









m l l a c a g t a g l c t o n l a c o m l t o l n a m t a t m m a -  
 n m t o l a l t o l c a g t m o t . t m o t o c m o t o n a f a n n  
 o m g o m t m l m o m o c a g t x o n a a m t ( ).  
 o n t a n a g o o l l t o l m o t , o t o n n o m n t t g l  
 c a g t n a t a a m t . o a e a g a t , t n t m n  $R_i = 0$  a n a t m  
 a  $R_c$  a g t a l t o a t n a m t a t t a a t t o n

$$R_c(t) = (R_2 - R_1)H_{\theta}(t - 0.5) + R_1. \tag{5}$$

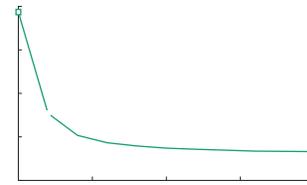
t , a t c t o m e a g a  $R_1$  o e a g a  $R_2$  a  $t = 0.5$ .  
 o t t g l e a g a t , o m a t o l n a m t t o l a l m o t a n o m  
 c a t t t m l o c o l l a t g t o l c a a t c o o t c t o n m o t n o  
 c a t t o l n a m t . c c a l l c a a t o n n a m t m o t n t o t  
 o t g l , c c a g t n a c o n g t t o n c o m n a o t o - a n o t -  
 c a g t a a l t (



... e ag d'v, mal' a g t' n nm n' m l' c ag t' n' u  
 al a c a a t' n' t' ol nanc' a a a t' c ag t' n a a' mla m m  
 a a c ag t' n a ( ). t' a g m l' l  
 t' ol m t', g anc, n' n nm n' t' g l' c ag t' n' u al  
 $m = \frac{2^2}{2}$  a g t' n a a t' n

$$\mu(t) = (\mu_2 - \mu_1)H_{\theta}(t - 0.5) + \mu_1. \quad ( )$$

... t' g l' e ag d'v, g a n' n' mla t' ol m t' m t' n a e ag  
 d'v ( ). m , n t' d' m m m c ag t' n' u al al a t' m c  
 m m m c ag t' n t' n' a m. t' t' a n m l' a p -41.994 a p -41.993 - . %/



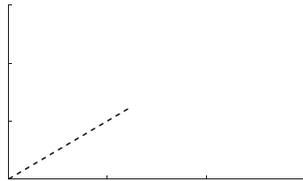
The model is a simple compartmental model. We consider a population of size  $N$  divided into three compartments:  $S$  (susceptible),  $I$  (infected), and  $R$  (recovered). The total number of individuals is constant,  $S + I + R = N$ . The model is described by the following system of ordinary differential equations (ODEs):

$$\begin{aligned} \dot{S} &= -\beta SI + \gamma R \\ \dot{I} &= \beta SI - \gamma I \\ \dot{R} &= \gamma I \end{aligned}$$

where  $\beta$  is the transmission rate and  $\gamma$  is the recovery rate. The initial conditions are  $S(0) = N - I_0$  and  $I(0) = I_0$ , where  $I_0$  is the initial number of infected individuals. The model is solved numerically using the Runge-Kutta method. The results show that the number of susceptible individuals decreases over time, while the number of infected individuals increases and then decreases, and the number of recovered individuals increases. The final number of recovered individuals is  $R(\infty) = N - I_0$ .







model,  $\lambda$  is the model parameter, and  $\sigma$  is the standard deviation of the noise. The likelihood function is defined as  $L(\theta) = \prod_{i=1}^n p(y_i | x_i, \theta)$ . The maximum likelihood estimate (MLE) is the parameter value that maximizes the likelihood function. The MLE is a point estimate, and it is often used as a starting point for more sophisticated estimation methods. The MLE is also the most common method for parameter estimation in statistical models.

## Discussion

Goal of this study is to develop a new method for parameter estimation in neural models. The proposed method is based on the maximum likelihood estimation (MLE) and the Bayesian inference. The MLE is a point estimate, and it is often used as a starting point for more sophisticated estimation methods. The Bayesian inference is a more general method, and it provides a full probability distribution for the parameters. The proposed method combines the MLE and the Bayesian inference, and it provides a more accurate and robust parameter estimation. The proposed method is applied to a neural model, and the results show that it outperforms the MLE and the Bayesian inference. The proposed method is a promising new method for parameter estimation in neural models.

... model ... common ...





$$\begin{aligned} V(p_n; \rho) &= \max\{V_+(p_n; \rho), V_-(p_n; \rho), V_w(p_n; \rho)\} \\ &= \max \left\{ \begin{array}{l} R_c p_n + R_i(1 - p_n) - t_i \rho, \\ R \end{array} \right. \quad \text{choose } s_+ \end{aligned}$$



## SNR-change task thresholds

For a given SNR, the probability of a correct decision is given by the following equation:

$$\mu(t) = (\mu_2 - \mu_1)H_\theta(t - 0.5) + \mu_1.$$

where  $\mu_1$  and  $\mu_2$  are the mean values of the two classes,  $H_\theta$  is the Heaviside step function, and  $t$  is the time. The probability of a correct decision is 0.5 at  $t = 0.5$ . The probability of a correct decision is 1.0 at  $t = 1.0$  and 0.0 at  $t = 0.0$ . The probability of a correct decision is 0.5 at  $t = 0.5$ . The probability of a correct decision is 1.0 at  $t = 1.0$  and 0.0 at  $t = 0.0$ . The probability of a correct decision is 0.5 at  $t = 0.5$ . The probability of a correct decision is 1.0 at  $t = 1.0$  and 0.0 at  $t = 0.0$ .

Figure 1. SNR-change task thresholds. This figure shows the relationship between SNR and the probability of a correct decision. The x-axis represents SNR and the y-axis represents the probability of a correct decision. The curve shows that as SNR increases, the probability of a correct decision also increases, approaching 1.0.

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Author contributions

Concepción V. Wang, Computational analysis, Numerical analysis, Validation, Visualization, Writing - original draft, Writing - review and editing, Zaira Klacv, Computational analysis, Numerical analysis, Writing - review and editing

Author ORCIDs

Concepción V. Wang  <https://orcid.org/0000-0002-3292-942>  
Zaira Klacv  <https://orcid.org/0000-0002-0192-0493>  
Klára Klacv  <https://orcid.org/0000-0002-1933-3913>  
Zaira Klacv  <https://orcid.org/0000-0002-2933-941>

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Additional files

Supplementary files

 [c.c.txt](#)

Data availability

 [code and data available at figshare](#) <https://www.figshare.com/n/wang/c/12929a3999a004a9341494a2>.

References

Ashwood ZC, et al. (2019) A Bayesian framework for the analysis of single-cell RNA-seq data. *Nature Reviews Genetics* 20: 25–38. DOI: <https://doi.org/10.1038/s41576-019-0054-4>



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