	Data fitted with:		
	Asymptote model	Exponential model	Gamma model
$d/\bar{d}_\alpha/k$	2.87 (2.22—3.65)	1.94 (1.46—2.6)	0.12 (0.09—0.17)
$\bar{d}_1$, % day^{-1}	0.57 (0.5—0.67)	0.59 (0.51—0.7)	0.62(0.53—0.78)
$\bar{d}_2$	0.41 (0.34—0.5)	0.44 (0.36—0.53)	0.43 (0.34—0.54)
$\bar{d}_3$	0.38 (0.31—0.47)	0.41 (0.33—0.5)	0.37 (0.27—0.48)
$\bar{d}_4$	0.41 (0.33—0.5)	0.44 (0.36—0.54)	0.43 (0.32—0.57)
τ_1, day	1. (0.91—1.51)	1. (0.93—1.53)	1. (0.93—1.57)
τ_2	0.78 (0.28—1.)	0.81 (0.35—1.)	0.8 (0.31—1.)
τ_3	1.97 (1.—2.65)	2.06 (1.14—2.7)	1.87 (0.73—2.67)
τ_4	1.7 (0.98—2.45)	1.83 (1.—2.54)	1.79 (1.—2.58)
RSS, 10^{-3}	6.19	5.94	5.87

Table S2: Average turnover rates of $CD4^+$ T cells from four healthy humans as estimated by fitting the data from Mohri et al. [2] using the Asymptote model, the Exponential model, and the Gamma model. The best fits of the models resulted in different average rates of cell turnover $\bar{d}_i$ and initial delays of labeling τ_i. Other parameters, that could be assumed to be identical between different individuals, are the death rate of labeled cells d (Asymptote model), the rate of turnover $\bar{d}_\alpha$ of the turning-over sub-population in the Exponential model, and the shape parameter k in the model with gamma distributed turnover rates. For the model with gamma distributed turnover rates, an asymptote level $\alpha = 1$ provided the best fit of the data. The quality of the fit is illustrated by the residual sum of squares (RSS). The 95% confidence intervals were obtained by bootstrapping the residuals with 1000 simulations.