

# Cell Fate Clusters in ICM Organoids Arise from Cell Fate Heredity & Division – A Modelling Approach

## Supplemental Material

Tim Liebisch<sup>1,\*</sup>, Armin Drusko<sup>1</sup>, Biena Mathew<sup>2</sup>, Ernst HK Stelzer<sup>2</sup>, Sabine C Fischer<sup>3</sup>, and Franziska Matthäus<sup>1</sup>

<sup>1</sup>Faculty of Biological Sciences & Frankfurt Institute for Advanced Studies (FIAS), Goethe Universität Frankfurt am Main, Ruth-Moufang-Straße 1, Frankfurt 60438, Germany

<sup>2</sup>Faculty of Biological Sciences & Buchmann Institute for Molecular Life Sciences (BMLS), Goethe Universität Frankfurt am Main, Max-von-Laue Str. 15, Frankfurt 60438, Germany

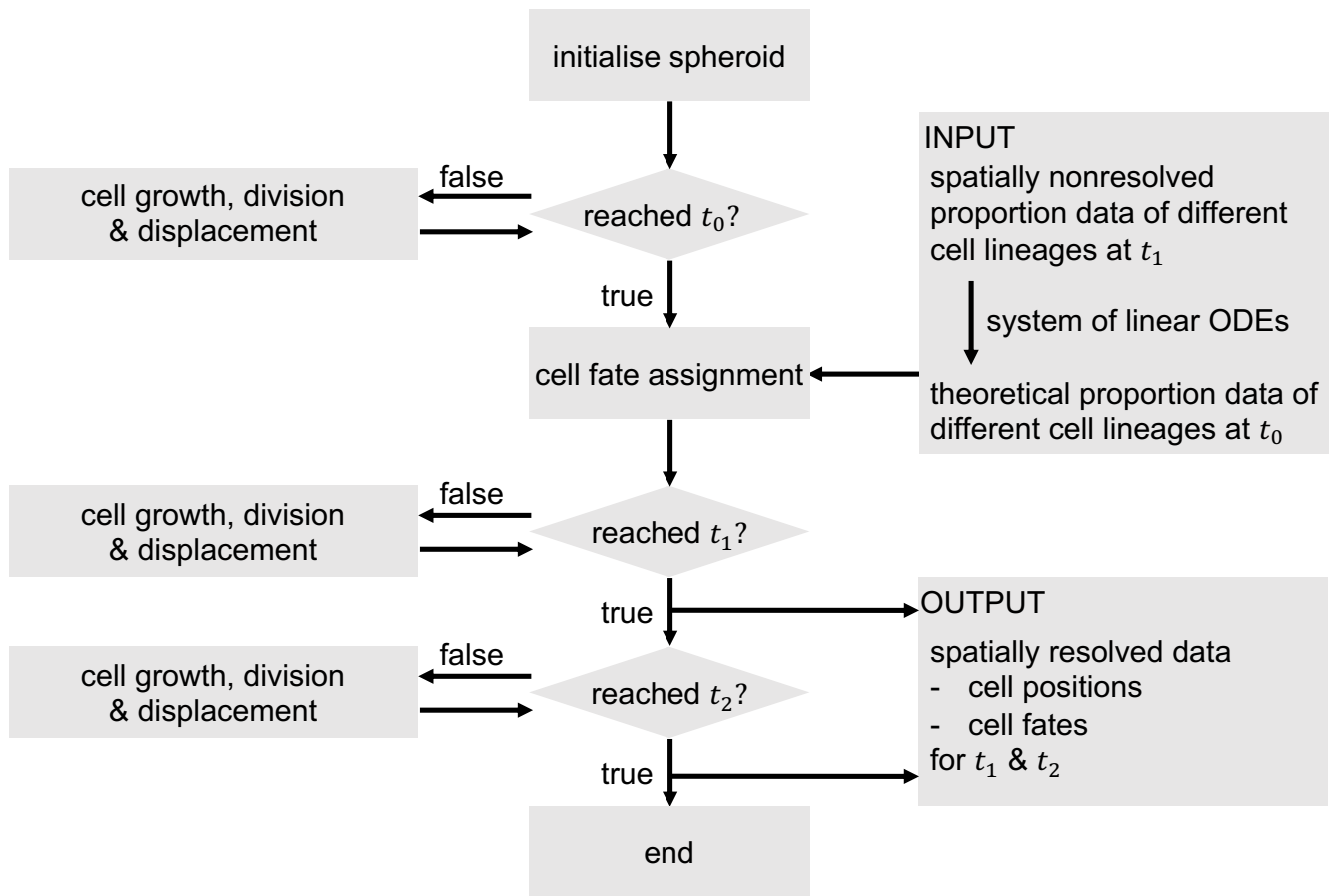
<sup>3</sup>Center for Computational and Theoretical Biology (CCTB), Julius-Maximilians-Universität Würzburg, Campus Hubland Nord 32, 97074 Würzburg, Germany

\*liebisch@fias.uni-frankfurt.de

### ABSTRACT

During the mammalian preimplantation phase, cells undergo two subsequent cell fate decisions. During the first decision, the trophectoderm and the inner cell mass are formed. Subsequently, the inner cell mass segregates into the epiblast and the primitive endoderm. Inner cell mass organoids represent an experimental model system, mimicking the second cell fate decision. It has been shown that cells of the same fate tend to cluster stronger than expected for random cell fate decisions. Three major processes are hypothesised to contribute to the cell fate arrangements: 1) chemical signalling; 2) cell sorting; and 3) cell proliferation. In order to quantify the influence of cell proliferation on the observed cell lineage type clustering, we developed a mechanical agent-based model accounting for mechanical cell-cell interaction, i.e. adhesion and repulsion, cell division, stochastic cell fate decision and cell fate heredity. The model supports the hypothesis that initial cell fate acquisition is a stochastically driven process, taking place in the early development of inner cell mass organoids. Further, we show that the observed neighbourhood structures can emerge solely due to cell fate heredity during cell division.

## Flowchart



**Figure A1.** Flowchart of the implemented model.

### Parameter estimation for different hypotheses

The model can be used to test several assumptions addressing cell fate heredity. In total, four different hypotheses are tested. Each hypothesis is considering cell fate switches during cell division according to Fig. 1d. During cell division, the cell fate is passed on to the daughter cells. A cell fate switch is possible with a given rate. The model considers the following cell fate switches: N.G. remain N.G. ( $\zeta_1$ ) or become N<sub>+</sub>G<sub>+</sub> ( $\alpha_3$ ). N<sub>+</sub>G<sub>+</sub> remain N<sub>+</sub>G<sub>+</sub> ( $\zeta_2$ ) or become N<sub>+</sub>G. ( $\alpha_1$ ) or N.G. ( $\alpha_2$ ). N<sub>+</sub>G. and N.G. remain N<sub>+</sub>G. ( $\zeta_3$ ) and N.G. ( $\zeta_4$ ) or switch to the opposite cell fate ( $\alpha_4$ ) and ( $\alpha_5$ ), respectively. These cell fate transitions form a system of linear ordinary differential equations, which can be written as

$$d\mathbf{f}/dt = \mathbf{A}\mathbf{f} \quad (\text{A1})$$

$$\begin{pmatrix} dN_+G_+/dt \\ dN.G./dt \\ dN_+G./dt \\ dN.G_+/dt \end{pmatrix} = \begin{pmatrix} \zeta_2 - \alpha_1 - \alpha_2 & \alpha_3 & 0 & 0 \\ 0 & \zeta_1 - \alpha_3 & 0 & 0 \\ \alpha_1 & 0 & \zeta_3 - \alpha_4 & \alpha_5 \\ \alpha_2 & 0 & \alpha_4 & \zeta_4 - \alpha_5 \end{pmatrix} \cdot \begin{pmatrix} N_+G_+ \\ N.G. \\ N_+G. \\ N.G_+ \end{pmatrix}, \quad (\text{A2})$$

with the analytical solution:

$$\mathbf{f}(t) = c_{N_+G_+} \mathbf{v}_{N_+G_+} e^{\lambda_{N_+G_+} t} + c_{N.G.} \mathbf{v}_{N.G.} e^{\lambda_{N.G.} t} + c_{N_+G.} \mathbf{v}_{N_+G.} e^{\lambda_{N_+G.} t} + c_{N.G_+} \mathbf{v}_{N.G_+} e^{\lambda_{N.G_+} t}, \quad (\text{A3})$$

with  $\mathbf{v}$  and  $\lambda$  the eigenvectors and eigenvalues of the coefficient-matrix  $\mathbf{A}$ , respectively. The unknown prefactor  $c$  values can be determined by inserting the known cell counts of the different cell types at  $t_1$ . The rates for the different cell fate switches vary for the different hypotheses (see Tab. A1).

**Table A1.** Cell fate transition rates for the four different hypotheses.

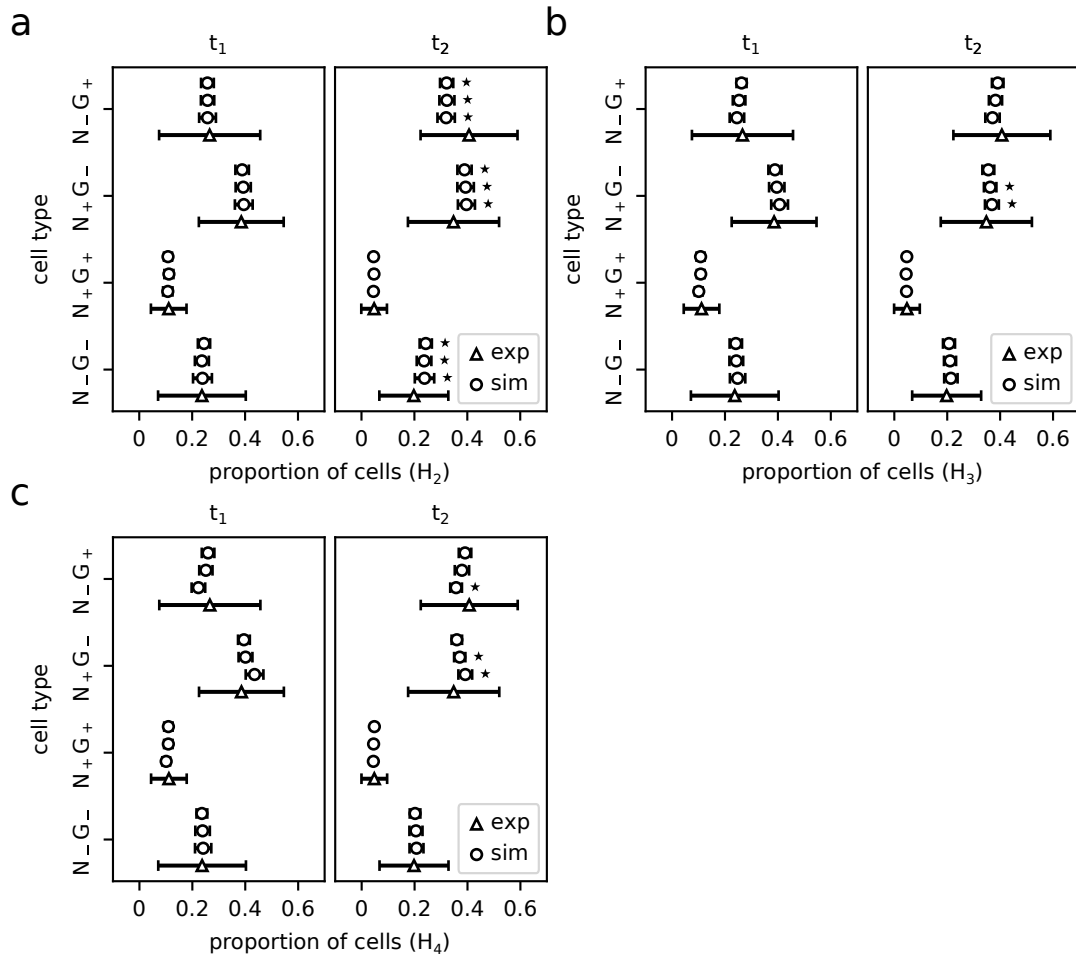
	hypothesis			
	H <sub>1</sub>	H <sub>2</sub>	H <sub>3</sub>	H <sub>4</sub>
$\zeta_1$	1	1	1	1
$\zeta_2$	1	1	1	1
$\zeta_3$	1	1	1	1
$\zeta_4$	1	1	1	1
$\alpha_1$	0	1	0.7863	0.7863
$\alpha_2$	0	0	0.7863	0.7863
$\alpha_3$	0	0	0.2123	0.2123
$\alpha_4$	0	0	0.2997	0.3927
$\alpha_5$	0	0	0	0.1

## Hypothesis 2, 3 and 4

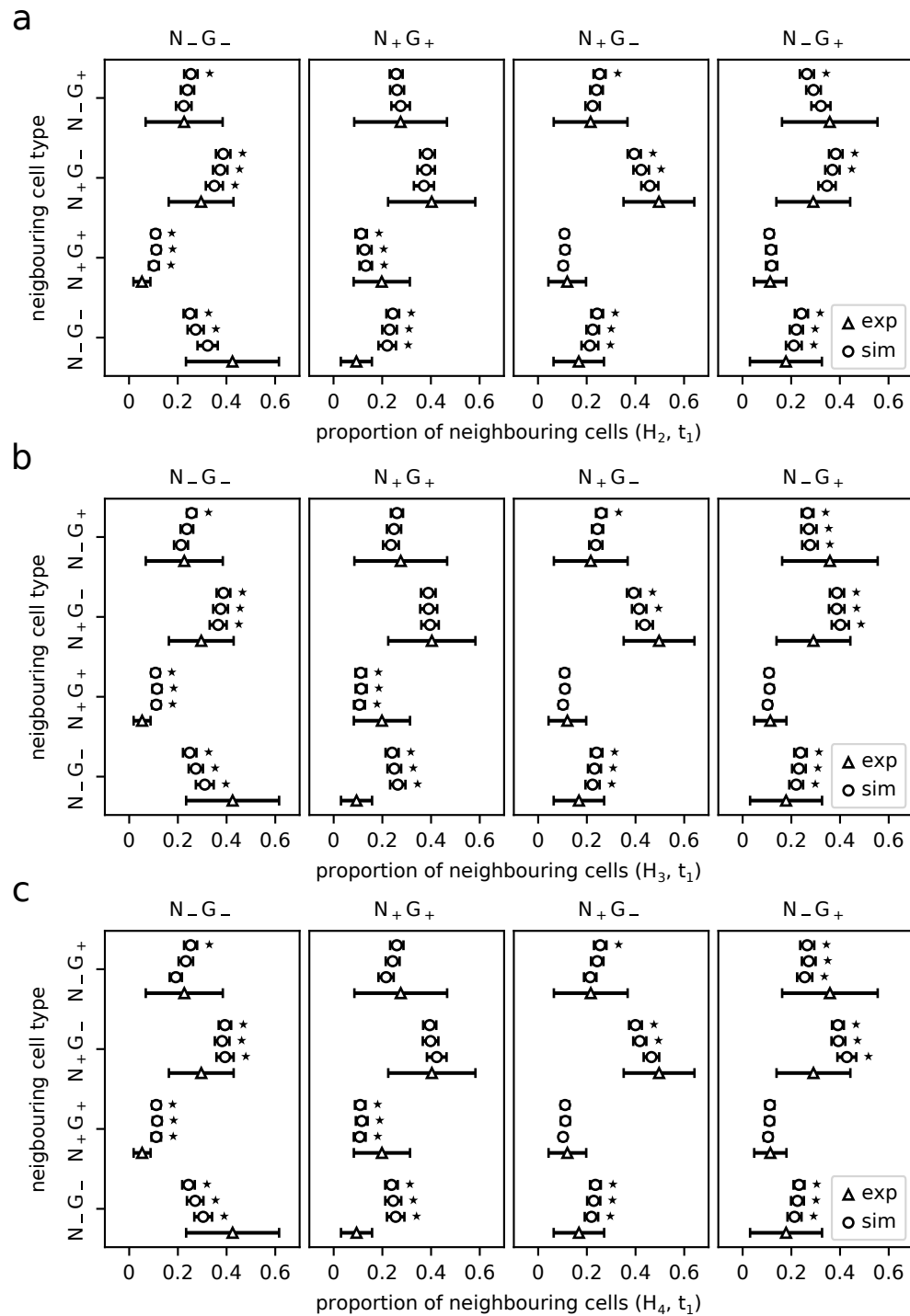
The neighbourhood statistics for  $H_2$  agreed reasonably well with the experimental data (see Fig. A3). The neighbourhood pattern of cells with the expression types N.G. and  $N_+G_+$  at  $t_1$  were similar to the neighbourhood structures obtained under assumption  $H_1$ , including the misfit involving N.G. cells. In addition, simulated  $N_+G_+$  cells were significantly less often neighbours of other  $N_+G_+$  cells than the experimental data suggests (see Tab. A4). The latter speaks against a cell fate change of  $N_+G_+$  cells into N.G. cells. If performed under the assumption of the  $H_2$  model, the evaluated proportions for  $t_2$  showed a better agreement with the experimental data. In particular, the predicted neighbourhood statistics of  $N_+G_+$  cells differ statistically less substantially from the *in vitro* measured proportions compared to the simulated cell neighbourhood statistics under the assumption  $H_1$  (see. Fig. A2 and Tab. A2).

If we consider cell fate switches from  $N_+G_+$  to N.G. and vice versa, which according to the literature are considered as unlikely, a third and a fourth hypothesis can be formulated. In both hypotheses, the strong increase in the amount of N.G. is explained by cell fate switches from  $N_+G_+$  to N.G. While  $H_3$  permits only the cell fate switches from  $N_+G_+$  to N.G.,  $H_4$  is considering a small flux between both cell fates. The parameter values for both hypotheses are shown in Tab. A1. As expected, the simulated proportions for  $H_3$  and  $H_4$  agree very well with the experimental data at  $t_1$  and  $t_2$  (see. Fig. A2 and Tab. A2).

Comparing  $H_3$  and  $H_4$  to  $H_1$  and  $H_2$ , we observe that their  $\psi$  values are higher, thus the quality of the fit of the neighbourhood statistics is lower (see. Fig. 2c). The neighbourhood distributions largely agree with experimental data at  $t_1$  for the neighbourhood of double positive and NANOG positive cells. The simulated proportions of GATA6 positive cells adjacent to other GATA6 positive cells are significantly lower compared to experimental data, independent of the cell count of the ICM spheroid at which the initial cell fate is determined (see. Fig. A3 and Tab A5 and A6).

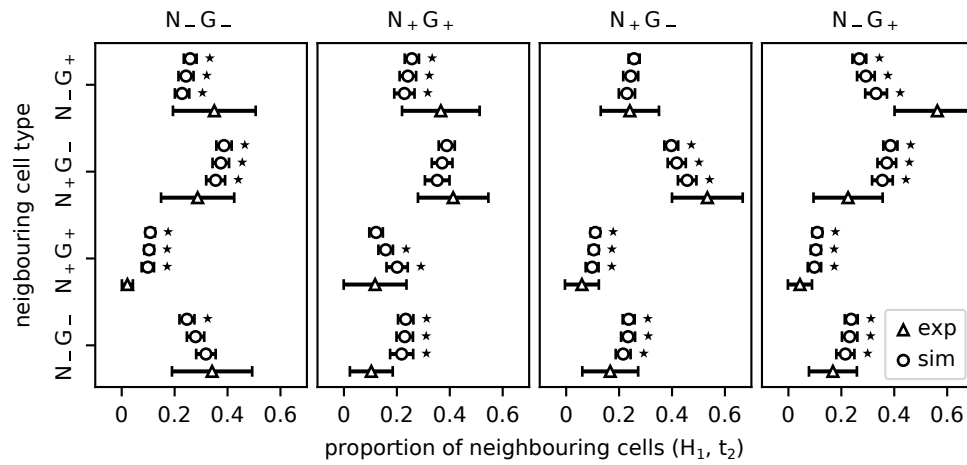


**Figure A2.** Expression type composition of ICM spheroids for H<sub>2</sub>, H<sub>3</sub> and H<sub>4</sub>. Expression type composition of ICM organoids and ICM spheroids as percentage of the total number of cells within ICM organoids at t<sub>1</sub> and t<sub>2</sub>. Simulations were performed under the assumption H<sub>2</sub> (a), the assumption H<sub>3</sub> (b) and the assumption H<sub>4</sub> (c). Experimental data from Mathew *et al.* (2019) are indicated by triangles. Simulation results for different t<sub>0</sub> are indicated by circles. The error bars indicate the standard deviation. t<sub>0</sub> from lowest line to top: 200, 300 and 400 cells. Statistically significant differences between the cell fate proportion of ICM organoids and ICM spheroids are indicated by stars (p < 0.05; using a Wilcoxon-Mann-Whitney test with Bonferroni correction).

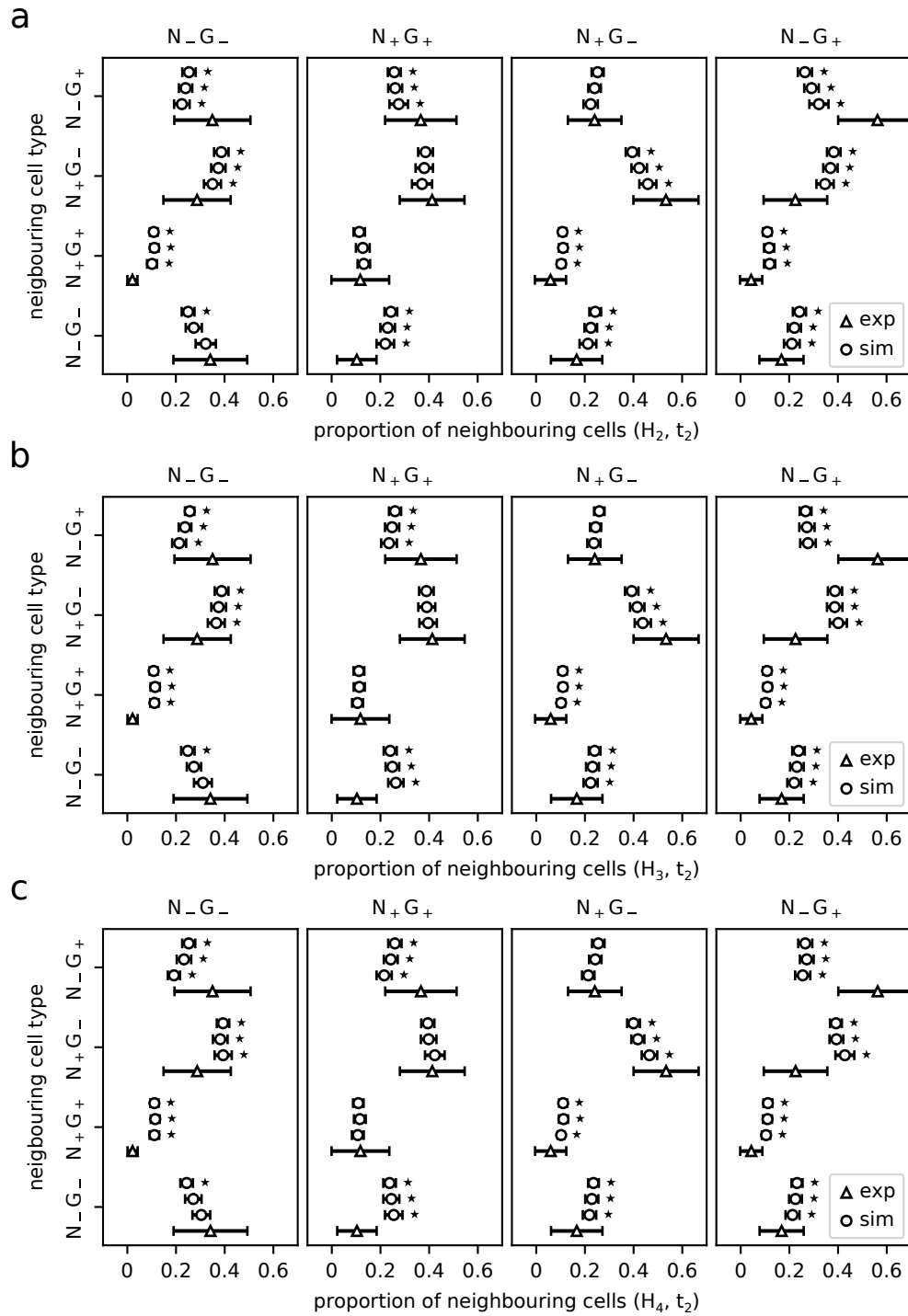


**Figure A3.** Expression type composition of neighbouring cells as percentage of the total of neighbouring cells at  $t_1$ . Simulations were performed under the assumption  $H_2$  (a), the assumption  $H_3$  (b) and the assumption  $H_4$  (c). Experimental data from Mathew *et al.* (2019) are indicated by triangles. Simulation results for different  $t_0$  are indicated by circles. The error bars indicate the standard deviation.  $t_0$  from lowest line to top: 200, 300 and 400 cells. Statistically significant differences between the neighbourhood structure of 24 h old ICM organoids and ICM spheroid patterns are indicated by stars ( $p < 0.05$ ; using a Wilcoxon-Mann-Whitney test with Bonferroni correction).

### Expression type composition of neighbouring cells at $t_2$



**Figure A4.** Expression type composition of neighbouring cells as percentage of the total of neighbouring cells at  $t_2$ . Simulations were performed under the assumption  $H_1$ . Experimental data from Mathew *et al.* (2019) are indicated by triangles. Simulation results for different  $t_0$  are indicated by circles. The error bars indicate the standard deviation.  $t_0$  from lowest line to top: 200, 300 and 400 cells. Statistically significant differences between the neighbourhood structure of 24 h old ICM organoids and ICM spheroid patterns are indicated by stars ( $p < 0.05$ ; using a Wilcoxon-Mann-Whitney test with Bonferroni correction).



**Figure A5.** Expression type composition of neighbouring cells as percentage of the total of neighbouring cells at  $t_2$ . Simulations were performed under the assumption  $H_2$  (a), the assumption  $H_3$  (b) and the assumption  $H_4$  (c). Experimental data from Mathew *et al.* (2019) are indicated by triangles. Simulation results for different  $t_0$  are indicated by circles. The error bars indicate the standard deviation.  $t_0$  from lowest line to top: 200, 300 and 400 cells. Statistically significant differences between the neighbourhood structure of 24 h old ICM organoids and ICM spheroid patterns are indicated by stars ( $p < 0.05$ ; using a Wilcoxon-Mann-Whitney test with Bonferroni correction).



*p*-values

**Table A2.** *p*-values for the statistical comparison of the simulated expression type composition of ICM spheroids to the experimental data at  $t_1$  and  $t_2$ . Simulations were performed under the assumption  $H_1$ , the assumption  $H_2$ , the assumption  $H_3$  and the assumption  $H_4$ . For statistical comparison a Wilcoxon-Mann-Whitney test with Bonferroni correction is performed. Statistically significant differences between simulated and experimental data are indicated in red ( $p < 0.05$ ).

neighbouring expression type	cell count at $t_0$	$t_1$				$t_2$			
		$H_1$	$H_2$	$H_3$	$H_4$	$H_1$	$H_2$	$H_3$	$H_4$
N.G <sub>+</sub>	400	0.240	0.345	0.150	0.244	8e-8	3e-4	0.207	0.190
	300	0.399	0.325	0.638	0.624	8e-8	3e-4	0.087	0.070
	200	0.468	0.340	0.955	0.208	9e-8	2e-4	0.031	0.006
N <sub>+</sub> G.	400	0.675	0.645	0.685	0.775	4e-4	5e-4	0.027	0.018
	300	0.743	0.822	0.888	0.992	6e-4	3e-4	0.012	0.005
	200	0.935	0.941	0.727	0.053	4e-4	3e-4	0.006	3e-4
N <sub>+</sub> G <sub>+</sub>	400	0.978	0.767	0.713	0.896	4e-12	0.039	0.023	0.021
	300	0.910	0.955	0.771	0.908	5e-12	0.023	0.048	0.045
	200	0.927	0.747	0.311	0.355	1e-11	0.051	0.028	0.059
N.G.	400	0.240	0.061	0.068	0.083	0.002	0.001	0.042	0.067
	300	0.399	0.078	0.061	0.070	0.001	0.002	0.032	0.049
	200	0.468	0.072	0.526	0.067	0.001	0.002	0.021	0.043

**Table A3.**  $p$ -values for the statistical comparison of the simulated expression type composition of neighbouring cells of ICM spheroids to the experimental data at  $t_1$  and  $t_2$ . Simulations were performed under the assumption  $H_1$ . For statistical comparison a Wilcoxon-Mann-Whitney test with Bonferroni correction is performed. Statistically significant differences between simulated and experimental data are indicated in red ( $p < 0.05$ ). Not statistically significant differences between experimental data and simulated expression type compositions of neighbouring cells for  $H_1$  (excluding N.G. cells) with  $t_0 = 200$  cells are indicated in blue.

neighbouring expression type	cell count at $t_0$	$t_1$ expression type				$t_2$ expression type			
		N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>	N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>
N.G <sub>+</sub>	400	6.9e-4	0.388	0.001	0.001	9.4e-5	1.8e-6	0.230	4.4e-16
	300	0.005	0.154	0.018	0.018	7.5e-6	3.0e-7	0.993	4.7e-14
	200	0.030	0.091	0.144	0.144	3.8e-7	4.7e-8	0.312	1.1e-11
N <sub>+</sub> G.	400	1.1e-8	0.963	6.7e-5	2.5e-5	3.3e-11	0.895	5.2e-14	9.9e-12
	300	1.7e-8	0.506	9.1e-4	6.0e-4	5.0e-10	0.137	1.4e-10	1.1e-11
	200	1.2e-5	0.189	0.059	0.007	1.1e-7	0.004	3.0e-4	2.7e-11
N <sub>+</sub> G <sub>+</sub>	400	5.0e-13	1.5e-4	0.480	0.560	8.0e-21	0.036	6.2e-10	6.4e-16
	300	3.1e-11	0.061	0.240	0.248	1.3e-20	3.8e-5	3.8e-9	5.6e-15
	200	1.8e-9	0.625	0.092	0.116	4.4e-20	1.1e-8	7.6e-8	2.4e-13
N.G.	400	1.3e-7	4.4e-15	0.18e-4	8.3e-7	0.001	8.8e-15	1.6e-5	1.6e-6
	300	1.7e-5	5.6e-15	0.008	1.7e-6	0.081	1.3e-14	2.4e-5	8.7e-6
	200	0.002	2.7e-14	0.144	3.0e-5	0.936	1.0e-13	4.3e-4	3.2e-4

**Table A4.**  $p$ -values for the statistical comparison of the simulated expression type composition of neighbouring cells of ICM spheroids to the experimental data at  $t_1$  and  $t_2$ . Simulations were performed under the assumption  $H_2$ . For statistical comparison a Wilcoxon-Mann-Whitney test with Bonferroni correction is performed. Statistically significant differences between simulated and experimental data are indicated in red ( $p < 0.05$ ).

neighbouring expression type	cell count at $t_0$	$t_1$ expression type				$t_2$ expression type			
		N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>	N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>
N.G <sub>+</sub>	400	0.001	0.405	0.003	0.15e-4	4.7e-5	1.9e-6	0.435	2.4e-16
	300	0.006	0.496	0.023	0.005	5.0e-6	3.6e-6	0.862	3.6e-14
	200	0.061	0.943	0.297	0.139	2.7e-7	3.8e-5	0.141	3.5e-12
N <sub>+</sub> G.	400	9.9e-9	0.919	6.5e-5	3.4e-5	3.4e-11	0.775	3.6e-14	3.8e-12
	300	1.2e-7	0.751	0.001	6.7e-4	3.0e-10	0.429	1.3e-9	1.6e-11
	200	4.0e-5	0.539	0.074	0.018	4.4e-7	0.146	5.9e-4	5.0e-11
N <sub>+</sub> G <sub>+</sub>	400	1.1e-13	1.5e-5	0.352	0.627	8.3e-21	0.099	1.1e-9	3.8e-16
	300	6.6e-14	3.5e-4	0.523	0.870	7.6e-21	0.015	4.8e-10	9.6e-17
	200	6.8e-11	0.002	0.175	0.656	1.9e-20	0.008	6.1e-9	5.4e-17
N.G.	400	2.1e-7	1.4e-15	7.9e-10	3.6e-7	0.002	3.1e-15	3.7e-6	3.2e-7
	300	8.1e-6	4.0e-15	3.0e-8	1.1e-5	0.052	9.5e-15	8.1e-5	9.5e-5
	200	0.005	1.6e-14	1.4e-6	5.1e-5	0.982	4.8e-14	5.8e-4	7.6e-4

**Table A5.**  $p$ -values for the statistical comparison of the simulated expression type composition of neighbouring cells of ICM spheroids to the experimental data at  $t_1$  and  $t_2$ . Simulations were performed under the assumption  $H_3$ . For statistical comparison a Wilcoxon-Mann-Whitney test with Bonferroni correction is performed. Statistically significant differences between simulated and experimental data are indicated in red ( $p < 0.05$ ).

neighbouring expression type	cell count at $t_0$	$t_1$ expression type				$t_2$ expression type			
		N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>	N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>
N.G <sub>+</sub>	400	7.9e-4	0.472	6.4e-4	1.3e-4	7.5e-5	2.5e-6	0.159	2.9e-16
	300	0.008	0.228	0.012	4.4e-4	2.2e-6	7.5e-7	0.993	1.4e-15
	200	0.191	0.108	0.048	8.3e-4	3.4e-8	1.3e-7	0.543	2.7e-15
N <sub>+</sub> G.	400	8.8e-9	0.996	3.5e-5	1.9e-5	6.2e-11	0.939	2.0e-14	7.0e-12
	300	9.7e-8	0.927	3.9e-4	2.4e-5	3.4e-10	0.932	2.6e-11	5.8e-12
	200	1.2e-6	0.771	0.008	1.4e-6	7.3e-9	0.823	2.4e-7	2.9e-12
N <sub>+</sub> G <sub>+</sub>	400	3.1e-13	1.1e-5	0.402	0.490	6.2e-21	0.119	8.4e-10	8.0e-16
	300	2.1e-14	2.2e-5	0.413	0.649	6.7e-21	0.092	6.5e-10	4.0e-16
	200	5.6e-14	2.3e-6	0.148	0.205	7.0e-21	0.181	8.3e-9	6.9e-15
N.G.	400	2.4e-7	1.9e-15	1.3e-9	9.7e-7	0.001	3.6e-15	5.6e-6	1.4e-6
	300	7.9e-6	1.1e-15	7.6e-9	2.2e-6	0.043	2.0e-15	3.5e-5	8.5e-6
	200	0.001	4.5e-16	7.5e-8	1.3e-5	0.676	8.3e-16	1.1e-4	1.1e-4

**Table A6.**  $p$ -values for the statistical comparison of the simulated expression type composition of neighbouring cells of ICM spheroids to the experimental data at  $t_1$  and  $t_2$ . Simulations were performed under the assumption  $H_4$ . For statistical comparison a Wilcoxon-Mann-Whitney test with Bonferroni correction is performed. Statistically significant differences between simulated and experimental data are indicated in red ( $p < 0.05$ ).

neighbouring expression type	cell count at $t_0$	$t_1$ expression type				$t_2$ expression type			
		N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>	N.G.	N <sub>+</sub> G <sub>+</sub>	N <sub>+</sub> G.	N.G <sub>+</sub>
N.G <sub>+</sub>	400	0.002	0.455	0.002	1.9e-4	4.3e-5	2.5e-6	0.292	5.1e-16
	300	0.021	0.164	0.018	3.3e-4	1.0e-6	2.9e-7	0.993	1.2e-15
	200	0.886	0.036	0.724	6.0e-5	1.5e-9	6.4e-9	0.024	6.1e-17
N <sub>+</sub> G.	400	3.5e-9	0.846	9.2e-5	5.0e-6	6.8e-12	0.701	1.5e-13	7.5e-12
	300	2.6e-8	0.620	5.8e-4	4.7e-6	8.8e-11	0.636	3.7e-11	5.0e-12
	200	8.3e-9	0.134	0.128	1.7e-8	3.6e-11	0.101	0.002	1.8e-13
N <sub>+</sub> G <sub>+</sub>	400	7.1e-14	6.2e-6	0.484	0.728	7.6e-21	0.155	6.0e-10	2.8e-16
	300	1.5e-14	2.6e-5	0.645	0.645	7.0e-21	0.073	3.1e-10	7.4e-16
	200	1.5e-13	2.6e-6	0.126	0.265	6.5e-21	0.163	7.5e-9	2.6e-15
N.G.	400	5.6e-8	2.4e-15	2.8e-9	1.4e-6	6.3e-4	5.2e-15	1.8e-6	8.5e-6
	300	7.9e-6	1.8e-15	1.7e-8	5.1e-6	0.031	3.0e-15	4.7e-5	4.5e-5
	200	5.8e-4	1.2e-15	1.8e-7	4.4e-5	0.517	1.6e-15	2.7e-4	5.1e-4