain roles*.* R *is an ordered tuple of* outcomes*. A tuple* $(x_1, x_2...x_n) \in X_1, X_2...X_n$ *is an* interaction*.*

Test-based co-optimisation problems are a specific case of interactive domain, where the domain roles are a set of *candidates* C and set of *tests* T. There exists a single function $f : C \times T \rightarrow \Re^n$ which maps each candidate-test pair to a vector of real numbers. A *binary outcome* problem is an instance of this in which a test has a single outcome, a pass or failure such that $f : C \times T \rightarrow \{1, 0\}$. The goal of a test-based problem is to attain a set of candidates such that they satisfy a particular *solution concept* or definition of optimality [1]. For example, for binary outcomes, a simple solution concept is the set of candidates which pass the largest number of tests. In general more complex solution concepts are often required. We may be interested in finding candidates which maximise outcomes over a unique range of tests, or minimise losses.

Our analysis focuses on the well-established solution concept of *pareto- optimality*, as applied to test-based problems [2]. A pareto-optimal solution concept

[1] The term solution concept originates in game theory. A more complete discussion of solution concepts in test-based problems can be found in [3].

is defined on test-based problems by considering each test as a separate objective. The solution concept applies a strong dominance relation $\succ$ between each pair of candidates $(c, c') \in C \times C$, with respect to each subset of tests $T_s \subseteq T$:

$$c \succ c' \;\mid\; \forall\, t \in T_s,\; f(c,t) \geq f(c',t) \wedge \qquad (1)$$
$$\exists\, t \in T_s \;,\; f(c,t) > f(c',t)$$

From Equation (1) we can say with reference to the whole test set T, there is a dominating subset of candidates (the pareto-optimal set). Removing the second condition gives the corresponding weak relation $\succeq$,

$$c \succeq c \;\mid\; \forall\, t \in T_s,\, f(c',t) \geq f(c',t) \qquad (2)$$

Hence, Equation (2) induces a partial order on the candidate set. Informally, this dominance relation orders candidates into layers or *pareto fronts*. Members of each pareto-front are non-dominated $c \not\succ c'$ with respect to each other, over all tests.

2.3 Coevolutionary Algorithms

Evolutionary algorithms carry out heuristic search through the principles of selection, variation and reproduction through successive generations. One or more populations of genotypes are maintained which represent semantic elements of the problem domain by means of the genotype to phenotype map. Selection occurs by comparison using a known, objective fitness function against one or more other genotypes. Variational operators act to mutate or recombine successful genotypes into ‘offspring’, giving rise to subsequent populations.

Distinct from evolutionary algorithms, coevolutionary algorithms lack an explicit guiding objective function for single individuals. Selection is instead carried out on the basis of evaluation of functions from the interactive problem domain. Thus, a coevolutionary algorithm explores a space of interactions, across potentially multiple populations, rather than a space of individual fitness values.

The absence of an individual objective function (notion of fitness) in CoEA can lead to *coevolutionary pathologies*. Examples have included issues such as cycling behaviour between states or loss of gradient (disengagement). To ensure convergence towards a particular solution concept, practitioners have introduced coevolutionary archives [1, 2, 6, 9]. An archive maintains a record of historically successful genotypes, which are then used to bias the current evolutionary process. In this model, the CoEA can be considered to be composed of two high level elements - a generator, which delivers novel genotypes through the evolutionary heuristic and a (set of) archives which act as an accumulator.

Test-based co-optimisation problems are addressed in this fashion by *competitive* or adversarial coevolutionary algorithms. Analogous to competitive coevolution in nature, the intention is to generate genotypes which represent successively more capable candidates and more challenging tests. Generators feature two distinct populations of candidates and tests, which are co-evolved simultaneously. Efficient archives have been proposed for test-based problems using the pareto solution concept [2]. However, the question of how to best design an appropriate generator is still open. To address this, we need to understand the effect of different maps on the coevolutionary search process.

3 Locality and Representation

3.1 A Normalised Locality Metric

Qualitatively, the concept of *locality* reflects the idea that small changes in an individuals genotype should lead to small changes in phenotype. Another way of stating this is that the application of a search operator to an element in the genotype space should result in a new phenotype, which is semantically similar to the old.

To our knowledge, the first quantitative definition of locality was introduced by Rothlauf [10]. Rothlauf considered a finite set of discrete genotypes G and of phenotypes P, with a surjective mapping function between the two $m : G \rightarrow P$. Under Rothlauf's work [2], distance metrics are paired with each set, d_G and d_P respectively such that (G, d_G) and (P, d_P) become distinct metric spaces. The metrics assume an appropriately chosen measure of similarity between members of each set - for example, the Hamming distance on binary strings. The minimum distance between genotypes over the whole space is then written as d_G^- (respectively, d_P^- for phenotypes). We can then refer to the *local neighbourhood* or adjacency set of a genotype, the subset of genotypes $adj(g) \subseteq G$ for which $d_G(g, g') = d_G^-$. Finally, the image of $adj(g)$ in the phenotype space under m is given by $adj^*(g) \subseteq P$. The operator $adj^*(g)$ therefore gives the subset of phenotypes which correspond to the local neighbours of g in genotype space, illustrated in Figure (1) below. Using these definitions Rothlauf's measure of locality is expressed as a summation

$$L = \sum_{g \in G} \sum_{p' \in adj^*(g)} d_P(p, p') - d_P^- \tag{3}$$

where $p = m(g)$. This summation provides information on the distance of neighbours when mapped to the phenotype space. In a mapping function where all neighbouring genotypes correspond to neighbouring phenotypes, $L = 0$. We term this situation *fully local.* For $L > 0$, the mapping is increasingly *non-local.*

Whilst the original Equation (3) gives a useful relative measure, it is not normalised to the size of the search space. In other words, comparison is limited to two different mappings of the same search space. Ideally, we would like to extend the measure so that it scales conveniently and permits comparison between mappings used in different domains. To scale L, we introduce d_G^+ and d_P^+, which are the maximal distances in genotype space and phenotype space respectively. Secondly, we normalise by the number of genotypes in G and the size of each

[2] The mathematical notation here is our own, introduced for later clarity.

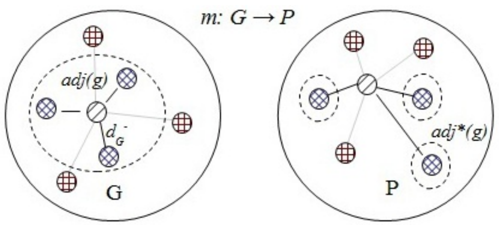

Figure 1: A non-local genotype to phenotype map. The relative distance of neighbouring genotypes increases under the new metric.

local neighbourhood. This leads to the adjusted measure:

$$L_N = \frac{1}{\mid G \mid} \sum_{g \in G} \frac{1}{\mid adj^*(g) \mid} \sum_{p' \in adj^*(g)} \frac{d_P^+ - d_P(p, p')}{d_P^+ - d_P^-} \tag{4}$$

L_N assumes the value 1 when all neighbouring genotypes have neighbouring phenotypes and 0 when all neighbouring genotypes give maximally different phenotypes. Values between 0 and 1 indicate intermediate levels of locality in the mapping. Note that for the specific case that m is a bijective function (i.e. there exists a one-to-one mapping between genotypes and phenotypes), it is possible to define an inverse map and the corresponding notion of locality in phenotype space. We refer to this concept here as the 'inverse' locality, L_N^{-1}.

3.2 Example: Locality in Gray Codes

For small genotype spaces, the measure of locality given in Equation (4) can be calculated directly. By way of example, we consider the calculation for a simple reflected binary or Gray code. Gray codes are commonly employed in genetic algorithms to avoid the so-called 'Hamming cliff', where a large change to the genome is required to move between adjacent binary strings [12]. Codes provide a useful test case for aggregated measures of locality, because by definition all phenotypes (integers) have neighbouring genotypes. Under Equation (4), the inverse locality of a Gray code (i.e. for integer to bit string) is equal to one, by definition. If we make a change to the code the inverse locality may decrease accordingly. Table 1 contrasts L_N^{-1} computed for a three bit word in binary, Gray and a random permutation. The distance metric d_G is the Hamming distance and d_P is the absolute difference between integers. The maximum and minimum distance d_G^+ and d_G^- are therefore 3 and 1 respectively. From the values of L_N^{-1} in Table (1), we can see that the Gray encoding preserves local neighbourhood structure (i.e. L_N^{-1}), but the random and binary encodings disrupt it. The partial sums in Table (1) are mean 'scaling factors' for each local neighbourhood. Small fractions are associated with phenotypes whose local neighbours have become more distant in the genotype space.

Table 1: Inverse locality for a 3-bit binary, Gray and randomised encoding. Rows show the scaled, partial sum of L_{NRM}^{-1} for each phenotype.

P	*Binary*		*Gray*		*Random*	
0	000	1.00	000	1.00	010	0.00
1	001	0.75	001	1.00	101	0.25
2	010	0.75	011	1.00	000	0.50
3	011	0.50	010	1.00	011	0.25
4	100	0.50	110	1.00	100	0.50
5	101	0.75	111	1.00	110	0.50
6	110	0.75	101	1.00	001	0.25
7	111	1.00	100	1.00	111	0.50
$\mathbf{L_N^{-1}}$	0.75		1.00		0.34	

4 Experiment

4.1 The Compare-on-one Problem

To analyse the effect of changes to the locality of a mapping on coevolutionary algorithms, we consider a standard co-optimisation benchmark, *Compare-on-one* [2]. Compare-on-one (CO1) is a binary outcome 'number game'. Candidates and tests are represented by fixed length vectors $c = [c_1...c_n], t = [t_1...t_n]$. The objective of CO1 is to maximise all dimensions of the candidate vector, guided by a binary payoff function

$$f(c,t) = \begin{cases} 1 & c_i > t_i \\ 0 & c_i \leq t_i \end{cases} \qquad i = argmax_x(t_x) \tag{5}$$

CO1 is a straightforward problem, but presents challenges to coevolutionary algorithms because of the propensity to induce overspecialisation on a single objective. Progress must be achieved in all dimensions, but comparison is only permitted on single elements of each vector. CO1 is intended to mimic larger scale problems, where a test may only examine a particular aspect of a system's performance. In our approach, we employ a modified version of CO1 which supports a binary to integer mapping. Each candidate or test is a 30 bit word (genotype), which is mapped to a pair of 15 bit integers (phenotype) by a Gray encoding (genotype to phenotype map). The objective performance of a candidate is therefore the smallest value of the pair of integers, $min(c)$.

4.2 Setup

Two populations of 20 candidates and tests were coevolved over a period of 100 generations. Populations are initialised randomly from a uniform distribution. At each generation, candidates accumulate a payoff equal to the total number of tests passed in the current test population. Tests are assigned payoffs equal to the number of candidates which fail that test. Both populations are ordered by payoff and the five highest ranked genotypes retained for the next generation. The remainder of the population is replaced with equal weight by mutated offspring from these members. Mutations (bit flips) occur with 0.1 probability for each element of the genotype. This approach is analogous to '*truncation selection*' in a standard GA .

Progress in the search is ensured by coupling the algorithm to an archive. The *Iterated Pareto Coevolutionary Archive* (IPCA) is an unbounded archive which maintains successive layers of pareto-optimal candidates (full details in [2]). The algorithm is coupled to IPCA by introducing the potential for offspring to be mutated from a randomly selected member from the archive. At generation t, this occurred with linearly increasing probability $\mu = (t/100)$. Therefore, as the search converges towards the pareto-optimal front, the likelihood of mutating from a dominating member of each population increases. Performance was measured on the best candidate member (objectively) in the IPCA archive.

Following from the example in Section (3.2), a simple greedy search was applied to generate sample encodings. For a given target locality T

```
1. Generate a reflected binary code $r$.
2. $l \leftarrow L(r)$.
3. while($|T - l| > tol$)
3.    Swap a randomly selected pair of integer values
        in $r$ to give $r'$
4.    If $|T - L(r')| < |T - l|$, $r \leftarrow r'$
5. end
6. return $r$
```

such that *tol* is a minimum acceptable tolerance on T. Five sets of 10 sample encodings were generated between $L_N^{-1} = (0.5 : 0.95)$, to a tolerance of ± 0.01.

5 Results & Discussion

Average performance measures were obtained for each of the sample sets over 100 runs. Figure (2) illustrates the average performance for two members of the first sample set ($L_N^{-1} = 0.51$ and 0.76). Comparison is made against performance using the standard Gray code, with and without archive feedback. Best performance is achieved by the Gray code and archive. As locality of the mapping decreases, average performance falls and benefits from archive feedback are lost.

This trend is supported over the full set of results. Figure (3) shows variation in the averaged performance, in response to changes in encoding. Each point represents the performance of an encoding at 50 generations. The trend indicates a strong correlation between locality and performance for this experiment, observable over all sample sets (Spearman coefficient $\rho = 0.98$). Locality and expected performance decrease nearly monotonically as the Gray code mappings are perturbed. Although this does not necessarily imply a causal relation between locality and performance, it does suggest that the L_N measure may prove a good indicator of a mapping's performance on simple coevolutionary problems.

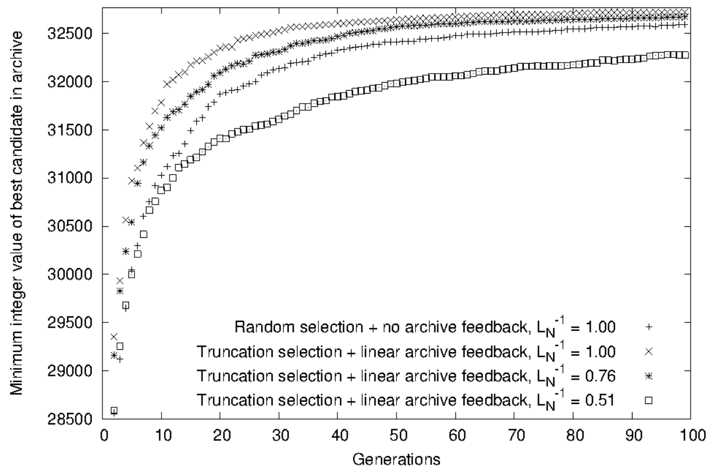

Figure 2: Example convergence plots on the 30 bit Compare-on-one problem. Expected performance is illustrated for selected members of the first sample set.

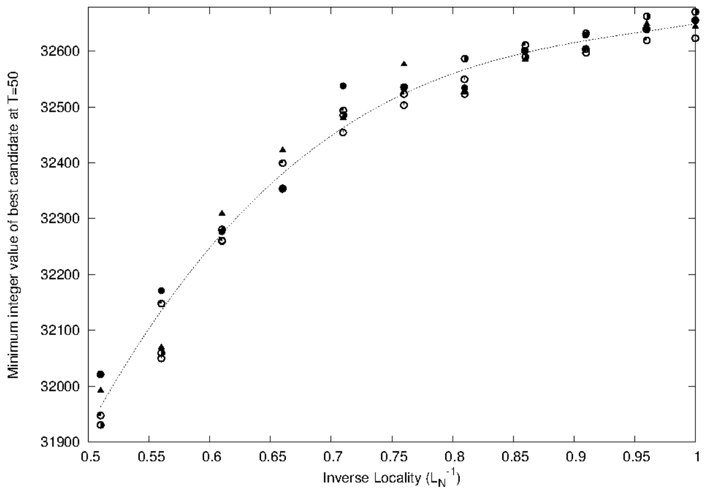

Figure 3: Correlation between performance and mapping locality for the 30 bit Compare-on-one problem, reported at 50 generations using 5 sample encoding sets.

6 Conclusion

This paper presented preliminary work investigating the role of locality in coevolutionary algorithms. We defined a normalised measure to analyse the effect of varying locality on a benchmark co-optimisation problem, *Compare-on-one*. Sample genotype to phenotype maps were generated over a range of different localities under greedy search. For this problem instance, locality in the genotype to phenotype map was strongly correlated with expected performance.

In realistic co-optimisation problems, calculating L_N directly is infeasible. One open question is how to accurately approximate L_N by sampling, to enable scaling of the measure to maps of practical interest. A second issue is the selection of appropriate measures of distance between genotypes and phenotypes. For the phenotype space, this is problem specific, though Galvan-Lopez. et. al. recently proposed the use of general measures of similarity such as Kolmogorov complexity or edit distances [4]. Within the genotype space, the challenge is to configure distance measures which correctly reflect the operators in use.

The definition of locality provided in this paper focuses on adjacent genotypes. An area of interest is the role of correlations between genotype and phenotype distances over longer scales beyond the immediate neighbourhood. We are currently investigating statistical approaches to explore this in more complex genotype to phenotype maps, such as those employed in genetic programming. Our future work will consider larger test-based problems and address whether the results observed here extend to more general interactive domains.

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Generating Models Using Metaheuristic Search

James R. Williams and Simon Poulding

Department of Computer Science,
University of York, UK
jw@cs.york.ac.uk

Abstract Model driven engineering is a software development practice that treats models as first-class artefacts in the development lifecycle. Automatically generating models is useful for tasks such as for testing *model transformations*. Our previous work utilises metaheuristic search techniques to automatically discover models with certain properties. This paper presents work in progress that extends our previous work to the more general problem of generating models that satisfy certain criteria.

1 Introduction

A *model*, in general terms, can be thought of as an abstraction of the problem under scrutiny. Model driven engineering (MDE) treats models as the primary development artefact. The focus of MDE is to model the system at the level of the application domain and, through a series of automatic transformations, generate code [11]. Modelling at the application domain level allows domain experts to specify the system. Models in an MDE context conform to a *metamodel* – another model which describes the model's concepts and semantics. *Model transformations* are the processes which move models from abstract representations of the system to more concrete, platform-specific, representations and eventually to code.

Automatically generating models that conform to some metamodel is useful for a number of reasons, in particular, for testing model transformations. Creating many models by hand is tedious, and so automation is desirable. Automated generation, however, needs to ensure that the set of generated models will sufficiently test the transformation (or be adequate for the task in hand). The test set should be an accurate representation of the kinds of models that will be transformed in practice, should have good coverage of both the transformation and the metamodel, and should limit similarities between models in order to keep the test set small, and not lead to superfluous testing.

A different approach to software engineering is *search-based software engineering* (SBSE). This approach is based on the observation that it is easier to determine whether one solution to a problem is better than another, than it is to construct an optimal solution to that problem [4]. Metaheuristic search algorithms focus on identifying (near) optimal solutions to a problem by searching over the space of all possible solutions to the problem. Arguably the most prominent type of metaheuristic search technique is the *genetic algorithm* (GA) [6].

GAs act upon a *population* of solutions, each of which has a *fitness* – a measure of how "good" that solution is. GAs then apply evolutionary concepts (mutation and crossover) to the population in an attempt to improve the overall fitness of the population. Each solution in a GA's population is commonly represented as strings of integers or bits (known as the *genotype*). These integer/bit strings need to be decoded into concrete representations of solutions (known as the *phenotype*) in order to calculate their fitness, and thus perform the evolution.

Our previous work [15] uses metaheuristic search to discover "interesting" characters in a fighting game. Characters in the game are described using a bespoke language, which conforms to a grammar that was defined using an MDE tool called *Xtext*[1]. Xtext creates a metamodel for the language, enabling any instances of the language to be treated as models, and thus be susceptible to MDE tasks (e.g. transformation). We use a metaheuristic search technique called *grammatical evolution* (GE) to try to evolve "good" characters. GE is a method for automatically deriving programs and works in the same way as a GA, but the mapping from genotype to phenotype uses the grammar of the target language. Each integer in the string is used in turn to select the next grammar rule to instantiate, and thus outputs a string conforming to the grammar. Our transformation from genotype (integer string) to phenotype (character definition) is achieved using a model transformation that acts upon the Xtext definition of the grammar. This transformation is applicable to any language whose grammar has been defined with Xtext, although the approach does not support cross-referencing other parts of the model.

This paper presents work in progress that extends our previous work in three ways. Firstly, the approach is not limited to Xtext models, and now supports Ecore[2] – arguably the most widely used metamodelling language. Secondly, we now support cross referencing other parts of the model. Finally, whereas our previous approach looked for a single, optimal model (the best character), we now focus on the more general problem of generating models. The paper is structured as follows. Section 2 briefly examines related work on model generation. Section 3 overviews our approach to utilising metaheuristic search to generate models. Finally, section 4 summarises our work and looks at future improvements that could be made.

2 Related Work

This section examines related work in the area of model generation. We first look at other approaches to model generation, before briefly examining an alternative approach to testing model transformations. We conclude with an overview of other research that combines model driven engineering and search based software engineering.

[1] Xtext website: `http://www.eclipse.org/Xtext`

[2] Ecore is part of the Eclipse Modeling Framework: `http://www.eclipse.org/emf`

2.1 Model Generation

Model generation is a relatively understudied field, compared to other MDE processes such as model transformation, model validation and model comparison. Brottier et al [3] present an algorithm for automatically generating models from a metamodel. The algorithm takes two forms of input: firstly, the metamodel to which the generated models should conform, and secondly, a set of *model fragments* – specific elements that must appear in the set of generated models. The size of the set of generated models is strictly limited by the specified model fragments, and as Mougenot et al [10] points out, forcing the generated models to have particular elements will produce models with lots of similarities.

Ehrig et al [5] devised an approach to generating model instances by creating a *graph grammar* from the metamodel and using the grammar to create instances. The authors note that this method suffers from not considering constraints on the metamodel, and does not consider which classes would be more likely to be instantiated often. Furthermore, they do not consider generating attribute values, which can have a great impact on the generated models. They suggest a post-processing approach to allocate attributes to the generated models, but this is not enough as it is the *combination* of object structure and attribute values that make models distinct, not just their structure (i.e. structural equivalence versus semantic equivalence). A similar approach is taken by Mougenot et al [10], but uses a special grammar called a *tree specification*. This approach also fails to consider constraints on the metamodel, and requires a complex transformation to create the set of procedures used to generate the trees. Furthermore, the trees then need to be mapped back into *models* that conform to the metamodel.

Sen et al [12] propose a way to generate models for testing model transformations by exploiting the constraint modelling of the Alloy language[3]. Their tool creates an Alloy specification from a set of input sources (including the source metamodel and the pre-conditions to the transformation). The specification is executed and the solutions returned by Alloy are converted into MDE models. This approach cannot handle infinite data types, such as strings or real numbers. Furthermore, Alloy is known not to scale well and so may struggle with large and complex metamodels [1].

2.2 Verification of Model Transformations

Complementary research to generating models for testing model transformations is the *verification* of model transformations. Anastasakis et al [1] utilise Alloy to analyse model transformations. Their approach captures both the source and target metamodels, and the transformation mappings, as an Alloy specification and then the Alloy Analyzer searches for inconsistencies in the transformation. Asztalos et al [2] have developed an approach that maps model transformation definitions into their *Assertion Description Language*, and then verifies the transformation using an automated reasoning system developed in Prolog.

[3] Alloy website: `http://alloy.mit.edu`

2.3 SBSE and MDE

The application of metaheuristic search techniques to solving MDE problems is very limited. Kessentini et al [8] present a search based approach that uses example source and target models to learn model transformations (this idea is known as *model transformation by example* [13]). Their approach applies metaheuristic search to "transformation fragments" – mappings between elements in example source and target models – in an attempt to match the best fragment (or mapping) to each construct in a given source model. The set of matched mappings then creates the target model. Goldsby et al [7] present work that extends an existing tool for evolutionary computation to generate UML state diagrams from class diagrams. Finally, Li et al [9] use metaheuristic search to analyse non-functional properties of architectures described using MDE.

3 Search Based Model Generation

To reformulate a software engineering problem as a search problem, we need to do two things [4]: firstly, we are required to find a characterisation of solutions – a description of the *solution space* or a type for the representation of solutions. Secondly, we need to define an *objective function* that can determine the fitness of candidate solutions – i.e. a measure of how close a solution is to solving the problem. This section explains how we address the reformulation of model generation as a search problem.

3.1 Encoding the Solution Space

As with our previous work [15], each solution (represented as an integer string) in the solution space represents a single model. We extend our previous work so that instead of generating *strings* from a grammar to create a program, we generate *objects* from a metamodel to create a model. In order to calculate the fitness of a solution, the objective function transforms the integer string (genotype) into a model (phenotype). Our transformation has been adapted to support Ecore models – arguably the most widely used metamodelling language. The transformation requires that the metamodel be treated as a grammar (similar to the approaches in [5] and [10]), and as such, the transformation demands that there is a starting rule in the grammar. Ecore metamodels enforce a container class – a class that all other objects in the model reside in (think UML composition). In order to apply our grammatical transformation, the user is required to annotate this container class as the starting node in the grammar (annotations are commonly used in Ecore to aid automation, and so are not unfamiliar to Ecore users). The transformation initially looks for this annotation and if it is non-existent, informs the user and exits. If the annotation is found, the transformation continues as follows:

1. Create an instance of the container class.

2. For every reference defined for the container class, keep creating objects of the reference type and adding them to the reference. To control the number of objects created, each referenced object is created with a 50% probability, based on the next value in the integer string: if the next integer is even, we create a new referenced object and try again. Otherwise, the process moves onto the next reference.
3. Examine all created objects (i.e. all children of the container class) For each child class that also possesses containment references, go to step 2. Repeat until all objects with containment references have been considered.
4. Populate all non-containment references from existing elements in the model. Objects are selected from the set of applicable objects for that reference using the next value in the integer string, and extra objects are added to the reference with a 50% probability.

The current implementation (explained above) does not consider setting the values of any attributes in each object – section 4 explains how we will implement this in the future. It is also our intention to allow the user to specify the probability with which referenced objects should be created.

3.2 The Objective Function

The transformation explained above is used for every kind of model generation. The body of the objective function, the fitness calculation, controls the kind of generation obtained. The types of generation that might be desired, and how different objective functions could be defined to achieve that generation, are explained below.

Random The user may desire the generation to be entirely random, ignoring constraints of any kind. This could be achieved by using the objective function to transform the population into models and save each model to disk. Setting the population's mutation rate to 100% and ignoring the notion of fitness, the GA can be executed for an arbitrary number of generations, randomising the population in each generation, until the desired number of random models is obtained.

Constrained The user may wish the generated models to satisfy certain constraints. To achieve this, the fitness of a solution relates to how closely it satisfies the constraints. To avoid population convergence, the objective function could save to disk any individual that satisfies the constraints, and the GA could be executed for a specified number of generations until the desired number of constrained models is obtained. Alternatively, the fitness function could aim to produce a population of constrained models, which are all saved to disk in the final generation.

Distinct Randomly generating models may result in a number of similar models, and thus the artefact under test is not satisfactorily tested. To generate distinct models, the objective function can compare the current model against those previously generated, and store models whose matching score is low. This scored-matching idea could be achieved using our proposed extensions to an existing model comparison language [14].

Example driven The user may wish the generated model set to be variations and mutations of a given model. This could be achieved by comparing each model to the example in the objective function and rewarding solutions that score well. Alternatively, annotations on the metamodel could be used to specify particular metaclasses that should be instantiated, and with what frequency.

These functions could be combined in order to further control the generation. For example, one might wish to created a set of constrained, distinct models. It is our hope that we can provide these functions to the user as part of an easy-to-configure tool integrated into the Eclipse IDE (the most widely used modelling environment). This tool would mean that the user needs to spend minimal effort to generate their models.

4 Conclusion and Future Work

In this paper we have overviewed work in progress on a new technique to generate MDE models. We have presented a powerful transformation from a simple string of integers to a model conforming to a given metamodel. This transformation is exploited in a genetic algorithm, with which different objective functions determine the kind of models generated. Our transformation targets Ecore models, but the underlying idea is generic and is applicable to any metamodelling language.

We have implemented the initial prototype transformation and are currently implementing the objective functions. As previously mentioned, we also plan to integrate our tool into the Eclipse IDE – the most widely used modelling environment. We plan on running an extensive experimentation phase in order to determine the validity and quality of the generation. For example, can we generate *all* distinct models up to a certain scope? Is our approach able to generate *all* possible models? Are there some models that, due to the nature of the transformation, can never be discovered? Does our approach lend itself to a simple way of achieving the desired coverage of the metamodel/transformation? Finally, how does our approach compare to the existing approaches discussed in section 2, in terms of performance and quality of the generated model set?

There are a number of challenges in the transformation that still need to be addressed. Firstly, our current implementation does not account for setting attribute values. To achieve this, we will look for inspiration from research into test-data generation. One possible solution would be to allow users to add annotations to their metamodels that express a number of "default" values for different attributes. The search can then pick one of the defaults using the integer string.

Another challenge to consider is the notion of cross-model referencing. Ecore models are allowed to reference objects in other models (including those with different metamodels). Presently, we only map one integer string to one model conforming to a single metamodel. In order to create references to other models, these models would need to exist and we would need to have knowledge of their existence. One possible solution would be to allow the user to specify a set of models that could be referenced and, during the mapping stage, use the integers to firstly select a target model, and then to select the specific element in that model to reference.

One final idea that we would like to pursue, is meeting with MDE practitioners and discussing their requirements for model generation. This would allow us to develop our toolset to be as usable and as useful to the community as possible.

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Digit distributions — What digits are really being used in hospitals?

Sarah Wiseman

UCL Interaction Centre, MPEB, Gower Street, London, WC1E 6BT
sarah.wiseman@cs.ucl.ac.uk

Abstract Typing studies have shown that common letters and bigrams have different error probabilities from less common ones. It is unknown as to whether the same effect can be seen when typing numbers. This paper presents an investigation into the distribution of digits being typed into hospital infusion pumps and shows that, as with letters in written English, there are common and uncommon characters being used. The number 0 is the most commonly typed digit, with 1 and 5 being the next most common. Digits such as 3, 4, 6, 7 and 8 are relatively rare. This information supports the study of the effect of number frequency on error rate. These results additionally provide more realistic data for use in infusions pump programming studies and also suggest design alterations and validations that are tailored to the numbers being entered on these devices with the aim of reducing error.

1 Motivation

The field of Human Computer Interaction (HCI) in the medical domain is a growing one. The number of cases of medical error caused by poor device design has spurred a large amount of investigation into this area. The aim of this work is to reduce blame on the medical worker when these medical errors occur, and highlight what work can be done to increase the quality of user centred design used by medical device manufacturers.

There are many examples of number entry error leading to serious medical errors. Be it from recording the height of a donor wrongly [1], calculating the wrong dosage amounts [5] or typing the wrong magnitude of number into an infusion pump [12]. A large amount of research for this field is completed in laboratory settings due to ethical constraints on testing within hospitals. It is imperative that lab based experiments mirror hospital settings as closely as possible if they are to be generalised in any way to a real life setting. This can range from creating realistic narratives within an experiment, to holding experiments in rooms set out to mimic the hospital environment. Currently, the data being used in the experiments has not been considered — that is the numbers being used in experiments in which participants are required to program devices or enter digits are being randomly generated [10, 14], thus ignoring any influence that digit frequency may play in our ability to enter numbers.

Early research into typing shows that the error rate associated with less frequent letters and letter combinations is different to that of more common instances. MacNeilage [8] notes that the least frequent letters (according to Baddeley's [2] analysis of printed English) are more likely to be typed in error or accidentally omitted than the more common ones. The opposite effect has been shown by Logan [7] in that when typists transcribe work from outside their domain of expertise, the newer and therefore less common words are more likely to be spelt correctly due to extra care and attention. It in unknown if a similar phenomenon exists with number entry.

There are examples of interfaces being designed with character frequency in mind outside of the medical domain. One example is the ".com" button that appears on certain touchscreen phones when the user is typing in the address bar. The ".com" URL suffix is the most common of all top level domains and designers of these interfaces have clearly taken this on board. Similarly, on many tills and financial calculators there will be a ".00" button to make entering round monetary amounts into the system quicker and easier. These shortcuts are based upon the frequency of digits and letters being entered in these particular settings. Context is important when designing these shortcuts: if the ".com" button appeared every time we wanted to send a text message, this would be considered a waste of screen space as, for that task, the occurrence of the characters in that order would not necessarily be significantly greater than other strings.

Domain specific knowledge is important in both the shortcut examples and the studies of typing. There are many examples of letter frequency analysis [2, 9] but the same attention has not been paid to number distribution. One famous example of digit analysis at this level is Benford's Law [3]. This law states that in naturally occurring numbers, the probability that the leading significant digit is 1 is close to 30% — greater than the expectation of around 11% if we assume all digits bar zero have an equal possibility of being the leading digit in a number. This trend continues with 2 being more likely than 3, which is in turn more likely than 4 and so on. This phenomena is noted in many datasets including stock market prices [6], fraud detection [4], country populations [11] to name a few. This distribution could be used to generate more realistic numbers for use within experiments however, it is unclear at the moment as to whether this law will apply to numbers used in hospitals for administering drugs.

Doctors' natural bias when choosing how to record blood pressure readings contributes towards the digit distribution literature. In a study by Wen et al. [13] it was shown that human preference has an effect upon which digit a blood pressure reading is likely to end in. 78% of the time the reading will end in 0, 5% will end in 5, 15% in an even digit and 2% of the time will end in an odd number other than 5. The volume and rate of drug infusions are ultimately also based upon human decision, be it as a result of a calculation or a set value used in certain treatments. These figures will therefore also be subject to human biases.

It can be seen from the literature that the frequency of a letter or number may have an effect upon the likelihood it will be typed in error. We cannot however, generalise these findings directly to the task of number entry so easily.

The processes involved in transcribing digits and numbers are not the same as typing letters and words. We are able to remember thousands of strings of letters in the form of words whereas the we may only be able to remember a few strings of digits in the form of, for example, a few phone numbers, our PIN and certain dates. Research therefore, needs to focus on the possible effects of digit frequency on error rate when typing numbers. For this to be possible, more needs to be known about the digit distributions occurring in the medical domain. In this study I present an analysis of numbers used when programming infusion pumps within a hospital with an aim to ascertain whether the digit distributions show that there are differences between the rate of occurrence of different digits.

2 Method

Information about what numbers are being entered into infusion pumps is not readily accessible. Hospitals do not keep records of dosage information separately to patient information, thus making the dosage data private information. The least intrusive method for collecting data on the numbers being entered into hospital infusion pumps therefore was to gather logs from machines currently in use. A total of 58 log files were collected from 32 pumps. The pumps had a numeric keypad to enter numbers with. On average, each log covered a period of 7 days, with the longest log lasting for 40 days and the shortest covering just a single day. The pumps used in this study were located in different wards throughout the hospital including oncology, surgery, paediatrics and midwifery.

The log files contained a large amount of information and recorded at an event level. An event could be anything from starting and stopping the machine, to an alarm going off if an infusion finished. At each stage, information about the rate of infusion, the volume of drug to be administered or "volume to be infused" (VTBI) and volume already infused was logged. For this study, the information needed included all numbers that a medical worker would have had to press to program the pump for a particular infusion. The pump being used required the rate and VTBI to be entered in order to start an infusion. The rate and VTBI were collected from the logs every time a new infusion was started. The rate is entered into the pump as the amount per hour to be infused. For example, a rate of 550 mL/hour would be entered simply as the number 550.

The log collected data to two decimal places. Trailing zeros after the decimal place were therefore ignored as they did not represent digits that a medical worker would have explicitly entered into the pump. The decimal point was also ignored if it was followed by zeros.

In the following text, 'number' refers to what was entered into the infusion pump, for example a VTBI of 500ml and 'digit' refers to the digits within that number, in the example case this is 5, 0 and 0.

3 Results

A total of 2442 numbers were gathered from the logs, 1051 of which included decimal places. This resulted in 6877 digits being collected.

Digit Distribution in the Hospital

Figure 1 shows that the most commonly used digit was 0, occurring over three times as often as the next most common digit, 1. Three digits in total occurred more frequently than expected: 0,1, and 5 (expected value based on each digit having an equal likelihood of being used). If 0 is treated as a special case and removed from the data set, due to its much higher frequency, and we then compare the other digits to one another, 2 and 9 also occur more frequently than the average distribution.

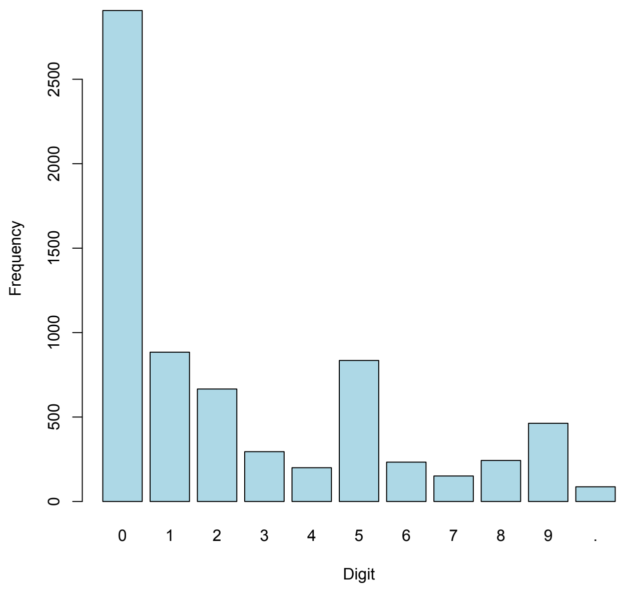

Figure 1: The frequency of all digits typed into infusion pumps across multiple hospital departments. This represents all data gathered for this study.

Figure 2 shows that the numbers initially adhere to a Benford distribution which is quickly disrupted by infrequent 3s and 4s and overly frequent 5s. This result is perhaps unsurprising as rate and VTBI are not strictly naturally occurring numbers, but come from a set of numbers chosen by humans whose tendency to round numbers to neat amounts does not mimic the random nature of naturally occurring numbers.

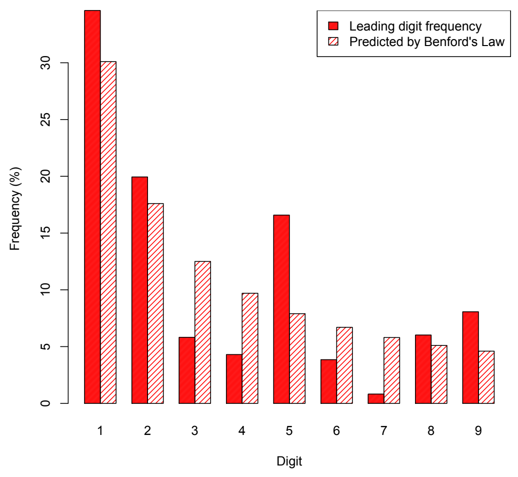

Figure 2: The frequency of all leading digits from pumps across multiple wards compared to the frequency as predicted by Benford's Law.

Digit Distribution in the Ward

There were notable differences in digit distribution between the wards of the hospital. Table 1 represents the distribution by ward, it is clear that all wards aside from surgery use a much larger number of 0s than other digits. We also see a trend of more 1s, 5s and 2s. On the surgical ward, the digit 9 is by far the most commonly used.

Figure 3 shows the variation in number length used on each ward. The numbers ranged in length between one and five characters long (both the number and decimal point). The most common number length for all wards was three, except for paediatrics with a most common length of two digits long. The difference in number length between paediatrics and the other wards may reflect the dosage sizes required for children compared to adults on the other wards. Below are the bar plots showing the distribution of digits.

4 Discussion

It can be seen that the digits used when programming infusion pumps are not evenly distributed. The abundance of 0s suggests that large numbers, rounded

Digit	Oncology		Midwifery		Surgery		Paediatrics	
0	2427	43.22%	192	40.42%	4	8%	39	30.95%
1	701	12.48%	77	16.21%	7	14%	28	22.22%
2	530	9.44%	60	12.63%	3	6%	20	15.87%
3	271	4.83%	3	0.63%	3	6%	1	0.79%
4	169	3.01%	3	0.63%	3	6%	0	0.0%
5	612	10.9%	104	21.89%	3	6%	30	23.81%
6	203	3.62%	20	4.21%	3	6%	2	1.59%
7	126	2.24%	0	0.0%	3	6%	1	0.79%
8	201	3.58%	6	1.26%	4	8%	2	1.59%
9	375	6.68%	10	2.11%	17	34%	3	2.38%

Table 1: Digit frequencies by ward. Table shows frequency of each digit and the percentage of total digits typed it accounts for.

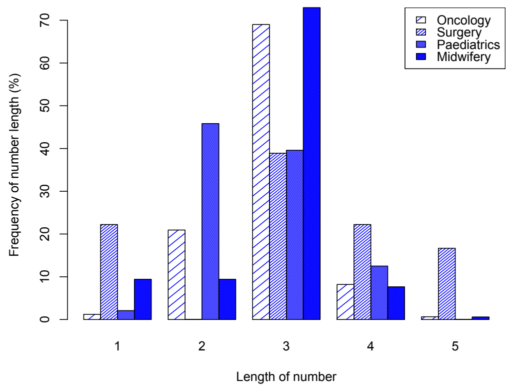

Figure 3: The length of numbers used on each ward.

to the nearest 10, 100 or 1000 are being used regularly. Of the 1420 numbers that had a 0 in the second place, 1418 of them were then completed with entirely 0s, only two then had any different digits following the first 0.

The high frequency of 1s, 2s and 5s is interesting and may be due to these digits being required to represent the natural quarter boundaries (25%, 50%, 75%, 100%). However, this does not account for the scarcity of the digit 7. Although as seen in Wen et al's study [13] we see more of a human bias towards digits 0-5 rather than 6-9 which would support the relative rarity of the digit 7. The discrepancy may also be due to a bias towards factors of 10 (1, 2 and 5).

The odd distribution of digits on the surgical ward could simply be caused by the relatively small sample for this ward compared to others. However, the prominence of the digit 9 could be due to the style of infusion used on this ward.

In some hospital departments, the liquid being infused has to be done so at a steady and specific rate for example in Oncology where a set amount of drug has been prescribed, whereas in other cases the infusion is used to simply get drugs into a patient as quickly as possible as may happen in an Intensive Treatment Unit. In this situation, it would be best to enter the highest possible number into the pump, which would mean typing the 9 key repeatedly. This could possibly explain the abundance of the digit 9 in the surgical ward.

There are multiple implications of these findings on future research. If more realistic numbers are to be used in future number entry experimentation, then they should not be generated using a Benford's Law distribution. New distribution patterns could be determined using the data gathered here. Future research may also look at the possibility of predicting an error depending upon the digits entered. If uncommon digits are entered, the system may want to question the user to ensure they have entered what they intended.

The results of this study have design implications too. The finding that that if a user has typed a 0, the remaining digits of the number are likely to be only 0s validates the design of infusion pumps that don't use a numeric keypad, but allow the user to increment each digit of a number separately. In these designs, each digit slot within a number defaults to 0, meaning entering of the number 12000 only requires the setting of two digits (1 and 2) whereas a number keypad would involve typing each of the digits (1, 2, 0, 0, and 0). It could be that devices using a numeric keypad could automatically complete a number with 0s when the user enters the first 0 as this is such a common occurrence.

This research shows that there are indeed vast differences in the distribution of digits being typed into infusion pumps on hospital wards. Research into how digit frequency affects error rate may therefore produce results relevant to the medical domain. This may also provide the basis for future device design and validation aimed at making the entry of numbers safer and less error prone.

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Part III

Extended Abstracts

Modeling Workloads, SLAs and their Violations in Cloud Computing

Rafidah Pakir Mohamad, Dimitris Kolovos, Richard Paige

Department of Computer Science,
University of York, UK
rafidah, dkolovos, paige {@cs.york.ac.uk}

Abstract Cloud computing is an evolution of data centres with a concept of utility computing. In utility computing, the service provider provides resources and infrastructure accessible to the customers and charges them in a pay-per-use base. Although this concept has been around for some time, it has become widely employed lately under the term "Cloud Computing". One of the challenges in the field of Cloud Computing is resource management, which includes capacity management with regard to SLAs (Service Level Agreements). This paper analyses the roadmap for achieving a solution to the problem of breaching server workload agreed in SLAs between service providers and customers by utilising domain specific modelling and model analysis techniques.

1 Introduction

Resource management in any computing environment is very important to avoid failure and maintain the performance of applications that run on it. In the cloud computing paradigm, infinite resources are possible in principle by creating virtual machines on top of physical machines. Cloud computing service providers need to allocate sufficient physical resources by performing capacity management based on workload [11]. This paper presents a literature survey with the aim to develop a resource and capacity management model for the service provider to perform costing and to estimate the resources required based on the actual workload with regard to SLAs using Domain Specific Modelling and model analysis techniques.

2 Background

Cloud computing technology is the latest paradigm in computing where services are accessed through the internet (cloud) by sharing hardware, software and/or applications remotely. Data Centres are dedicated places which contain servers and facilities for computing and most of these have cooling facilities and raised floors. Cloud Computing enables anyone to own their virtual data centre with pools of virtualised resources in a pay-per-use model. For primarily security-related reasons, some organisations prefer to own their own private cloud rather than using public clouds. This private cloud can be hosted in their own data centre or a third-party service provider based on SLAs. The existing conventional data centre is mostly utilised by implementing cloud computing with supported by virtualisation technology. However, managing actual physical resources that support these scalable virtualised resources is a significant challenge [5].

Resource and capacity management at the data centre owned by the service providers are very crucial and complex in order to maintain the Quality of Service (QoS) stated on the SLAs between both parties. Resources are allocated based on predicted and agreed workload patterns and resource demand stated in SLAs. However, the actual resource demand needed by the customers to support their businesses might differ from what was stated in the SLAs. As a cloud computing service provider, it is essential to provide resource demand to the customer with support for auto scaling and recalculating the costing when the initial SLAs are violated. The computation for the cost for pay-per-use model in cloud computing is different from other utilities bill calculation. Electricity is measured by Watts used, water and gas by volume. In Infrastructure as Service (IaaS), cloud customers are charged based on instances(virtual machines) used per unit of time. Furthermore, charges would differ based on instances specification because the instances will use physical resources in service provider's data centre based on its specifications such as CPU and storage size.

2.1 Data Centres

A data centre is a place which houses servers and facilities for computing in a special area with access controls and cooling facilities. There are four types of tiers of data centres based on selected criteria explained in TIA-942 [1]. As per TIA-942, the evolution of data centres was started with the creation of first computer UNIVAC in 1940s. Later in 1960s, IBM introduced its mainframe computer. The first distributed computing started with airline reservation system which went into full operation with two powerful IBM mainframes, sixteen data storage devises and 1,000 terminals in 1965 [6]. The mainframes were very powerful machines and also were very expensive to operate and to maintain. The next generation of computing involved microcomputers, which initially were focused on office usage. Microcomputers replaced terminals which were connected to mainframes. Then the technology moved on to grid computing, commodity clusters, virtualised clusters, and more recently to cloud computing [9]. Cluster computing focuses on traditional non-service applications, whereas clouds are service oriented and grid computing features are utilised by both technologies, but still there are differences between cloud and grid [9].

Cloud Computing The term cloud refers to hardware, software and/or applications remotely accessed via the internet under the principles of utility computing. The National Institute of Standards and Technology provides the following definition: *"Cloud Computing is a model for enabling convenient, on-demand network access to a shared pool of configurable computing resources (e.g., networks,* *servers, storage, applications, and services) that can be rapidly provisioned and released with minimal management effort or service provider interaction".* Software as a Services (SaaS), Platform as a Service (PaaS), Infrastructure as a Service (IaaS) are the three types of services provided by cloud computing [3, 20]. Utility computing [16] started receiving wide attention under the new name of *cloud computing* - when Amazon[1] introduced EC2 (Elastic Compute Cloud) in 2006. Today, with facility provided by Amazon, anyone can own a virtual datacenter at a minimum cost. However, it is a big challenge for the service providers to manage and provide physical resources to support in principle infinite virtual machines.

Server Utilization Studies show that server utilization in real world data centre is estimated between 5% and 20% [3, 4]. Furthermore, an observation for 5000 servers over 6 months showed that the servers are rarely completely idle and these servers operate between 10% to 50% of their maximum utilisation level [14]. This shows that servers in real data centres are under-utilised. However, these under-utilised servers still consume a lot of electricity to stay on [2, 18]. Additional energy is also needed for cooling the heat produced by the underutilize servers. Managing a big data centre is very costly and cloud computing service provider need to take all necessary actions to achieve cost-efficiency in data centre. Virtualisation and server consolidation have been proposed as solutions for maximising server utilisation [18]. The number of physical servers can be reduced, by having several virtual machines running on a single server. Intelligent resource management will reduce power consumption in data centres by having fewer servers and as such requiring less cooling.

Resource Management Resources in a data centre can be separated into physical and virtual resources. Virtual resources are completely isolated server installations within a normal physical server which work like real standalone servers while in reality they still share physical resources of the hosting server. The main advantage of virtual machine is that it can be migrated to another physical server and mirrored as much as needed for multi-processing. Virtual machines are typically called *instances*. To optimise physical server utilisation, virtual machines are allocated to physical servers based on the workload pattern stated in SLAs. Even though virtual machines are scalable, they need to be managed properly to minimise failure on physical machine [11]. On the other hand, customer's business demands might violate SLAs workload pattern and eventually increase the cost of operation for the service provider. The service provider needs to charge the customer and in this scenario a penalty calculation process is needed. Simultaneously, the service provider will have to find the actual resource demand based on real workload pattern by their customer for capacity management. We anticipate that capturing resource and capacity management models with Model Driven Engineering techniques will facilitate more intelligent

[1] http://aws.amazon.com/releasenotes/Amazon-EC2/532

resource and capacity management and enable more accurate costing. Kalman-filtering [12] is of the methods used to predict the need for additional resource demand before failure occurs in a server due to huge workload. Besides that, open source tools such as Ganglia [15] are widely used for resource monitoring and cloud federation [10] is one of the techniques that address the the issue of limited resources.

2.2 Model-Driven Engineering(MDE)

The use of models to capture information at a high level of abstraction reduces the complexity of understanding a domain or field of interest [17]. MDE is a well known approach in software engineering which advocates constructing rigorous models – often using Domain Specific Modelling Languages(DSMLs), and managing these models using automated tools such as transformation, analysis and validation engines, and model-to-text generators [17]. Domain Specific Modelling is principally known as the idea of creating models for a specific domain with a DSML suitable for that domain as an area of interest [19]. A DSML consist of five fundamental components [7]: abstract syntax, concrete syntax, syntactic mapping, semantic domain and semantic mapping. These components are used to formally represent a specific set of structure, behaviour and requirement features of a particular domain in the form of a meta-model which is also called *modelware* [8]. MDE focuses on exploiting as well as creating domain-specific models that capture information about the problem at hand at a suitable level of abstraction, instead of focusing on algorithmic or low-level computing concepts. MDE relies on automated model management and in particular on automated support for model transformation. Model transformation is divided into model-to-model (M2M), and model-to-text (M2T) transformation. In the former, input models are transformed to other models – possibly expressed in a different modelling language, and in the latter, models are transformed to textual artefacts such as code, documentation and human-readable reports.

3 Proposed work

Epsilon [13] is a platform for building consistent and interoperable task-specific languages for model management tasks such as model transformation, code generation, model comparison, merging, refactoring and validation [13]. In this work, Epsilon will be used to develop resource management models and then analyse and transform these models to other representations of interest. Test data for analysis will be attained by setting-up a cloud environment using Eucalyptus[2] private cloud. The server workloads will be observed by workload monitoring tools such as Ganglia [15]. Workloads will be simulated using scripts to generate workload patterns as stated in the SLAs case study. Again, workload simulation will be used to violate the expected patterns. Initially, resource monitoring data

[2] http://www.eucalyptus.com/

will be captured in the form of domain specific models and reports will be produced by transforming these model to text, but later on more types of analysis and model transformation are envisioned.

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Using Domain-Specific Modelling Languages for Requirements Engineering in Agile Software Development

Masoumeh Taromirad

Department of Computer Science, University of York, UK
mtaromi@cs.york.ac.uk

Abstract In this short paper we argue for greater integration of Agile Software Development techniques with techniques for Requirements Engineering; we argue that this is a promising development style that may allow enhanced delivery of software solutions even in the face of rapidly changing requirements. We also argue for the use of Domain-Specific Modelling Languages as a promising mechanism for addressing the perceived incompatibilities between Requirements Engineering and Agile Software Development.

1 Introduction

Change is an accepted fact of software development projects; during a project's lifecycle, its business context, system requirements, project schedule, development artefacts and even the development process may change [1]. In addition to this, reducing the development time to reduce time-to-value plays an essential role in being successful in the competitive business world [2]. On the other hand, recent studies show that eliciting, specifying and managing requirements is still a considerable challenge in developing a software system; errors in requirements lead to consistent project failure rate (about 50%) [3, 4]. Therefore, introducing appropriate practices and techniques for identification and specification of requirements that consider *change* and *short time-to-delivery* as critical concerns is essential.

Agile Software Development is considered to be an appropriate development style to effectively deal with changes during the project life cycle [5]. In this paper, we focus on Requirements Engineering (RE) practices in the context of agile development, considering current challenges in order to improve software development. We suggest to employ Domain-Specific Modeling (DSM) for requirements engineering, which may provide better understanding, validation & verification, and faster development.

In the rest of the paper, we are going to introduce Agile Software Development (Section 2), Requirements Engineering (Section 3) and Domain-Specific Modeling (Section 4) and briefly talk about their challenges and interactions. Finally, in Section 5, the problem and the proposed idea will be discussed in more detail.

2 Agile Software Development

Agile Software Development, formally introduced in 2001, is basically specified by Agile Manifesto [6] and Agile Principles [7], which contain four core values of agile development and 12 detailed statements supporting the core values. Agile Manifesto and Principles have been written by a group of practitioners of development methodologies dealing with modern software development needs and challenges: rapid changes and faster time-to-value. So, at the high-level, agile style of development directly addresses the problems of rapid changes and aims to effectively respond to changes within the project time frame and budget [1], which consequently leads to better time-to-delivery of software solutions.

Accordingly, in this short paper, we consider agile development as a way of thinking about software development taking into account two main concerns of the Agile Manifesto and Agile Principles (change and time-to-value) [8]. As well, there are some well-known agile development methodologies (XP, Scrum, ASD, DSDM, dX, Crystal Clear, and FDD). Studying their definitions and experimental reports will help in achieving better understanding of agile development and its current practices.

Although agile development initially targeted small projects (regarding project scope and team size) and experimental reports confirm this [9], agility is a concept that should be taken into account in any software development project (even large and critical projects) in order to maintain successful and satisfy customers' expectations [10]. Hence, these may arise the need to revise current assumptions and practices or introduce new ones for using agile in large and critical projects.

Communication complexity, which grows exponentially as project becomes larger, and complex and large solution domains are two aspects of the large projects which have not been properly addressed by Agile Manifesto or Agile Principles. In such cases, effective documentation, at least as a complementary practice, would be helpful to overcome these issues. This is because it provides knowledge transfer and is used to align common goals and achieve greater understanding of the problem and the solution [11, 12]. In spite of the general misunderstanding about agile development, documentation (requirements, design, and code documents) should be considered very carefully in agile development. Because lack of enough documentation might cause long-term problems for agile development when software needs to be maintained in the long run [13]. So, light-but-sufficient documentation to produce effective documents for requirements, design, and code is important, specially in large projects, to achieve the overall goal of agile development such as producing working software [14]. Consequently, in this text, we have focused on documentation in agile development specifically requirements documentation regarding the critical role of requirements in software development. The next section will introduce Requirements Engineering and existing difficulties.

3 Requirements Engineering

Requirements Engineering (RE) is the process by which the requirements are determined and generally includes requirements understanding, elicitation, evaluation, specification and documentation, and consolidation [15], which may be performed in different ways. Any project needs some forms of RE activities whatever its type, size, the way used for handling these activities, and how much each activity should be covered [16]. But, there are limited practical RE practices in terms of efforts, technologies, and supporting tools which subsequently defect the software development projects [17].

A RE process deals with requirements at different levels of abstraction: from early requirements to low-level technical ones. It usually begins with identifying high-level user-oriented requirements including business goals and user requirements, normally explained in natural languages, and ends in a Requirements Document (RD) containing lower level specification of the system (system requirements), described by a specification language to provide effective communication between users and developers about the problem and the solution (common understanding) [15]. RD, the formal output of RE activities which will be handed to developers, is the baseline for later activities (e.g. planning, design, test, and evaluation) and downstream artefacts [4, 13]. Thus, in this short paper, we focus on system requirements and RD which also comply with our concern about agile development.

Although not well-defined requirements and conflicting ideas for a proposed system are some of the difficulties in RE, requirements specification practices and techniques are more challenging. Requirements are usually explained in the problem domain terms while software needs to be explained in the software terms. So, producing a practical requirements specification document providing a common understanding to all stakeholders and easy to use, is critical. In addition, the requirements document should not be too big and complex, since it would be outdated during the project, and should not be far from executable code in order to be easily verified and implemented [4]. Existing RE processes, practices, techniques, and supporting tools are also too heavyweight and are not well-defined to integrate into coherent development processes, such as integrating with other development models and producing downstream artefacts from RE artefacts. These difficulties and problems still exist and somehow are more sever in the context of agile development. On the other hand, an agile style of development could help in addressing some of the difficulties of RE, such as dealing with conflicting ideas about the system. This is becuase it implements requirements in short iterations resulting in quick feedback to identify conflicts, incompleteness, errors, etc [13].

4 Domain-Specific Modeling

Domain-Specific Modeling (DSM) is a model driven development approach [18] which mainly aims at raising the level of abstraction, by using domain-specific modeling languages for modeling, and fully automatic generation of final output. DSM has main three parts:

1. Domain-Specific Modeling Language (DSML): A modeling language dedicated to the specific problem domain which closely maps to the problem domain concepts
2. Code Generator: A domain-specific automatic code generator which generate final output in the target programming language or any other format
3. Framework Code: Common areas of all application in the domain

By using DSM, models, specified with domain problem terms, should be easier to understand, read, and remember, and they are more usable for the requirements specification and documentation. Moreover, full code generation provides quick response and feedback and changes are faster and easier to make at a higher level of abstraction (any changes are made within domain concepts not in generated codes).

DSMs are defined to focus on narrow problem domain and narrow solution domain to raise the level of abstraction. So, applying DSM in larger projects would arise questions about scalability and change management such as techniques to deal with various changes in different parts and their effects on the existing codes.

5 Problem and Future Work

According to the previous sections, *agile* is a suitable development style to address some of main issues in modern software development projects. It effectively deals with changes during project life cycle and supports customers' business goals in a better way (competitive time-to-value). On the other hand, difficulties with RE activities hinder projects' success remarkably. To improve software development, agility should be considered as the high-level characteristic of the development process, addressing changes and time-to-delivery, while software development still needs more effective and practical RE practices regarding their current weaknesses.

As explained before, there are some challenges about using agile in large and critical projects. One of those is about sufficient documentation. Moreover, we explained that considering RD is very important due to the importance of requirements in the project and their changing nature. In Section 3, we showed that there are some obstacles in RE and existing RE practices and techniques are not suitable for agile development. This is because, traditionally, RE is a heavy and documentation-oriented process while agile development processes are light, in comparison with RE processes, and emphasize on face-to-face communication [13]. But, as mentioned in Section 3, agile development style would be useful to overcome some of the problems of RE. So, introducing appropriate requirement specification practices and techniques compatible with agile style of development is very challenging regarding current problems and shortcomings of RE which would be more serious in integration with agile concerns.

In this paper, we focus on practices and techniques for developing RD in the context of agile development and so we more emphasize on *system requirements* as they are more similar to the initial definition of requirements in existing agile development methodologies and, more important, they are closer to the solution domain and working software.

Requirements Specification and Documentation play an essential role in RE. Since their immediate output, Requirements Document (RD), covers the requirements (the main concerns of any project) and will be the first output of projects which shapes and affects other activities and artefacts along the development process. Regarding the current problem and existing characteristics for RD [4, 13, 15], an effective and practical RD should

- be understandable to all stakeholders while supporting software development.
- support inevitable changes in requirements and consequents changes/updates on existing artefacts.
- be light-but-sufficiet in order to be updated during the project life cycle.
- be close to the working software.
- support traditional RD characteristics and features such as traceability, smoothness, and seamlessness.

As mentioned in Section 2.3, DSM and Domain-Specific Modelling Languages aim to address many of the limitations of requirements documents, and some of the concerns of RE in general. At the same time, DSMLs appear to indirectly consider (or, at least, do not contradict) key agile concerns of managing change and time-to-delivery. Thus, a promising idea for future work is to consider DSMLs and DSM as an effective approach for requirements specification in the context of agile development. Modeling, especially graphical modeling carried out using DSMLs and in an iterative and incremental style may be a suitable approach for specifying requirements, and it will offer greater potential for *analysis, validation* and *downstream activities* through using DSMLs and their automated tools for describing and manipulating models. In particular, we envision using DSMLs and automated tools (such as Epsilon[1]) for automatic generation of consequent artefacts (e.g., architectural models, design models), impact analysis, change propagation, and production of better documentation.

Therefore, the proposed idea is to use DSML to introduced effective and practical RE practices for requirements specification, in a development process respecting agility in software development.

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Agent-Based Modelling and Simulation of the NF-κB Intracellular Signalling Pathway

Richard Alun Williams

Department of Computer Science and York Centre for Complex Systems Analysis, University of York, UK

Introduction

Cells receive information from their environment through extracellular signals interacting with a class of proteins located on their surfaces that are known as receptors. Signal transduction[1] involves the binding of these extracellular signalling molecules to the cell-surface receptors and the triggering of a cascade of intracellular signalling events inside the cell. This intracellular signalling forms part of a complex system of communication that acts to regulate cell activity and action relative to changes in the external environment [6]. The ability of cells to perceive and correctly respond to their environment is of particular importance for the immune system and the combating of infection. Gene activations and alterations to metabolism are examples of cellular responses to extracellular stimulation that require signal transduction. Errors in the processing of extracellular signals are responsible for the onset of many cancers and autoimmune diseases. The Nuclear Factor-κB (NF-κB) signalling pathway[2] is one of the key signal transduction pathways involved in control and regulation of the immune system [5]. It is hoped that through an increased understanding of cell signalling pathways, such as NF-κB, diseases may be treated more effectively, or even eradicated entirely through prevention of pathway dysregulation.

The systems that biologists wish to analyse and model show an increasing number of interdependencies and relationships, meaning that traditional modelling tools are no longer as appropriate as they once were. Computational biologists and computer scientists are beginning to take a more realistic view of these systems through recent advances in computational modelling techniques, such as agent-based modelling and simulation. Furthermore, computational power is advancing rapidly, providing the ability to run large-scale computer simulations of biological systems, which was not plausible in the last century [7]. We believe that computational modelling and simulation of the NF-κB signalling pathway will complement wet-lab experimental approaches, and will facilitate a more comprehensive understanding of this example of a complex biological system.

[1] Signal transduction is the process by which an extracellular stimuli (signalling molecule) activates a cell membrane receptor, which in turn initiates a cascade of internal biochemical reactions to generate a cell-level response.

[2] A signalling pathway is a network of intracellular biochemical reactions that link the receiving of an extracellular signal at the cell membrane to the cell response at the molecular level.

Project Objectives

The overall objective of this PhD research project is to use an agent-based modelling approach to further our understanding of the intracellular NF-κB signalling pathway. This incredibly general aim will be achieved through a principled approach to design and development of the computational model, based upon the iterative nature of the CoSMoS framework [1]. In particular we will be developing three fully working iterations of the computational model, which will incorporate increasing levels of detail regarding the biological knowledge that they are based upon. The first version will replicate the functionality of an existing agent-based model developed in Matlab [9], but will be developed using the FLAME simulation framework[3] to allow large-scale simulations run over high-performance clusters. The second version will incorporate increased intracellular signalling components, and will be scaled up to much larger numbers of agents. The scope of the third and final version is yet to be confirmed, and will be decided, subject to time constraints later on in the PhD; we currently have two options which relate to (i) development of a corresponding model using another development framework, such as Java and MASON[4], to investigate any differences in simulation results across platforms; or (ii) continue with the FLAME model and further augment for massively parallel simulations, using numbers of agents within the order of those found in biology, to investigate whether an increase in resolution (with respect to numbers of agents) leads to enhanced predictive capacity of computational models.

Preliminary Results

We have been given access to the code of an NF-κB model that was written in 2004 by Mark Pogson and Simon Coakley and served as a *Proof of Concept* (POC) during the development of the FLAME agent-based simulation framework [4]. Simon Coakley developed FLAME for his PhD [3], which was submitted in 2007, therefore this NF-κB model developed in 2004 was very much a *work in progress* model. We initially encountered a large number of issues in getting the FLAME framework to parse and compile the NF-κB POC model. The code (XML and C) was updated to reflect the latest syntax for the current version (0.16.2) of the parser which was stored on ccpforge and maintained by the EURACE project[5]. Additional *teething problems* were encountered regarding software compatibility and hardware drivers, which have been resolved on a case-by-case basis, and we have recently successfully run our first set of initial simulations using the POC.

The reverse engineering exercise through a systematic code walkthrough and generation of UML diagrams is virtually complete, with just the UML state

[3] www.flame.ac.uk
[4] http://cs.gmu.edu/ eclab/projects/mason/
[5] The EURACE Project is a FP6 European Project involving a collaboration of researchers from various backgrounds (computer scientists and economists) to work together to derive a simulated model of the European economy.

diagram outstanding. The time-course data generated through the initial simulations has also furthered our understanding of the POC model, and in particular has highlighted that there is no biochemical dissociation reaction of NF-κB from it's inhibitor IκBα (termed the NF-κB-IκBα complex), degradation of IκBα, or indeed transcription[6] and translation[7] of the inhibitor IκBα. Analysis of the code has highlighted that the POC model does have some very elegant features regarding the 3D spatial environment of the cell, and the 3D Brownian motion dynamics of individual NF-κB and IκBα molecules. We propose to harness this functionality in our future agent-based models.

Experimental data for use within this PhD research programme has been provided by the Qwarnstrom lab, within the Department of Cardiovascular Science, at the University of Sheffield Medical School. We have been given access to some of the experimental data generated by single-cell analysis of NF-κB-IκBα dynamics. This data relates to the degradation of inhibitor of IκBα over time, which is the key biochemical reaction for activation of the signalling pathway. The wet-lab experimentation observes the degradation of IκBα through use of fluorescent protein tags which are linked to the inhibitor; the decrease in fluorescence directly correlates to the degradation of the IκBα inhibitor protein, and thus activiation of NF-κB. Of particular interest is the data from: Yang et al, who in 2001 examined IL-1[8] mediated IκBα degradation [11]; Yang et al, who in 2003 identified the RelA[9] control of IκBα phosphorylation [12]; and Zhang et al, who looked at the novel interleukin1 receptor (IL-1R) co-receptor TILRR[10] within amplification of NF-κB activation [13].

A number of statistical techniques have been used on the data to understand the biological domain related to this project. Linear statistical analysis advised that the distribution of the data closely resembled a negative binomial distribution, and therefore non-parametric techniques are required to summarise the data. Box-whisker diagrams were used to visually compare the differences in fluorescence between control and IL-1 stimulated experiments with various components (e.g. IκBα, IκBα-RelA, and IκBα-RelA-p50). The addition of RelA or RelA-p50 showed a marked decrease in fluorescence, signifying a decrease in IκBα.

[6] Transcription is the first step of the process known as gene expression and is where a DNA sequence is read and a corresponding sequence of RNA is produced.

[7] Translation is the process were the RNA sequence produced during transcription is read and a corresponding sequence of amino acids is produced, thus resulting in a protein being generated from the initial DNA sequence.

[8] Interleukin1 (IL-1) is a cytokine (chemical messenger developed by a cell to communicate with other cells) and one of the key extracellular stimuli which activates the NF-κB signalling pathway.

[9] The term NF-κB actually relates to a family of five different proteins (RelA, RelB, cRel, p50 and p52), with RelA being the most prevalent.

[10] A novel IL-1R co-receptor has recently been discovered and has been named 'Toll and Interleukin like Receptor Regulator' (TILRR), which amplifies IL-1 induced activation of the NF-κB signalling pathway.

Multivariate statistical techniques were also used to analyse the data. Preliminary analysis used scatterplot matrix and hierarchical clustering, with more detailed analysis being performed using principal component analysis. The fluorescence data was consistently shown to consist of three clusters with regards to the fluorescence at time 0min. We believe that the large variability within the observations is consistent with a negative binomial distribution and is due to the stochasticity inherent to biological populations (from cells to organisms). We also believe that a certain degree of variability may be due to the overexpression of fluorescent protein constructs used with the single-cell analysis work, e.g. the work of Carlotti et al [2] and Yang et al [11, 12] have optimal functional levels of RelA at 7-fold endogenous level and of IκBα at 3.5-fold endogenous level. We therefore propose that in the short term, data used for calibration of the resulting NF-κB FLAME Model and subsequent validation and simulation should be confined to that which has an initial fluorescence less than 1.5 units. We also believe that in order to get rational results, each cell needs to form it's own control (which was also the approach taken for the Pogson et al model [10]), which would eliminate the wide variations observed when averaging dynamics over multiple cells, and by implication simulations. Furthermore, it is believed that such an approach would yield more consistent results as cell time-course dynamics would be expressed as a percentage of initial fluorescence for each cell.

Future Work

Areas of future work within the immediate timeline are to complete the multivariate statistical analysis for the single-cell data that we have been provided with, namely the Zhang et al [13] data regarding the TILRR co-receptor. Following this data analysis exercise, we will develop a domain model to formally document which aspects of the biology of the NF-κB signalling pathway we will look at. We will then reverse engineer the Pogson model [8, 9], which has been developed in Matlab, and replicate this functionality within the platform model that will correspond to our NF-κB FLAME model. This work, will then be completed through development of the associated simulation platform, calibration against the subset of wet-lab single-cell data highlighted above, and validated and verified through *in silico* experimentation to generate a baseline simulator which may be used in the future within a predictive capacity. We would like to stress here that *in silico* models should not be considered as definitive descriptions of networks within the cell, but should instead be considered as one approach that allows us to understand the capabilities of complex systems, and devise wet-lab experiments to test these capabilities.

It is our intent to use the previously generated single-cell analysis data from Yang et al [11, 12] and Zhang et al [13], and re-interpret in the context of agent-based modelling and *in silico* experimentation. We hope that this approach will further our understanding of the NF-κB signalling pathway, and potentially make an incremental step towards understanding and controlling the transcription factors role in inflammatory disease.

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Part IV

Poster Abstracts

Dirt Spot Sweeping Random Strategy

Mian Asbat Ahmad and Manuel Oriol

Department of Computer Science
University of York, UK

In this poster, an enhanced and improved form of automated random testing called Dirt Spot Sweeping Random (DSSR) strategy is introduced. DSSR is a new strategy that not only combines ordinary random strategy and random plus strategy to achieve their combined benefits but additionally sweeps the dirt spots in the program code for faults. It is based on two intuitions, first is that values from the boundaries of equivalence partition have interesting values and using these values in isolation can locate many faults which can produce high impact on test results while second is that faults reside in block and strip pattern of the program and when a fault is found it is most likely that it lies on this pattern therefore using neighbour values of the fault finding value can reveal more faults quickly which will consequently increase the test performance. DSSR is implemented in an open source automated random testing tool called York Extensible Testing Infrastructure (YETI). After implementation several experiments were performed on two groups of classes. First group contain error seeded programs written specifically for performance evaluation of DSSR while the second group contain classes from Java Development Toolkit (JDK). Experimental results of both groups showed that DSSR perform up to 30 % better than pure random testing.

Model-Driven Engineering for Specifying, Analysing and Monitoring Cloud Computing SLAs

Fatima Alkandari, Richard F. Paige, Simon Poulding

Department of Computer Science,
University of York, UK
{fatma, paige, smp}@cs.york.ac.uk

Cloud computing is a paradigm for the development and deployment of service-based applications on shared infrastructure. It focuses on delivering IT resources (hardware and software) on-demand, and on a pay-as-you-go basis [3, 8]. Cloud computing has different deployment models: public clouds, private clouds and hybrid clouds [5]. There are many commercial offerings that differ in technology maturity level, service level and system architecture, as well as service-level agreements and other features. One key challenge associated with cloud computing is *contracting for the cloud*: how are cloud service-level agreements (SLAs) – which are effectively contracts between cloud consumer and provider – best defined, negotiated, monitored and managed? [1, 2]

Model Driven Engineering (MDE) is an approach to software engineering that utilizes models as first-class artifacts. The aim of using models is to raise the level of abstraction and increase the potential for automation in the software development process [4]. Models may be constructed using general modelling languages (UML) or Domain Specific Languages (DSLs), which have specialist concepts and logic for capturing domain knowledge. DSLs may be easier to use for domain experts to understand, validate and modify programs [6, 7].

My research investigates the use of MDE for enabling cloud computing. The use of MDE in cloud computing may help to provide easier development of cloud-based applications, in particular making it easier to take into account concerns of different stakeholders. Specifically, I am investigating the use of MDE principles for capturing and analysing cloud SLAs, so that inconsistencies, incompleteness, inaccuracies, and desirable properties in SLAs can be analysed and checked before they are deployed on a cloud platform. Additionally, I am investigating ways of making cloud SLAs easier to write and use by domain experts (who may not be cloud computing experts), and to make it easier for non-experts to take decisions by comparing different cloud SLAs. For example, when two SLA providers promise a specific up-time and one of the SLA providers include the scheduled maintenance time while other provider excludes it, I would like to be able to notify consumers of this in a domain-specific and contextually relevant way (i.e., in their own vocabulary, and in terms of the cloud SLA, not the infrastructure that triggered the violation).

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Data mining of audiology data for procuring hearing aids and tinnitus maskers

Muhammad Naveed Anwar and Michael Philip Oakes

Department of Computing, Engineering & Technology, University of Sunderland, St. Peters Way, Sunderland SR6 0DD, England
{Naveed.Anwar,Michael.Oakes}@sunderland.ac.uk

This poster describes the data mining of a large set of patient records from the hearing aid clinic at James Cook University Hospital in Middlesbrough, UK. As is typical of medical data in general, these audiology records are heterogeneous, containing the following three different types of data:

– Audiograms (graphs of hearing ability at different frequencies)

– Structured tabular data (such as gender, date of birth and diagnosis)

– Unstructured text (specific observations made about each patient in a free text comments field)

There are two research questions for this research:

– To find factors influencing the selection of ITE (in the ear) opposed to BTE (behind the ear) hearing aids. James Cook University Hospital is unique in that it supplies ITE hearing aids on the National Health Service

– Among those patients diagnosed with tinnitus (ringing in the ear), to find the factors influencing the decision whether or not to prescribe a tinnitus masker (a gentle sound source, worn like a hearing aid, designed to drown out tinnitus)

A range of statistical techniques, including clustering, the chi-squared test, principal component analysis, a Naïve Bayesian approach and multiple logistic regression have been used on this set of audiology data. These enabled us to discover candidate variables (including individual words in the free text fields) which may influence the dichotomies identified above. The findings of this research are compared with the experience of the professional audiologist at James Cook Hospital. The candidate variables are combined using both a Naïve Bayesian approach and multiple logistic regression to produce decision support systems, where unseen patient records are presented to the system, and the relative probability that the patient should be fitted with an ITE as opposed to a BTE aid or a tinnitus masker as opposed to no tinnitus masker will be returned. The advantage of these techniques for the combination of evidence is that it is easy to see which variables contributed to the final decision, facilitating the production of explanation facilities for decision support systems to be used in the real world.

Dynamics and Chaos for Worst Case Execution Time Analysis

David Griffin and Alan Burns

University of York

One of the problems to overcome in Worst Case Execution Time (WCET) analysis is that the complexity of modern computer systems means that a small change in the initial conditions of the system can lead to a large change in the execution time of the system. The leads to static analysis techniques which attempt to explore the entire state space of the system, thus becoming intractable, or measured analysis techniques which struggle to give absolute guarantees.

An alternative method to existing techniques is to directly examine the unpredicatabilitiy within the system. Recent advances in mathematics allow the use of dynamical systems to describe the WCET problem. In turn, the use of dynamical systems enables the use of chaos theory, a branch of mathematics specialised to the analysis of a class of systems which have the property that two initial states which are similar diverge significantly with the progression of time. As chaos theory is already used in safety critical systems, it provides a valid set of techniques to apply to the WCET problem.

This work introduces a dynamical system which describes the WCET problem, and presents both theoretical results and empirical evidence that some common computer components, such as a cache, may behave chaotically. Applications of the use of chaos theory to the WCET problem are introduced, to either identify and limit chaotic behaviour or to embrace chaos and gain confidence bounds that the system will not exceed a certain execution time.

Self-repairing Robot Swarms

Alan G. Millard and Jon Timmis

Department of Computer Science
The University of York, UK

It has long been assumed that swarm systems are robust, in the sense that the failure of individual robots will have little detrimental effect on a swarm's overall collective behaviour. However, a recent study by Bjerknes [1] has shown that this is not always the case. The task of emergent beacon taxis was used as a case study, which requires an aggregated swarm of homogeneous autonomous robots, with limited sensing abilities, to traverse an empty arena towards an infrared beacon. The failure mode found to have the most damaging effect upon the swarm's emergent beacon taxis behaviour, was motor failure. This fault renders a robot stationary, but does not affect its other electronic systems, allowing the robot to continue to contribute to the emergent behaviour of aggregation. When the swarm is required to physically translate its position during beacon taxis, a robot experiencing motor failure will *anchor* the swarm, impeding (or at worst, preventing) the swarm's progress towards the beacon [2].

In our previous work [3] we investigated whether the anchoring issues observed by Bjerknes [1] could be alleviated through the development of self-repair mechanisms that enable a swarm to take some form of corrective action in response to the failure of individual robots[1]. Extending the work of Ismail et al. [4], an equivalent failure mode was considered, whereby a fault in a robot's power unit causes a sudden loss of stored energy. The amount of remaining energy is sufficient to allow for simple signalling, but insufficient to power the robot's motors, resulting in a loss of mobility. A robot experiencing this type of failure may be 'repaired' by having its battery recharged by functional robots. The specialised hardware required to implement such self-repair mechanisms has only recently become available, in the form of the Symbricator robot — a new robotic platform designed for the SYMBRION/REPLICATOR projects [5] — which facilitates the sharing of energy between physically connected robots.

We have developed a novel decentralised self-repair algorithm for the Symbricator robotic platform, inspired by the emergent aggregation behaviour of cellular slime moulds, using software available from the Player/Stage Project [6]. A simulated swarm of robots executing this algorithm is observed to self-organise to form a physically connected ad hoc robotic 'organism' around a faulty robot, which serves as a conduit for energy transfer. The swarm's collective energy is then evenly redistributed throughout the organism, and once the faulty robot has been repaired, the robots simply disperse to resume beacon taxis. Experimental results have shown that our algorithm enables a simulated swarm of ten robots to recover from up to five simultaneously injected faults, thus affording the swarm a high degree of fault-tolerance [3].

[1] Abandoning faulty robots is not a scalable strategy in the long term.

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Developing a Simulation and Hardware for a Robot Swarm Using Sound to Communicate

Jennifer Owen

Department of Computer Science, University of York, York, UK
jowen@cs.york.ac.uk

In our research we are interested in getting a swarm of E-Puck [1] robots to communicate and cooperate with each other using audio messages. To perform these experiments we need a simulation of our robot swarm, as well as a hardware extension to the E-Pucks that is capable of detecting an audio signal and determining its frequency and the direction it came from. Robotic swarm experiments are enormously time consuming, so a simulation is needed to predict which experimental parameters are worth testing on a real robotic swarm.

1 Simulation

Our simulation was made following the CoSMoS process [2], which is an iterative design process for developing simulations of complex systems. CoSMoS consists of four deliverables. First there is the *Domain Model*. In simulation, the *Domain* is the thing we wish to model. In our simulation, the domain is E-Pucks with hardware that is still under construction. The *Domain Model* is an aggregation of everything we know about the domain. In our simulation this is the specification of the E-Pucks and the requirements for our custom hardware, everything else about the domain is still unknown. Second is the *Platform Model* which is everything we will use in our simulation from the domain model. We will simulate ideal E-Pucks with ideal custom hardware without attempting to add noise to their actions, this may need to be modified later if our simulation proves to be too innaccurate. Next there is the *Simulation* which is the implementation of the platform model. We will use Player/Stage, which is an open-source robot simulator [3]. The final deliverable is an *Analysis Model* which is the testing and verification of the model as it compares with the original domain. Since our domain involves robot hardware that has ot yet been built, we cannot yet verify our simulation against reality.

2 Hardware

To detect audio and the direction it came from, in the real robots, we will be using a *phased array* of microphones. Three or more microphones are evenly spaced along a plane, an approaching sound will reach each microphone at slightly different times. This delay is dependent on the angle the sound came from. If a sound originates from directly in front of the robot, it will hit the microphones at the same time. If it comes from 90° to the side there is the most delay between microphones receiving the sound. In a *phased array* we use this principle, but the process is reversed. We can effectively point the phased array of microphones in any direction by applying a delay to each microphone. This delay is calculated such that all the microphones will receive the sound at the same time only if the sound originates from the desired angle. If the delayed data from all the microphones is summed, this will give us a peak if the sound originates from the desired angle.

Our hardware records sound entering each microphone, the data is delayed and summed for 5 different angles. A Fourier transform is performed on each resulting waveform to give us a measure of which frequencies came from each angle.

3 Future Work

The next stage in our research is to finalise the hardware and test its limitations. Specifically we need to know its maximum range, the maximum frequency it can detect, its ability to measure a sound's direction and the minimum duration a sound can have for it to be detected. This information will be fed back into our simulation to improve its accuracy. Finally we will verify the simulation against a real robotic system performing basic audio communication.

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Trans-DV: A Framework for Developing and Formally Verifying Model Transformation Specifications

Asmiza A. Sani, Fiona A. C. Polack, and Richard F. Paige

Department of Computer Science
University of York
Deramore Lane, York, YO10 5GH, UK
asmiza,fiona,paige@cs.york.ac.uk

Abstract The Trans-DV framework proposes a set of languages for specifying model transformations with attached verification properties. The languages are based on a corpus of transformation patterns, which support automatically generating a formal specification using templates that are amenable to simulation and analysis. Trans-DV also provides several phases for capturing transformation requirements, structural and behavioural features and finally simulate and formally verify the transformation specification using model checkers. Currently, Trans-DV supports automated verification via the Alloy Analyzer.

Keywords: Model transformation, verification, formal methods

1 Introduction

Model Driven Engineering is defined by two basic principles; *conformation* of a model to a domain model and *representation* of a model for a real world system [2]. Transformation is the core mechanism at the basis of any model manipulation process in Model Driven Engineering (MDE). A transformation defines a relationship between models; a transformation specification enables a process of transforming source models automatically into target models. Specifications are read, analysed and implemented by transformation tools [3].

Though typically developed following an ad-hoc process, transformations are engineering artefacts and can be developed in a disciplined way, like other software artefacts. As such, typical software engineering practices and techniques can and should be applied to them. In particular, formally verifying transformation implementations against specifications may be valuable, in identifying flaws, omissions or errors, and in promoting a more disciplined approach to engineering transformations. Formally verifying a model transformation can be complex, but introducing patterns and templates as part of this process may enable a light-weight and pragmatic verification approach [7].

2 Motivation

Often transformation adopts testing for verification [4] [6] and formal methods is less considered due to common perception regarding its difficulty. Trans-DV is a framework that provides a systematic process for specifying and verifying transformations, using a language for capturing both structural and behavioural patterns in a model. The motivation of Trans-DV is two fold; one is to provide a way to visually specifying transformation and the other is to do it, particularly, for supporting automatic formal analysis and simulation of the specification. Trans-DV uses templates which, when instantiated, automatically produce an equivalent formal specification from a transformation, attached with assertions that are tractable and amenable to formal analysis and simulation, hence, hiding the rigour of formal methods from transformation engineers. For now, Trans-DV supports verification via Alloy [5] and Alloy Analyzer [1].

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Agent-Based Modelling and Simulation of the NF-κB Intracellular Signalling Pathway

Richard Alun Williams

Department of Computer Science and York Centre for Complex Systems Analysis, University of York, UK

Poster Abstract

The ability of cells to perceive and correctly respond to their environment is of particular importance for the immune system and the combating of infection. Errors in the processing of extracellular signals are responsible for the onset of many cancers and autoimmune diseases. The NF-κB signalling pathway is one of the key signalling pathways involved in the control and regulation of the immune system [4]. Computational biologists and computer scientists are beginning to take a more realistic view of these systems through recent advances in computational modelling techniques, such as agent-based modelling and simulation. Furthermore, computational power is advancing rapidly, providing the ability to run large-scale computer simulations of biological systems, which was not plausible in the last century. It is hoped that through an increased understanding of cell signalling pathways, such as NF-κB, diseases may be treated more effectively, or even eradicated entirely through prevention of pathway dysregulation. We believe that computational modelling and simulation of the NF-κB signalling pathway will complement wet-lab experimental approaches, and will facilitate a more comprehensive understanding of this example of a complex biological system.

We will be developing an agent-based model and simulation of NF-κB using the FLAME simulation framework [3]. FLAME was developed for the simulation of large-scale agent-based models over high-performance computer clusters. The agents are designed and modelled as communicating X-machines, which allow them to communicate with each other through a centralised message board. Experimental data [2, 6–8] for use within model development, calibration and ultimate simulation has been provided by the Qwarnstrom lab, within the Department of Cardiovascular Science, at the University of Sheffield Medical School. This data relates to the degradation of inhibitor of NF-κB (IκBα) over time, which is the key biochemical reaction for activation of the signalling pathway. The wet-lab experimentation observes the degradation of IκBα through use of fluorescent protein tags which are linked to the inhibitor; the decrease in fluorescence directly correlates to the degradation of the IκBα inhibitor protein, and thus activiation of NF-κB.

A number of statistical techniques have been used on the data to understand the biological domain related to this project. Linear statistical analysis advised that the distribution of the data closely resembled a negative binomial distribution, and therefore non-parametric techniques are required to sum-

marise the data. Negative binomial distributions are widely seen throughout biology due to the inherent stochasticity within biological processes. As such, these processes generate large variation, due to the compound effects of scale (DNA-RNA-Protein-Cell), and result in large variability of observations within datasets [1, 5]. Multivariate statistical techniques were also used to analyse the data. Preliminary analysis used scatterplot matrix and hierarchical clustering, with more detailed analysis being performed using principal component analysis. The data was consistently shown to consist of three clusters with regards to the fluorescence at time 0min.

It is difficult to calibrate an agent-based model with data that shows such large variability, which is inherent to a negative binomial distribution. We therefore propose that in the short term, data used for calibration of the resulting NF-κB FLAME Model and subsequent validation and simulation should be confined to the first cluster from multivariate statistical analysis, which has an initial fluorescence less than 1.5 units. Further iterations will then incorporate the additional data, and we intend to perform *in silico* experimentation to predict differences in system dynamics due to the amount of IκBα inhibitor (degree of initial fluorescence).

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