		Parameter	Simulation Parameter	Domain Value	Platform Value	Description
Environment:	Γ	Initial Tract Circumference	initialGridHeight	0.976 mm	244 pixels	Initial circumference of the intestine tract when the process begins.
	Δ	Initial Tract Length	initialGridLength	28.80 mm	7203 pixels	Initial length of the intestine tract when the process begins.
	K	Upper Tract Circumference	upperGridHeight	1.016 mm	7303 pixels	Circumference of the intestine tract at the end of the development.
	P	Upper Tract Length	upperGridLength	29.22 mm	254 pixels	Length of the intestine tract at the end of the development period.
	T	Developmental Time	simulationTime	20 Hours	20 Hours	Time period from start to end of this stage of the process. Closely matches that performed in the laboratory
	Υ	Intestine Growth Time	growthTime	20 Hours	20 Hours	Number of hours at which the intestine tract is growing from its initial size to end size
	Λ	Seconds Per Simulation Step	secondsPerStep		60 Seconds	Number of seconds of developmental time represented by 1 'tick' of the simulation. Used to calculate how many steps the simulation runs for, and the cell speed range
Interaction	χ	Probability of bind upon cell contact	thresholdBindProbability	50.00%	0.50%	Probability that where an LTin or LTi cell comes into contact with an LTo cell, a stable bind is formed, and signalling occurs. In the simulation, all probabilities fall between 0 and 1
Stromal Cells	ζ	Stromal Cell Density (LTo)	stromalCellDensity	20.00%	20.00%	The density of LTo cells along the tract surface
	θ	Percent of LTo Cells that express RET Ligands	percentStromaRETLigands	Unknown	0.20%	Percentage of LTo cells which express RET ligand, and therefore have the capacity to mature to form patches. Established through calibration
	ρ	Number of Hours RET Ligands are Active	numHoursRETLigandActive	20 Hours	20 Hours	Number of hours at which RET-ligand cells are present/express the ligand.
	H	Percentage of RET Ligands Cells that are Non-Stromal	probabilityLTinLTiRETLigands	Unknown	Not Used	It may be possible that other cells, such as LTin/LTi cells, also express RET Ligand, thus potentially they could bind together to slow the process down. This is a theory that the simulation could later test. The functionality is there but not currently in use
	ϖ	Number of Hours an Immature LTo remains active (if no interaction occurs)	imLToActiveTime	Unknown	20 Hours	Potentially an LTo cell, if it has not differentiated, may lose the capability to do so after a set period. Again the functionality exists to test the effect of removing such cells after a set period, though not yet used.
	N	LTo Division Time	lToDivisionTime	12 Hours	12 Hours	Number of hours before an LTo cell divides
	σ	Cell Size	LTO_DIAMETER	24 Microns	6 Pixels	Size of each LTo. 1 pixel = 4 microns
Generic LTi/LTin Cell Parameters	ω	Cell Speed Lower Bound	cellSpeedMinLowBound	3.8 Micrometres a Minute	0.95 pixels a minute	Lower bound cell speed. 1 pixel/min = 4 microns/min
	ξ	Cell Speed Upper Bound	cellSpeedMinUpBound	8.8 Micrometres a Minute	2.2 pixels a minute	Upper bound cell speed. 1 pixel/min = 4 microns/min
	Π	Simulation Run Cell Speed Low Bound	cellSpeedLowBound		Calculated	As it is possible to change the number of seconds represented by one 'tick' of the simulation, the correct cell speed range needs to be calculated to ensure the right speed is set. This is calculated using the cell speed per minute and the seconds represented by one 'tick'
	Θ	Simulation Run Cell Speed Upper Bound	cellSpeedUpBound		Calculated	Calculates the upper bound cell speed for the reasons specified above
	τ	Cell Size	HCELL_DIAMETER	8 Micrometres	2 Pixels	Size of each LTin/LTi. 1 pixel = 4 microns
LTin Cells	δ	Percentage of LTin Cells at E15.5	percentLTinfromFACStain	0.45%	0.45%	If whole tract was populated with cells of this size, this would be LTin cell population at E15.5 – used to estimate LTin input rate
	ε	LTin Input Time	lTinInputTime	20 Hours	20 Hours	Time at which migration of LTin cells into the tract ceases
	ς	LTin Input Rate	lTinInputRate		Calculated	In this model, LTin cells enter right up to the time point above. As we know the number of cells in the tract at E15.5, an input rate is used so that the correct number enter over the period to ensure this figure is reached. The input rate is calculated using the input time and percentage parameters above, if a linear increase is followed. The model is also capable of using exponential and square root increases
	κ	LTin Input Rate Function	lTinInputRateGraphType		linear	Sets the input rate to follow either a linear trajectory, or exponential or square root function, in order to investigate different migration rates.
	λ	LTin Input Rate Constant	lTinInputRateGraphConstant		Not Used	Constant to generate either an exponential or square root input rate
LTi Cells	ϕ	Percentage of LTi Cells at E15.5	percentLTifromFACStain	0.37%	0.37%	If whole tract was populated with cells of this size, this would be LTi cell population at E15.5 – used to estimate LTi input rate
	γ	LTi Input Delay Time	lTiInputDelayTime	Unknown	0 Hours	Hour point at which LTi migration commences
	η	LTi Input Time	lTiInputTime	20 Hours	20 Hours	Time at which migration of LTi cells into the tract ceases
	Ψ	LTi Input Rate	lTiInputRate		Calculated	Calculates LTi input rate in a similar way to LTin input rate
	ϒ	LTi Input Rate Function	lTiInputRateGraphType		linear	Sets the input rate to follow either a linear trajectory, or exponential or square root function, in order to investigate the effect of different migration patterns.
	A	LTi Input Rate Constant	lTiInputRateGraphConstant		Not Used	Constant to generate either an exponential or square root input rate
Chemokine	φ	Threshold Chemokine Level at which Chemotaxis occurs	chemoThreshold	Unknown	0.3	The amount of chemokine which triggers a cell to follow the path towards a forming patch
	B	Sigmoid Curve Adjustment Constant	chemoSigCuveThreshold		3	Chemokine expression is calculated using an inverse sigmoid function. Therefore, chemokine expression close to an LTo cell is strong, and this decreases, following an 's' curve, as distance increases from the cell. This constant is here to move the curve so that the y axis meets the top of the curve, rather than the axis passing through the middle.
	I	Upper Limit for Chemokine Sigmoid Function	chemoUpperLinearAdjust		0.2	Controls the 'tightness' of the curve and therefore the distance at which the chemokine is diffused – therefore the curve starts tight (so that when chemokines begin to be expressed, the distance affected is small)
	Z	Lower Limit for Chemokine Sigmoid Function	chemoLowerLinearAdjust		0.04	Controls how linear the curve becomes as chemokine expression increases. When this point is reached, the chemokine will be diffusing over a large distance, and it is assumed that further expression ceases at this point
	ι	Chemokine Function Adjuster	chemoLinearAdjustmentReducer		0.005	The amount to adjust the curve with each stable contact between an LTo and LTin/LTi cell
Cellular Adhesion	M	Initial Expression Level of adhesion factors from LTo		0	0	Initial adhesion molecule expression level for each LTo. This will rise with interactions between the LTo and LTin/ LTi Cells
	Ξ	Probability adhesion holds cell in place around patch	maxAdhesioneffectProbabilityCutOff	Unknown	0.65	The maximum probability of a cell responding to the adhesion level when around an LTo cell. Ensures that some stochasticity is retained in the LTin and LTi behaviour
	E	Amount adhesion increases with each stable interaction	adhesionIncrement	Unknown	0.05	As interactions between LTin/LTi cells and LTo cells increases, the amount of cellular adhesion factors expressed also increases. The increase is not restricted. 0.05 was established in calibration
	ν	Slope at which the probability of a cell being affected by the level of adhesion factors increases with adhesion level	adhesionSlope	n/a	1	Expression of adhesion factors is modelled as a straight line, passing through the origin, plotting expression against probability the cell is held in place. As expression increases, the probability increases. The slope adjusts this line – determining whether much expression is needed for the probability to increase, or the probability is high with little expression.
Output Control		Enable Cell Tracking	cellTrackingEnabled		TRUE	Boolean to determine if cell tracking is enabled
		Enable LTo Stats	generateLToStats		TRUE	Boolean to determine if generation of LTo statistics is enabled
		Enable Step by Step Snaps	stepBystepTrackingImages		FALSE	Boolean to determine whether snapshots should be taken each step
		Cell Tracking Start Hour	trackingSnapStartHr		12 Hours	Hour to start tracking (if enabled)
		Cell Tracking End Hour	trackingSnapEndHr		13 Hours	Hour to end tracking (if enabled)
		Enable 12 Hour Snapshots	twelveHourSnaps		FALSE	Boolean to determine whether 12 hour snapshots should be taken.
Knockouts		Chemokine KnockOut	chemoKnockOut		FALSE	Boolean to determine if chemokines should be knocked out.
		RET Ligand KnockOut	retLigandKnockOut		FALSE	Boolean to determine if RET should be knocked out.