Supporting Information

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SI1. Table 1. The fraction of all the cell types from E10.5 to E18,5 mouse embryonic stages

stage (E)	f_neuron (%)	f_NE (%)	f_bIP (%)	f_gliaP (%)	f_GABA (%)	f_RG (%)
10.5	0.845571108	90.28406957	0.127226463	0	0	7.769108819
11.5	11.80248988	60.68040374	0.975890699	0	0	32
12.5	23.39400222	31.64503913	2.361291507	0	0	44.69682432
13.5	34.1993264	20.44139306	6.862271538	0	0.978648858	40.68457
14.5	42.71070425	7.853673648	4.653398698	0	7.217990392	32.55542824
15.5	57.41456307	5.04806366	6.201175178	0	9.41505857	22.67529465
16.5	68.29161543	3.247719875	7.932708172	1.169447197	11.58025907	12.87298949
17.5	68.21109828	1.519037493	4.448543791	2.124757068	13.65369756	9.672291539
18.5	69.88534977	0.357770876	3.380929081	5.024485716	17.03225748	6.597338797

sem_neuron	sem_NE	sem_bIP	sem_gliaP	sem_GABA	sem_RG
0.197615708	1.652851304	0.127226463	0	0	2.126814588
2.010652241	3.201937518	0.124361452	0	0	5.542280026
0.447644187	3.876815793	0.621867876	0	0	2.056630212
3.892021873	3.361393601	1.137055772	0	0	3.23289547
5.264768257	1.728452574	0.808030687	0	0	0.893415138
5.184228918	0.24893758	1.023955256	0	0	2.174084039
1.901258292	0.523752827	1.106654324	0.434565785	0.434565785	2.228536169
2.263722124	0.430639833	2.280864764	0.354942669	0.354942669	3.834065794
3.409491769	0.16	1.435636474	0.439707402	0.439707402	2.090878471

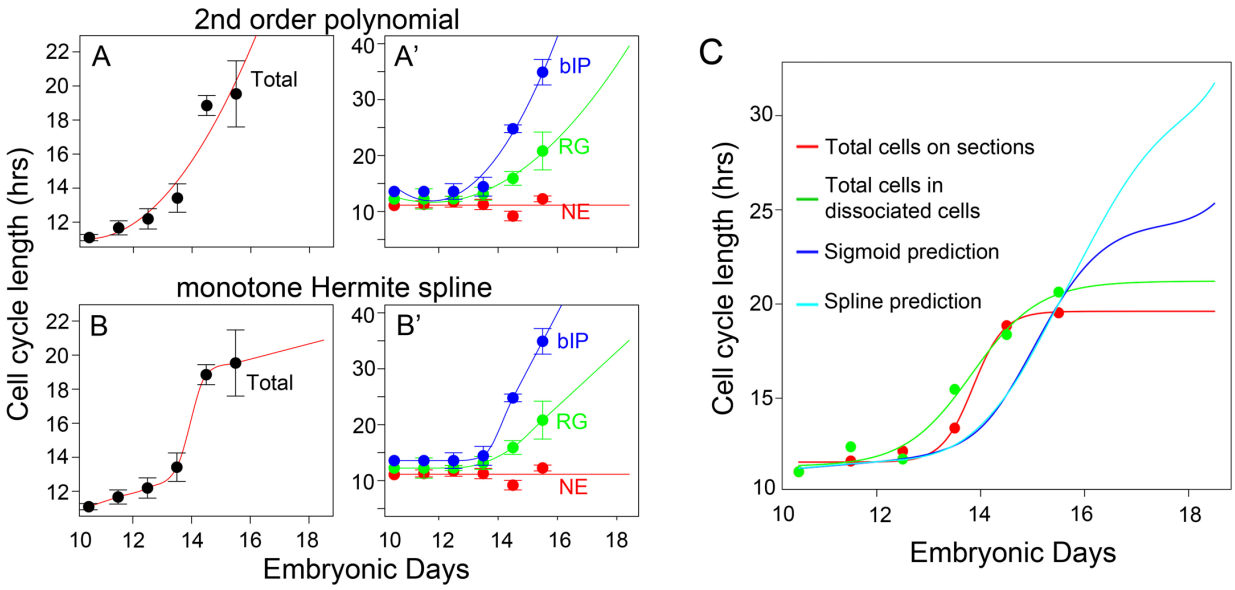
SI2. Table 2. The fraction of cell death from E10.5 to E14,5 mouse embryonic stages

Embryonic stages (E)	Cell death (%)
10.5	0.798190768
11.5	0.465611281
12.5	0.665158973
13.5	1.463349741
14.5	0.199547692

SI3. Table 3. Cell cycle length data of published and this study

	Takahashi et al (1996)	**This study**				
Embryonic stages (E)	the VZ on sections (hr)	the VZ on sections (hr)	dissociated total cells (Nestin+) (hr)	Dissociated NE cells (Blbp-Glast-Tbr2-, Nestin+) (hr)	Dissociated RG cells (Blbp+Glast+) (hr)	Dissociated RG cells (Tbr2+) (hr)
10.5	NA	11.1	11	11	NA	NA
11.5	NA	12.4	11.7	11.3	11.8	NA
12.5	10.2	11.8	12.2	11.7	11.4	13.6
13.5	11.4	15.5	13.4	11.3	13.1	13.2
14.5	15.1	18.4	18.9	9.2	19.6	25.3
15.5	17.5	20.6	19.5	12.3	19	34.9
16.5	18.4	NA	NA	NA	NA	NA

SI4. Figure S1 Comparison of fitting methods for the estimation of each progenitor type



(A-B') Alternative models of the cell cycle data. 2nd order polynomial fitting curves (A, A') or a monotone Hermite spline interpolation to the same data corresponding to the Figure 2K-M. The cell cycle length of NE is fitted by a constant. (C) Predicted average cell cycle length of total progenitor population calculated from the estimated cell cycle lengths of NE, RG, bIPs, and glial progenitors. Cell cycle length of RGs and bIPs are modeled by sigmoid function (blue) or spline interpolation (light blue). The cell cycle length of glial progenitors is set to a constant based on published data (22.5 hours; Knapp et al., 1992, shorter than 24 hours; Burns et al., 2009) (1, 2). Experimentally measured average cell cycle length of total progenitor population using total cells on section (red) and that of total dissociated cells (green) are shown for comparison. Prediction with the sigmoid function models is closer to experimentally measured results.

SI5. Modelling of NE and RG behaviors with cell type-specific cell cycle length for Figure 3

NEs, RGs, and bIPs have distinct cell-cycle lengths (Figure 2). To incorporate the different cell cycle lengths in estimation of expansion coefficients (α_s, α_r), the model described in the main text is evolved as follows. We exclusively consider cells derived from NEs, and the developmental stages in which the fraction of RG-derived glial progenitor is negligible (from E10.5 to E17.5). That is,

$$s(t) + r(t) + p(t) + \nu(t) = 1 \qquad (1)$$

where $s(t)$, $r(t)$, $p(t)$, and $\nu(t)$ are the fractions of NEs, RGs, bIPs, and excitatory neurons at time t (E10.5 ≤ t ≤ E17.5).

In a short period of time (Δt), in which cell cycle lengths of the progenitors ($T_x(t)$, with $x = s, r, p$) can be regarded as constants, the fraction of the progenitors that undergo cell division is $\Delta t/T_x(t)$ (assuming equal cell density throughout the cell cycle). When $N(t)$ is the total number of cells at time t, $N(t+\Delta t)$ is;

$$N(t+\Delta t) = \overbrace{\left(1-\frac{\Delta t}{T_s(t)}\right)s(t)N(t) + 2\frac{\Delta t}{T_s(t)}s(t)N(t)}^{cells\ from\ NEs} + \overbrace{\left(1-\frac{\Delta t}{T_r(t)}\right)r(t)N(t) + 2\frac{\Delta t}{T_r(t)}r(t)N(t)}^{cells\ from\ RGs}$$
$$+ \overbrace{\left(1-\frac{\Delta t}{T_p(t)}\right)p(t)N(t) + 2\frac{\Delta t}{T_p(t)}p(t)N(t)}^{cells\ from\ bIPs} + \overbrace{\nu(t)N(t)}^{neuron}$$

Applying (1) to the equation above yields;

$$N(t+\Delta t) = \left(1+\frac{\Delta t}{T(t)}\right)N(t) \qquad (2)$$

where

$$\frac{1}{T(t)} = \frac{s(t)}{T_s(t)} + \frac{r(t)}{T_r(t)} + \frac{p(t)}{T_p(t)}$$

A. Evolution of expansion coefficient of NE (α_s)

Let $n_s(t)$ be the number of NEs at time t.

$$n_s(t+\Delta t) = \overbrace{\left(1-\frac{\Delta t}{T_s(t)}\right)n_s(t)}^{no\ division} + \overbrace{\alpha_s\frac{\Delta t}{T_s(t)}n_s(t)}^{NE\rightarrow NE} = \left\{1+(\alpha_s-1)\frac{\Delta t}{T_s(t)}\right\}n_s(t) \qquad (3)$$

Dividing this equation (3) by (2) results

$$s(t+\Delta t) = \frac{1+(\alpha_s-1)\varphi_s(t)}{1+\varphi(t)} \cdot s(t) \qquad (4)$$

where $\varphi(t) = \Delta t/T(t)$, $\varphi_x(t) = \Delta t/T_x(t)$ (with x = s,r,p).

In (4), all the variables but α_s are known. Solving (4) for α_s yields;

$$\alpha_s = \frac{s(t+\Delta t)\big(1+\varphi(t)\big)-s(t)}{s(t)\varphi_s(t)} + 1 \qquad (5)$$

B. Evolution of expansion coefficient of RG (α_r) from NE and RG fractions

Let $n_r(t)$ be the number of RGs at time t.

$$n_r(t+\Delta t) = \overbrace{\left(1-\frac{\Delta t}{T_r(t)}\right)n_r(t)}^{no\ division} + \overbrace{\alpha_r\frac{\Delta t}{T_r(t)}n_r(t)}^{RG\to RG} + \overbrace{\beta_s\frac{\Delta t}{T_s(t)}n_s(t)}^{NE\to RG} \qquad (6)$$

With $\alpha_s+\beta_s = 2$, summing (6) and (3) yields;

$$n_s(t+\Delta t) + n_r(t+\Delta t) = \big(1+\varphi_s(t)\big)n_s(t) + \big\{1+(\alpha_r-1)\varphi_r(t)\big\}n_r(t)$$

Dividing the above equation by (2) results;

$$s(t+\Delta t) + r(t+\Delta t) = \frac{\Big(1+\varphi_s(t)\Big)s(t) + \big\{1+(\alpha_r-1)\varphi_r(t)\big\}r(r)}{1+\varphi(t)}$$

Solving the above equation for α_r yields;

$$\alpha_r = \frac{\big(s(t+\Delta t)+r(t+\Delta t)\big)\big(1+\varphi(t)\big)-\Big(1+\varphi_s(t)\Big)s(t)-r(t)}{r(t)\varphi_r(t)} + 1 \qquad (7)$$

C. Evolution of expansion coefficient of RG (α_r) from RG, bIP, and neuron fractions

Let $n_p(t)$ be the number of bIPs at time t.

$$n_p(t+\Delta t) = \overbrace{\left(1-\frac{\Delta t}{T_p(t)}\right)n_p(t)}^{no\ division} + \overbrace{\alpha_p\frac{\Delta t}{T_p(t)}n_p(t)}^{bIP\to bIP} + \overbrace{2\Phi_2\big(1-\mu_2\big)\frac{\Delta t}{T_r(t)}n_r(t)}^{RG\to 2bIP} + \overbrace{\Phi_1\big(1-\mu_1\big)\frac{\Delta t}{T_r(t)}n_r(t)}^{RG\to 1bIP}$$

(8)

where Φ_1 and Φ_2 denote probabilities that that RGs generate one neuron or two neurons, respectively.

Let $n_n(t)$ be the number of neurons at time t.

$$n_n(t+\Delta t) = \overbrace{n_n(t)}^{neuron} + \overbrace{\beta_p\frac{\Delta t}{T_p(t)}n_p(t)}^{bIP\to neuron} + \overbrace{2\Phi_2\mu_2\frac{\Delta t}{T_r(t)}n_r(t)}^{RG\to 2neuron} + \overbrace{\Phi_1\mu_1\frac{\Delta t}{T_r(t)}n_r(t)}^{RG\to 1neuron} \qquad (9)$$

With $\alpha_p+\beta_p = 2$ and $\beta_r = 2\Phi_2+\Phi_1$, summing (8) and (9) yields;

$$n_p(t+\Delta t)+n_n(t+\Delta t) = n_n(t)+\Big(1+\varphi_p(t)\Big)n_p(t)+\beta_r\varphi_r(t)n_r(t)$$

Dividing the above equation by (2) results;

$$p(t+\Delta t)+n(t+\Delta t) = \frac{n(t)+\Big(1+\varphi_p(t)\Big)p(t)+\beta_r\varphi_r(t)r(t)}{1+\varphi(t)}$$

Solving the above equation for β_r yields;

$$\beta_r = \frac{\big(p(t+\Delta t)+n(t+\Delta t)\big)\big(1+\varphi(t)\big)-\Big(1+\varphi_p(t)\Big)p(t)-n(t)}{r(t)\varphi_r} \qquad (10)$$

α_r is obtained by;

$\alpha_r = 2-\beta_r$ (11)

References

1. P. E. Knapp, The cell cycle of glial cells grown in vitro: an immunocytochemical method of analysis. *J Histochem Cytochem.* **40**, 1405–1411 (1992).

2. K. A. Burns, B. Murphy, S. C. Danzer, C.-Y. Kuan, Developmental and post-injury cortical gliogenesis: A Genetic fate-mapping study with Nestin-CreER mice. *Glia* **57**, 1115–1129 (2009).