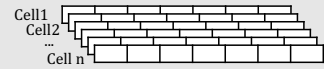


Each cell is stored as a 7-integer array in a monodimensional vector (cell population vector). The integers represent the cell attributes as follows:

Clone ID	CellCycle Length	CellCycle Timer	position (x)	position (y)	position (z)	Proliferating
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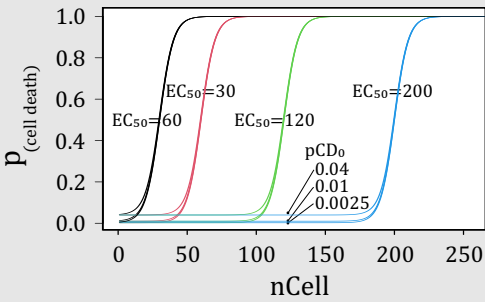


Clone ID: A unique identifier for the cell's lineage.
Cell cycle length: The cycle length of the cell.
Cell cycle timer: remaining time before the cell is ready to divide.
Position (x, y, z): The 3D coordinates of the cell in the simulated space.
Proliferating: whether the cells is proliferating (1) or resting (0)

A cell-density map is computed by tessellating the continuous space in a 3D-grid and by tallying the number of cells from each lineage within every voxel. This map is subsequently employed to calculate the survival probability of each cell in the following step.

For any given cell **Q**, death probability is modelled as:

$$p_{(\text{cell death})} = pCD_0 + \frac{1 - pCD_0}{1 + e^{-k(nCell - EC_{50})}}$$

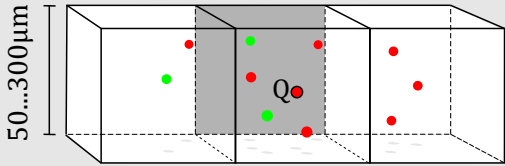


where pCD_0 is the basal cell death probability, $k=0.2$ and EC_{50} was one of the explored parameters. $nCell$ is the number of cells in the voxel occupied by **Q** and is calculated as:

$$nCell = nLCell \times Lw + nACell \times Aw.$$

nLCell is the number of cell in the voxel belonging to the same clone of **Q** (lineage cells).

nACell is the number of cell in the voxel belonging to other clones than that of **Q** (alien cells).



$$nCell = 4 \times Lw + 2 \times Aw$$

Lw and Aw are respectively the weight of lineage and alien cells. When clonal competition is not implemented $Lw=Aw=1$

Each newborn cell inherits attributes form its mother cell. Some attributes may undergo changes depending from simulation parameters. Cell cycle lenght changes by a Gaussian value. If the variation is negative, it is scaled to prevent cell cycle length to shorten below `LOW_CYCLE_LIMIT` parameter.

This mechanism allows for a balance between lineage-specific cycle lengths, introducing fluctuations while ensuring no unrealistically short cycle durations.

If the parameter governing the Gaussian variation (`SD_DELTA_CYCLE`) is set to 0, it leads to fixed cell cycle lengths within each lineage.