A stochastic model of adult neurogenesis coupling cell cycle progression and differentiation

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Abstract

Long-term tissue homeostasis requires a precise balance between stem cell self-renewal and the generation of differentiated progeny. Recently, it has been shown that in the adult murine brain, neural stem cells (NSCs) divide mostly symmetrically. This finding suggests that the required balance for tissue homeostasis is accomplished at the population level. However, it remains unclear how this balance is enabled. Furthermore, there is experimental evidence that proneural differentiation factors not only promote differentiation, but also cell cycle progression, suggesting a link between the two processes in NSCs. To study the effect of such a link on NSC dynamics, we developed a stochastic model in which stem cells have an intrinsic probability to progress through cell cycle and to differentiate. Our results show that increasing heterogeneity in differentiation probabilities leads to a decreased probability of long-term tissue homeostasis, and that this effect can be compensated when cell cycle progression and differentiation are positively coupled. Using single-cell RNA-Seq profiling of adult NSCs, we found a positive correlation in the expression levels of cell cycle and differentiation markers. Our findings suggest that a coupling between cell cycle progression and differentiation on the cellular level is part of the process that maintains tissue homeostasis in the adult brain.

1 Introduction

It is now widely accepted that a precise balance of stem cell self-renewal and differentiation is required to maintain long term tissue homeostasis. There are two strategies to achieve this task: asymmetry on the cellular or on the population level [1, 2, 3]. In mammals, the applied homeostatic strategies are different for every regenerating tissue, among which are the skin, intestine, lung, blood, bone marrow, heart, testis, uterus and mammary gland [4, 5, 6]. For instance, approximately 85% of the stem cells in the skin divide asymmetrically [7], whereas stem cells in the intestine divide mostly symmetrically [8]. The mammalian brain also regenerates [9], whereas it remains unclear which homeostatic strategy is applied. For a long time, it has been thought that the strategy to maintain tissue homeostasis in the adult brain would rely on asymmetry on the cellular level [10]. This thinking is likely to have originated from the fact that during embryo neurogenesis, primary neural progenitors in the ventricular zone (VZ) divide mostly asymmetrically [11]. However, Obernier et al. have recently shown that stem cells in the adult brain divide mostly symmetrically [12]. This implies that for adult neurogenesis the strategy to maintain homeostasis is population asymmetry rather than asymmetry on the cellular level. Although the sustainment of adult organs via population asymmetry is a well-established concept and is found in other tissues, there are still many open questions. For example, how can a stable stem cell population be achieved when stem cells divide exclusively symmetrically?

Homeostasis via population asymmetry could, for instance, be achieved by limited access to a stem cell niche in combination with a short-range cell fate determining signal [2, 13]. Conversely, if the stem cell population asymmetry is based on an internal regulation that is either intrinsic or coupled to an extrinsic signaling, it is unknown what mechanisms could govern the process. Is a molecular regulator enabling a balanced stochastic cell fate decision for a stem cell population? Interestingly, an experimental study revealed a molecular link between cell cycle progression of neural progenitors and neuronal differentiation through the proneural gene *Ascl1* [14]. Furthermore, recent results have shown that the transcription factor *Ato* in *Drosophila*, regulating the expression of *Ase*, the non-mammalian homolog of *Ascl1*, has a dual role in proliferation and differentiation of neural progenitors [15]. These findings suggest that the cell cycle progression and differentiation of embryonic NSCs are regulated in a coupled manner through the expression of proneural genes. At present it remains unclear, whether cell cycle progression and differentiation of adult NSCs is also regulated in a coupled manner, and, in addition to that, whether such a coupled regulation would have an effect on tissue homeostasis.

Over the years, a number of insightful studies on renewal dynamics of stem cells have been conducted, ranging from models on stem cell dynamics in general [16, 17, 18, 19, 20, 21, 22, 23] to brain specific models [24, 25, 26, 27, 28, 29, 30, 31, 32]. The latter were used to explore

specific characteristics of neurogenesis, such as the role of fate determining signaling factors during development [28], or the migration of neuroblast cells to the olfactory bulb in adults [26]. Other models explored the conditions for homeostasis without further specifying the studied regenerating tissue [17, 19, 20, 21, 22, 23]. For instance, the dynamics of mutant accumulation in homeostatic tissues over time has been explored, showing that type and number of mutants depend on the division-tree length [23]. Especially the role of feedback signals controlling the balance between stem cell self-renewal and differentiation was investigated. It was shown that homeostasis based on stochastic processes needs to be regulated by negative regulatory feedback loops [20]. Furthermore, it was found that, depending on the applied feedback network, symmetric stem cell divisions can both stabilize or destabilize the homeostatic state of a population [21].

In order to study how a coupling between cell cycle progression and differentiation on the single cell level affects homeostasis, we developed a model in which stem cells have an intrinsic probability to progress through cell cycle and to differentiate. In our model, stem cells divide symmetrically, representing for instance adult NSCs [12]. We chose a stochastic approach as it allows to study how fluctuations that emerge at the cellular level affect population dynamics. With our model, we investigated the dynamics of stem cell populations with uncoupled and coupled cell cycle activity and differentiation. We evaluated how robust populations are maintained and how many pre-differentiated cells are produced. Furthermore, we analyzed single-cell RNA-Seq data of adult NSCs for a qualitative comparison to our simulation results.

This paper is organized as follows. In Section 2 we define our model and discuss the biological background underlying our assumptions. In Section 3 we present the results of our simulations (Section 3.1 and 3.2) and the RNA-Seq profiling analysis (Section 3.3), offering biological interpretation of the results. In Section 4 we discuss our findings.

2 Methods

2.1 Modeling a stem cell

We developed a stochastic model of stem cell dynamics in which the fate of a stem cell is determined by its probability to progress through cell cycle within a time frame Δt and its probability to differentiate.
In our model, we assign each stem cell a factor ϵ, where ϵ corresponds to:

$$\begin{cases} \epsilon : & \text{probability to progress through cell cycle within } \Delta t, \\ (1-\epsilon) : & \text{probability to not progress through cell cycle within } \Delta t, \end{cases} \tag{1}$$

with $\epsilon \in [0, 1]$. The cell cycle activity ϵ is inverse proportional to the cell cycle time τ_{cc} and given by $\epsilon = \frac{\Delta t}{\tau_{cc}}$. Further, each stem cell has a

$$\begin{cases} \alpha : & \text{probability to differentiate, and a} \\ (1-\alpha) : & \text{probability to maintain stemness,} \end{cases} \tag{2}$$

with $\alpha \in [0, 1]$.

Recent findings revealed that the divisions of NSCs in adult mice are mostly symmetrical [12]. Our model mimics the dynamics of adult NSCs by allowing stem cells to divide only symmetrically, either into two stem cells (symmetric proliferative division) or into two pre-differentiated cells (symmetric differentiative division). If a stem cell does not progress through cell cycle, it remains unchanged while keeping its typical stem cell properties. The dynamics of a stem cell are described by a discrete-time Markov chain, where each iteration has a set of 3 states: symmetric proliferative division, symmetric differentiative division and no division. A graphical representation of one iteration is shown in Figure 1(a). The probability of differentiation and self-renewal are given by $\epsilon\alpha$ and $\epsilon(1-\alpha)$, respectively.

2.2 Modeling a stem cell population

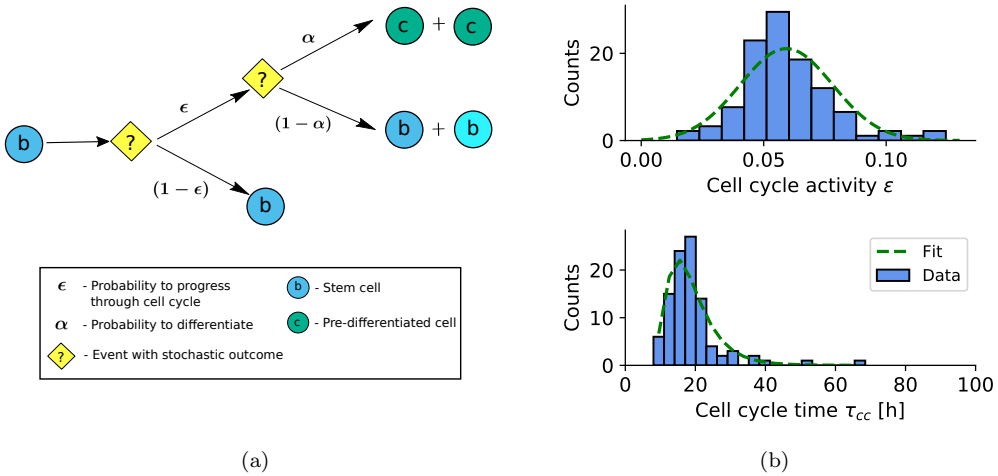
Several factors can lead to inhomogeneous populations, e.g. the spatial distribution of stem cells or biomolecular signaling. Our model allows for extrinsic and intrinsic sources of heterogeneity by assigning an individual value pair of cell cycle activity and differentiation probability (ϵ_k, α_k) to every stem cell. In case of a symmetric proliferative division, the daughter cell does not inherit the properties of its mother cell, being in line with an experimental study that revealed independent cell cycle times between mother and daughter cells in the rat retina [33].

We investigated stem cell populations with uncoupled and coupled cell cycle and differentiation probabilities. The probabilities (ϵ_k, α_k) for every stem cell of a population were generated according to a multivariate normal distribution $\mathbf{X} \sim \mathcal{N}_2(\mathbf{k}, \mathbf{\Sigma})$ with vector $\mathbf{k} = (\mu_\epsilon \ \mu_\alpha)^\mathsf{T}$ and covariance matrix

$$\mathbf{\Sigma} = \begin{pmatrix} \sigma_\epsilon^2 & c\sigma_\epsilon\sigma_\alpha \\ c\sigma_\epsilon\sigma_\alpha & \sigma_\alpha^2 \end{pmatrix}. \tag{3}$$

The mean values μ_ϵ, μ_α and standard deviations $\sigma_\epsilon, \sigma_\alpha$ determine the normal distribution of cell cycle activities and differentiation probabilities, respectively. The correlation coefficient $c \in [-1, 1]$ defines the type of coupling between cell cycle activity and differentiation.

For our simulations, we assumed average cell cycle times of $\tau_{cc} \simeq 20h$, which is close to measured cell cycle times for stem cells in the ventricular-subventricular zone (V-SVZ) of the adult mammalian brain [34]. We chose a time step of $\Delta t = 1h$. Figure 1(b) shows an exemplary histogram of cell cycle activities $\{\epsilon\}$ and the corresponding histogram of cell cycle times $\{\tau_{cc}\}$. We chose σ_ϵ such that the resulting distribution of the cell cycle times $\{\tau_{cc}\}$ resembles experimental measurements [33, 35]. Consequently, about 90% of all stem cells have a cell cycle time of $(20 \pm 10)h$, while the remaining ones are slow cycling stem cells that accumulate over time.



(a) (b)

Figure 1: (a) *Schematic representation of one iteration step. The probability of differentiation and self-renewal are given by* $\epsilon\alpha$ *and* $\epsilon(1-\alpha)$*, respectively.* (b) *Exemplary histogram of cell cycle activities* $\{\epsilon\}$ *and corresponding histogram of cell cycle times* $\{\tau_{cc}\}$*, with normal and log-normal fit, respectively.*

To study the dynamics of a stem cell population in a tissue, we summed over all stem cells at each iteration step to track the stem cell population size. The expected net change of the stem cell population B after one time step is given by

$$\Delta B = B_{t+1} - B_t = \sum_{k=1}^{B_t} \epsilon_k \cdot (1 - 2\alpha_k), \tag{4}$$

where B_t is the number of stem cells before the iteration step. For homeostasis, we assumed the stem cell population to be constant in size:

$$\langle \epsilon_k (1 - 2\alpha_k) \rangle_{k,t} = 0. \tag{5}$$

For all relevant parameter areas in our study, the differences in the solution for $\langle \alpha_k \rangle_k = \mu_\alpha$ between the statistically dependent and independent case, are negligible. Thus, we solve $\langle \epsilon_k \rangle_k \cdot \langle 1 - 2\alpha_k \rangle_k = 0$ to determine μ_α for the homeostatic case. The non-trivial solution is $\mu_\alpha = 0.5$, which implies that the stem cells are on average as likely to maintain stemness as to differentiate. We analyzed the average stem cell population dynamics for the non-homeostatic cases and found that a deviation from the homeostatic conditions ($\mu_\alpha \neq 0.5$ and $\mu_\epsilon > 0$) leads to a measurable change in the stem cell population size within approximately two days (Section A.1).

To evaluate and compare our simulations, we analyzed the number of differentiated daughter cells and the probability to maintain a stem cell population (robustness). We defined the differentiation rate D as the number of pre-differentiated cells C that were generated on average per time step, normalized by the initial stem cell population size B_0:

$$D = \frac{C_{t_{end}}}{t_{end} \cdot B_0}, \tag{6}$$

with t_{end} being the simulation time. We simulated the stem cell population dynamics for different t_{end} and we set $B_0 = 50$. For every t_{end}, we simulated $n = 300$ populations and evaluated how many stem cell populations $\tilde{n}$ could maintain their size, i.e. were neither lost ($B_{t_{end}} = 0$) nor did overgrow ($B_{t_{end}} \geq 2B_0$) within the given time period t_{end}. We calculated the robustness R as follows:

$$R = \frac{\tilde{n}}{n}. \tag{7}$$

2.3 Analysis of single-cell RNA-Seq data

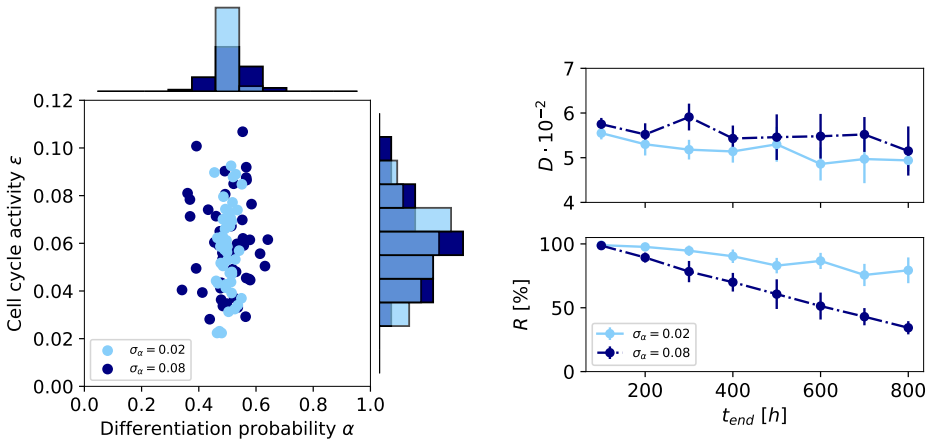
We analyzed public single-cell RNA-Seq data of adult NSCs [36] for a qualitative comparison to our simulation results. From the RNA-Seq data, we extracted cell cycle and differentiation marker expression levels, which we related to the cell cycle activity ϵ and differentiation probability α in our model. The goal of this analysis was, to extract information on the coupling between cell cycle activity and differentiation of adult NSCs.

For our analysis, we plotted the expression levels of cell cycle markers (*Mki67, Mcm2, Ccnd1* [36, 37, 38]) and differentiation markers (*Ascl1, Neurog2, Neurod2* [34, 39, 40]) on a $\log_2$ scale against each other, excluding data points with zero expression for both marker types. We then computed the Pearson correlation coefficient (PCC) and did a bootstrapping analysis to evaluate the accuracy of the determined PCC.

3 Results

3.1 Uncoupled cell cycle progression and differentiation

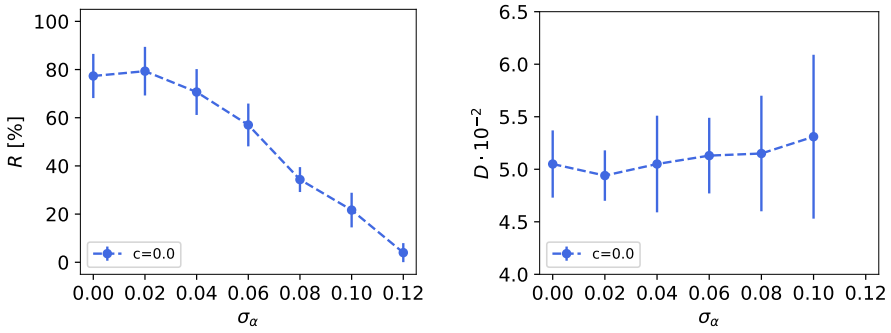
First, we studied the dynamics of stem cell populations with uncoupled cell cycle activity and differentiation. To do so, we generated probabilities as described in Section 2.2 with various σ_α and $c = 0$. Two exemplary distributions are shown in Figure 2(a) and further exemplary distributions are shown in Figure A.2. We simulated the dynamics of two stem cell population types with distinct differentiation heterogeneity levels ($\sigma_\alpha = 0.02, \sigma_\alpha = 0.08$) for different simulation times t_{end}. We found that for both population types the average differentiation rates D are not significantly changing for different simulation times, while a population with higher differentiation heterogeneity tends to generate more differentiated progeny (Figure 2(b), top). Evaluating the robustness R, we observed that for both differentiation heterogeneity levels, the probability to maintain a population decreases for increasing simulation times (Figure 2(b), bottom). Although the robustness of populations with lower differentiation heterogeneity decreases significantly slower, there is no life-long homeostasis for a population with uncoupled cell cycle and differentiation activities.



(a) (b)

Figure 2: (a) *Two exemplary stem cell populations with uncoupled cell cycle and differentiation and distinct differentiation heterogeneity levels. The histograms show an overlay of cell cycle activity and differentiation probability distributions, respectively, where the bars for* $\sigma_\alpha = 0.02$ *are transparent.* (b) *Average differentiation rates* D *(top) and average robustness* R *(bottom) of two stem cell population types with uncoupled cell cycle and differentiation for different simulation times* t_{end}*. The level of heterogeneity affects the probability for maintaining homeostasis significantly, while the production of differentiated progeny is not affected.*

Focusing on long-term simulations ($t_{end} = 800h \simeq$ one month), we observed that the level of heterogeneity in the differentiation probabilities has a strong impact on homeostasis: the higher the differentiation heterogeneity level, the lower the probability to maintain a stem cell population (Figure 3(a)). Furthermore, the probability for overgrowth among the unstable cases increases from around 50% for $\sigma_\alpha = 0$ to 100% for $\sigma_\alpha = 0.12$. Both results are likely to be caused by the dynamics of stem cells that have a high cell cycle activity and are more likely to maintain stemness: these cells cause a stem cell population to (over-)grow and their number increases with increasing differentiation heterogeneity. Moreover, the long-term simulations revealed that the differentiation rates D of populations with a robustness $\geq 10\%$ do not significantly change for various differentiation heterogeneity levels (Figure 3(b)). However, stem cell populations with heterogeneous differentiation probabilities tend to be larger and thus have on average slightly higher differentiation rates than stem cell populations with homogeneous differentiation probabilities.

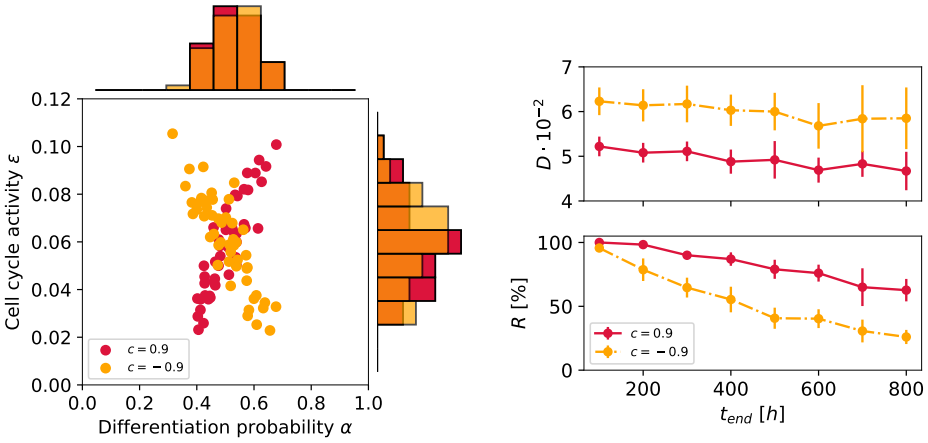


(a) (b)

Figure 3: *Long-term ($t_{end} = 800h$) robustness and differentiation rates of stem cell populations with uncoupled cell cycle and differentiation for various σ_α.* (a) *The higher σ_α, the lower the probability for a population to be maintained.* (b) *The level of heterogeneity in the differentiation probabilities does not affect the differentiation rates significantly. More heterogeneous differentiation probabilities induce the generation of more differentiated progeny.*

3.2 Coupled cell cycle progression and differentiation

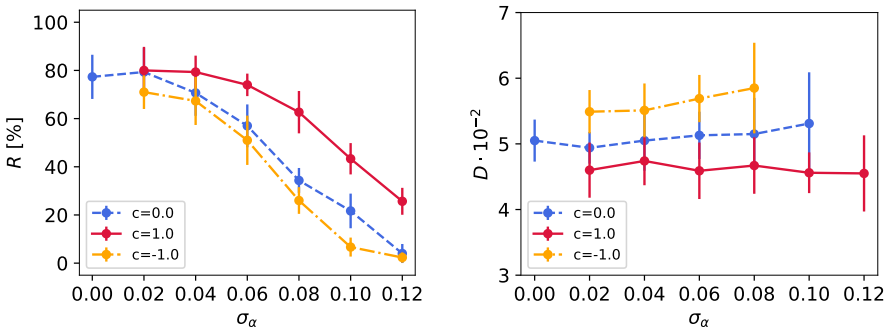
Having analyzed uncoupled stem cell populations, we investigated stem cell populations with coupled cell cycle and differentiation activities. Again, we generated probabilities as described in Section 2.2 with various σ_α and $c \neq 0$. Two exemplary distributions are shown in Figure 4(a) and further exemplary distributions are shown in Figure A.2. We studied the dynamics of stem cell populations with coupled cell cycle and differentiation activities and $\sigma_\alpha = 0.08$. We found that for all simulation times, a negative coupling results in significantly higher average differentiation rates D than a positive coupling (Figure 4(b), top). Evaluating the robustness R, we observed that for both, populations with positive and negative coupling, the probability to be maintained in the long term is lower than in the short term (Figure 4(b), bottom). The probability to maintain homeostasis decreases significantly slower for populations with a positive coupling than for populations with a negative coupling. However, there is no life-long homeostasis for a population with coupled cell cycle and differentiation activities.



(a) (b)

Figure 4: (a) *Two exemplary coupled stem cell populations with positive and negative correlation. The histograms show an overlay of cell cycle activity and differentiation probability distributions, respectively, where the bars for* $c = -0.9$ *are transparent.* (b) *Average differentiation rates* D *(top) and average robustness* R *(bottom) of two coupled stem cell population types for different simulation times* t_{end}*. A negative coupling increases differentiation rates, while a positive coupling increases the probability for maintaining homeostasis.*

Focusing on long-term simulations ($t_{end} = 800h \simeq$ one month), we observed that the type of coupling between cell cycle activity and differentiation has a strong impact on homeostasis. A positive correlation increases the probability for a tissue to be maintained in the long term (Figure 5(a)) and decreases its average differentiation rates D (Figure 5(b)). In contrast, a negative correlation decreases the probability for a tissue to be maintained in the long term. At the same time, it results in the highest average differentiation rates D for stem cell populations with a robustness $\geq 10\%$. Furthermore, we found that the probability for overgrowth among the unstable cases merely depends on the differentiation heterogeneity level and is independent of the coupling type. Stem cell populations with a coupling between cell cycle activity and differentiation mainly consist of two subpopulations: slow dividing stem cells and fast dividing stem cells, which are either more likely to maintain stemness or more likely to differentiate. For populations with a negative coupling, the slow dividing stem cells are more likely to differentiate and the fast dividing stem cells are more likely to maintain stemness, which causes populations to (over-)grow. At the same time, because these stem cell populations are larger, they enable the generation of more pre-differentiated progeny compared to populations with a positive coupling. For populations with a positive coupling, the fast dividing stem cells are more likely to differentiate, while the cells that are more likely to maintain stemness divide slowly, which enables robustness of a population in the long term.



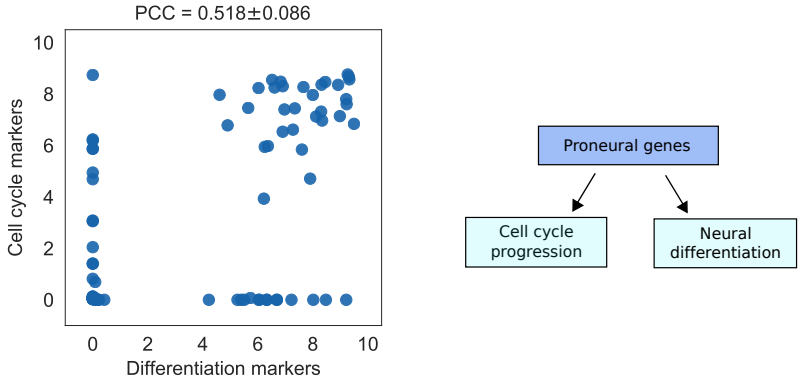
(a) (b)

Figure 5: *Long-term ($t_{end} = 800h$) robustness and differentiation rates of stem cell populations with coupled cell cycle and differentiation for various σ_α.* (a) *A positive coupling increases the probability for maintaining homeostasis.* (b) *A negative coupling increases differentiation rates, while a positive coupling lowers them.*

3.3 Single-cell RNA-Seq data of adult murine NSCs

In our simulations, we observed the most robust stem cell populations for a positive correlation between cell cycle activity and differentiation (Figure 5(a)). We also found a positive correlation between cell cycle and differentiation marker expression levels in the adult murine SVZ (Figure 6(a)). This finding indicates that an adult NSC population is likely to prioritize its robust maintenance rather than a high amount of differentiated progeny. We saw this positive correlation confirmed when we analyzed the subpopulation of stem cells which have non-zero expression levels in both, cell cycle and differentiation markers (A.3).

An underlying mechanism for a coupling of cell cycle and differentiation on the molecular level could be driven by proneural genes regulating both processes in a coupled manner (Figure 6(b)). Determining which molecular players might be involved in such a regulation will require further experimental investigation.



(a) (b)

Figure 6: (a) *Analysis of single-cell RNA-Seq data of adult mouse NSCs [36] reveals a positive correlation between cell cycle and differentiation marker expression levels.* (b) *Schematic representation of a possible underlying molecular mechanism of a coupled regulation of cell cycle progression and differentiation.*

4 Discussion

Homeostasis is an important mechanism for the sustainment of adult tissues during life. Various organs regenerate via tissue homeostasis, and there is evidence that also complex organs like the brain make use of it. Here, we presented a stochastic model to study stem cell dynamics in the adult brain. We focused on the interplay between cell cycle activity and differentiation on the cellular level and its impact on stem cell population dynamics. We also analyzed single-cell RNA-Seq data of adult NSCs for a qualitative comparison to our simulation results. In the following, we present and discuss the main findings of this study.

Our simulations showed that the probability to maintain homeostasis decreases with increasing differentiation heterogeneity. Furthermore, we found that a coupling of cell cycle and differentiation has an effect on stem cell population dynamics, and, depending on whether the coupling is positive or negative, increases or decreases the robustness of homeostasis in an adult tissue, respectively. A coupling between cell cycle activity and differentiation leads to the generation of two subpopulations within a stem cell population. There are slow dividing and fast dividing stem cells, which are either more likely to maintain stemness or more likely to differentiate. In a population with a positive coupling, the fast dividing stem cells are more likely to differentiate and the slow dividing stem cells are more likely to maintain stemness. This combination leads to an increase in the typical lifetime of a stem cell pool. How subpopulations within a stem cell population could be generated remains unclear. For instance, limited access to a stem cell niche in combination with a short range signal can possibly generate two or more subpopulations of stem cells.

Although a positive coupling between cell cycle and differentiation leads to a significantly higher long-term robustness for heterogeneous differentiation probabilities, it is also advantageous for a stem cell population to keep the heterogeneity level of differentiation low. Based on our theoretical analysis, we cannot conclude which of these scenarios is probably the case in the adult brain. Other studies report heterogeneous gene expression amongst stem cells within a population, suggesting the existence of differentiation heterogeneity within a NSC population. For instance, there is evidence for heterogeneity in gene expression among hematopoietic stem cells [41, 42, 43]. Furthermore, heterogeneity among the NSCs in the mammalian brain prevails in terms of proliferation dynamics and regional identity [44]. A central question is, whether the heterogeneity is a reflection of intrinsic differences of NSCs or is caused by an external signal [10].

Single-cell RNA-Seq is a powerful method to compare gene expression levels of cells within a population. Our qualitative analysis of single-cell RNA-Seq data of adult NSCs showed a positive correlation between the expression of cell cycle markers and differentiation markers, indicating that cell cycle activity and differentiation are indeed coupled. As RNA-Seq data has several limitations, such as providing a snapshot of gene expression in time and allowing for a relative quantification of gene expression levels only, we can neither conclude that the differentiation probabilities are heterogeneous and positively coupled nor that they are rather homogeneous. Nonetheless, the idea that both, cell cycle progression and differentiation, are controlled by the same molecular players could explain a positive correlation between these two key components of homeostasis. The proneural gene *Ascl1*, associated with differentiation of neuronal progenitor cells [14], could be part of a molecular network that regulates cell cycle progression and differentiation of NSCs in a coupled manner. The existence and the details of such a regulating network will require further experimental investigation, as well as the identification of additional molecular players.

In this study, our focus was on exploring the effect of a coupled internal regulation of cell cycle activity and differentiation on stem cell population dynamics. Explicit regulating factors are not part of our model, as they were intensively explored in former studies [17, 21]. As there is no long-term homeostasis without external control, we propose that feedback signaling among the stem cells or signaling from the stem cell niche are the building blocks to maintain a stem cell population. In addition, a coupling of cell cycle activity and differentiation of stem cells gives a stem cell population an internal robustness and is thus likely to be part of a homeostatic strategy. Furthermore, a certain, if only small, amount of adult NSCs dividing asymmetrically can further increase the stability of homeostasis, as well as stem cell quiescence.

If the balance between stem cell self-renewal and differentiation gets out of equilibrium, the

stem cell population suffers overgrowth or depletion of the stem cell population, resulting in fatal consequences for the organ such as tumorigenesis [3, 45, 46]. Our simulation results have shown that a stem cell population whose cell cycle activity and differentiation are negatively correlated is rather unstable: it tends to overgrow, while producing many differentiated cells at the same time. This results in the question whether in case of disease, a regulating molecular mechanism might possibly be altered and adopt a state that is similar to the negatively coupled one. In summary, in terms of neurogenesis and neural diseases related to tissue overgrowth, the molecular link between cell cycle progression and differentiation in NSCs is worthwhile to study further.

Materials

Code Availability

For simulations and data analysis we used Python programming language (Python Software Foundation, `https://www.python.org/`).
Our code is available on `https://github.com/astopka/StochasticModelNSC.git`.

Data Availability

For the analysis of single-cell RNA-Seq data we used the public dataset from [36] and the processed data was downloaded from `https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE67833`.

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A Appendix

A.1 Average stem cell population dynamics

We studied the average stem cell population dynamics, assuming constant average stem cell properties $\epsilon = \langle \epsilon_k \rangle_k, \alpha = \langle \alpha_k \rangle_k$ for any time. Equation (4) then becomes

$$\frac{dB}{dt} = [\epsilon \cdot (1 - 2\alpha)]B(t) \tag{8}$$

with the solution

$$B(t) = B_0 \cdot e^{[\epsilon \cdot (1-2\alpha)]t}. \tag{9}$$

We characterized the evolution of a stem cell population by bringing the initial population size B_0 in relation to the final population size $B_{t_{end}}$:

$$\rho_B = \frac{B_{t_{end}}}{B_0}. \tag{10}$$

There a three possible scenarios for the evolution of a stem cell population over time: it can be constant in size ($\rho_B = 1$), grow ($\rho_B > 1$) or shrink ($\rho_B < 1$), where the two latter cases occur under non-homeostatic conditions (Figure A.1). We analyzed the non-homeostatic cases and found that even a minimal deviation from the homeostatic cell cycle and differentiation activity leads to a vast change in the stem cell population size within the time of two average cell cycles ($t_{end} = 40h$). Both, overgrowth and depletion, become stronger with an increasing average cell cycle activity $\langle \epsilon_k \rangle_k$.

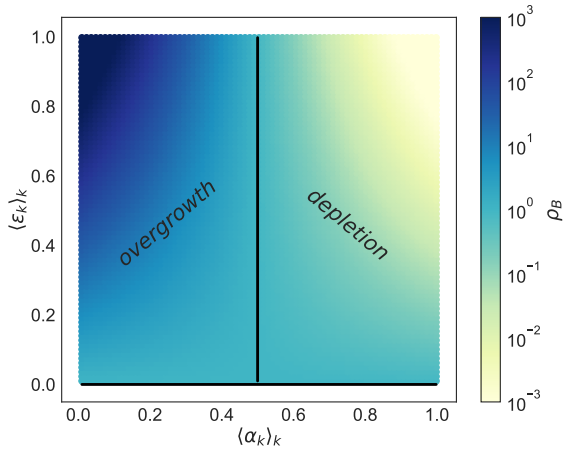

Figure A.1: *Average stem cell population dynamics for the homeostatic cases (black lines) and the non-homeostatic cases for* $t_{end} = 40h$.

A.2 Exemplary distributions of stem cell probabilities

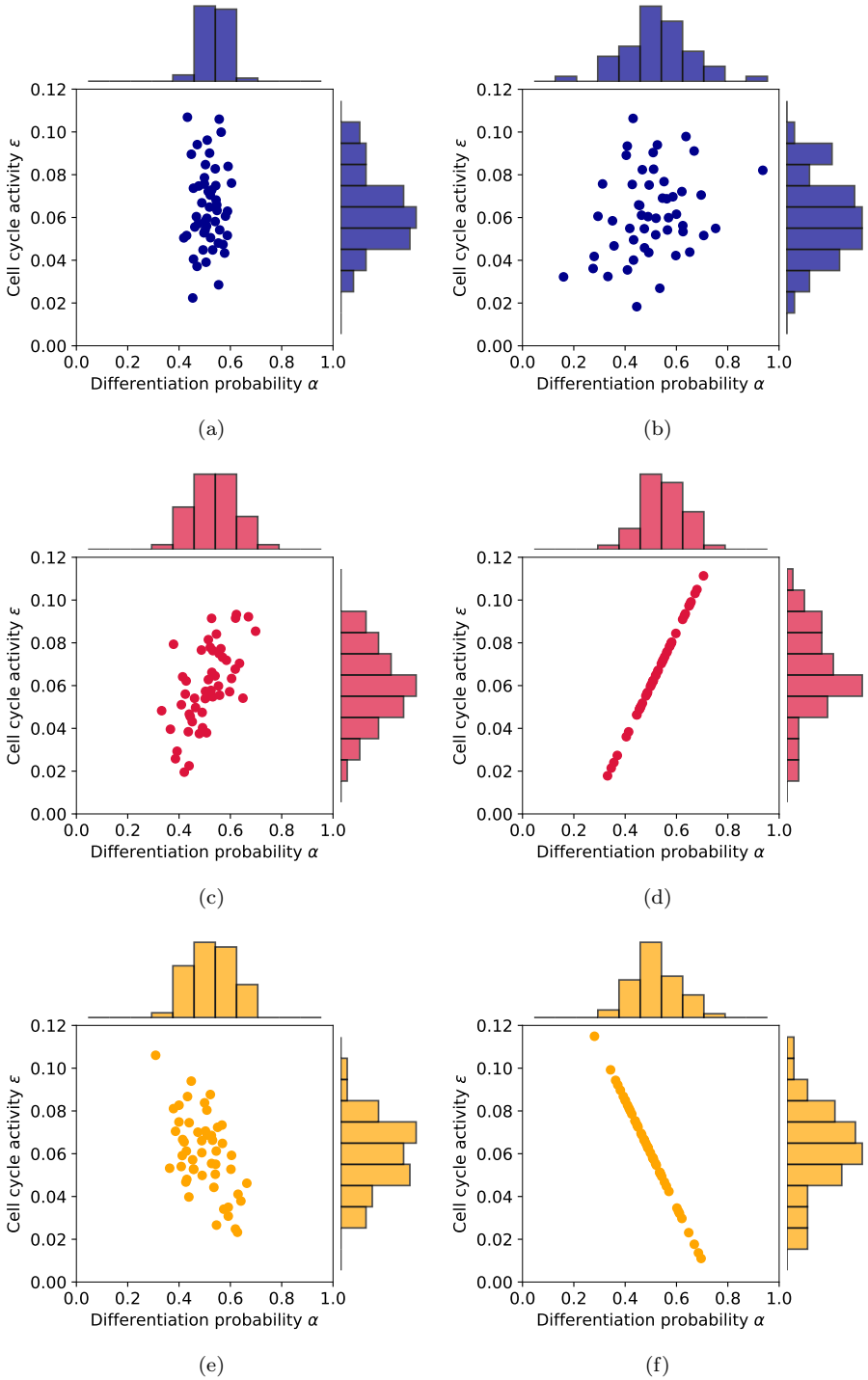

Figure A.2: (a) *Uncoupled probabilities with* $\sigma_\alpha = 0.04, c = 0$. (b) *Uncoupled probabilities with* $\sigma_\alpha = 0.12, c = 0$. (c) *Coupled probabilities with* $\sigma_\alpha = 0.08, c = 0.5$. (d) *Coupled probabilities with* $\sigma_\alpha = 0.08, c = 1.0$. (e) *Coupled probabilities with* $\sigma_\alpha = 0.08, c = -0.5$. (f) *Coupled probabilities with* $\sigma_\alpha = 0.08, c = -1.0$.

A.3 Subpopulation in single-cell RNA-Seq data of adult murine NSCs

Here, we analyzed the subpopulation of cells that do have non-zero expression levels in both gene marker sets. For this analysis, we excluded cycling cells that do not express differentiation markers and cells that do express differentiation markers without cell cycle activity. The results show, that also for this subpopulation there is a positive correlation between cell cycle and differentiation in the adult (Figure A.3).

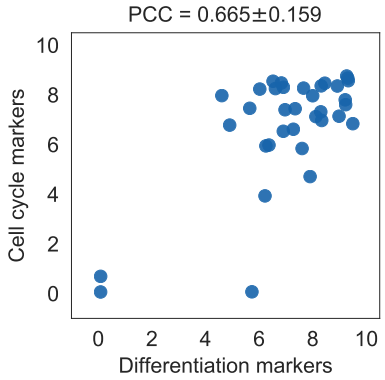

Figure A.3: *Cell cycle marker expression levels against cell differentiation marker expression levels of those adult mouse NSCs [36], that express both, cell cycle and differentiation markers.*