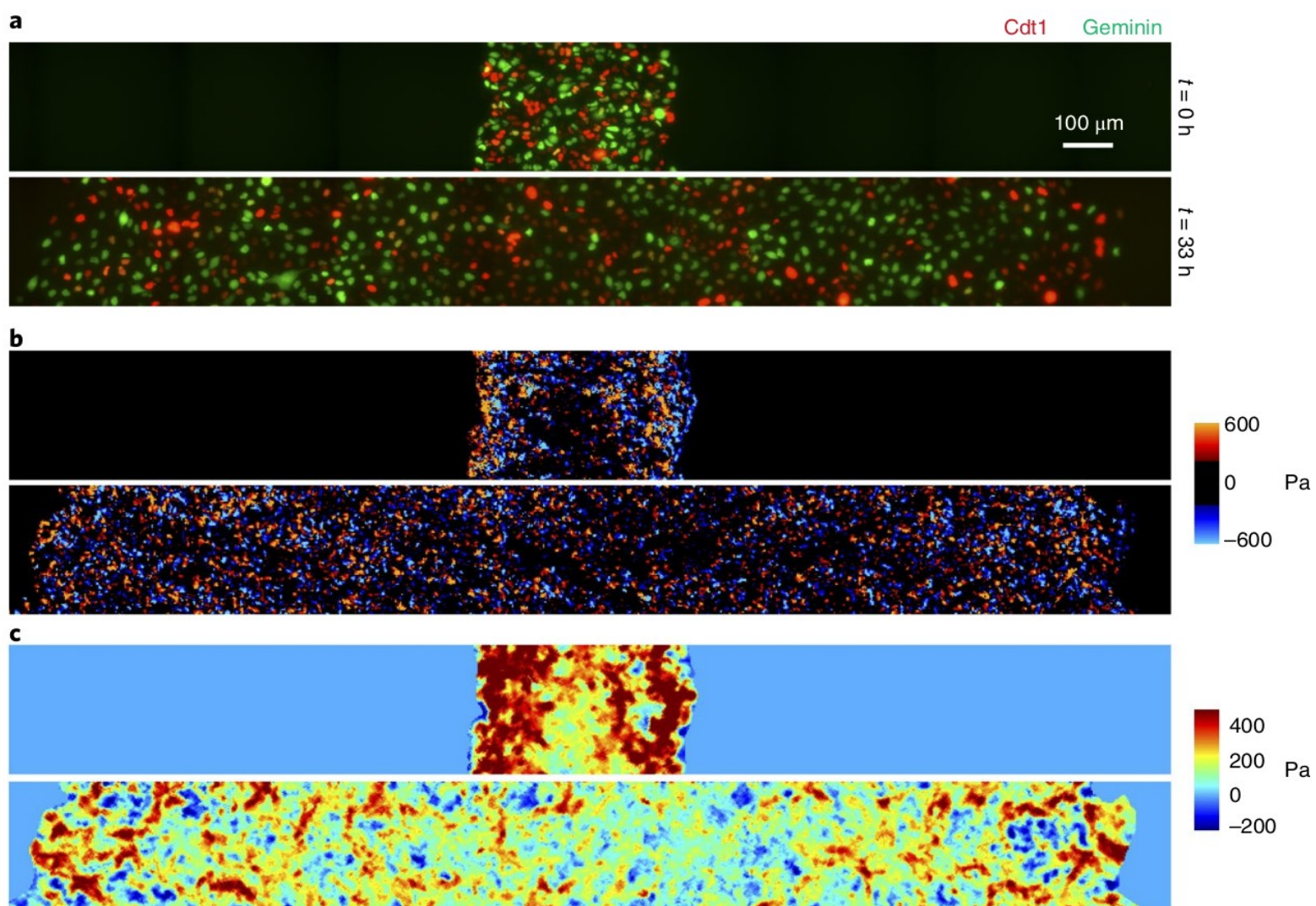
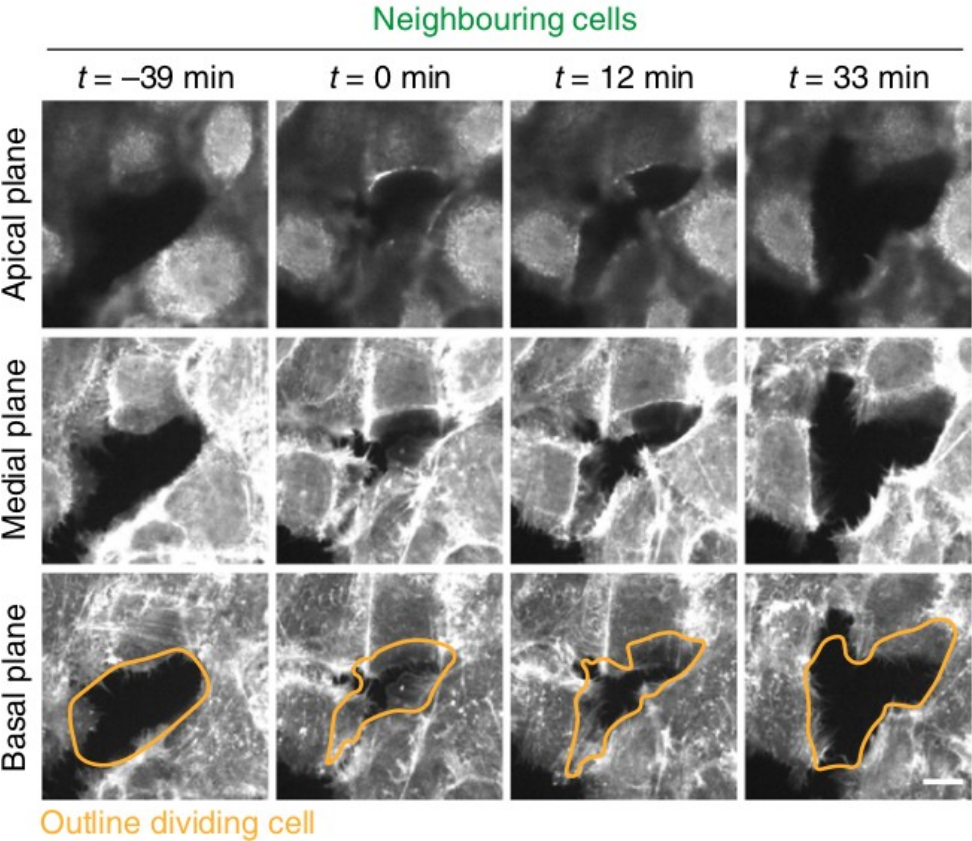
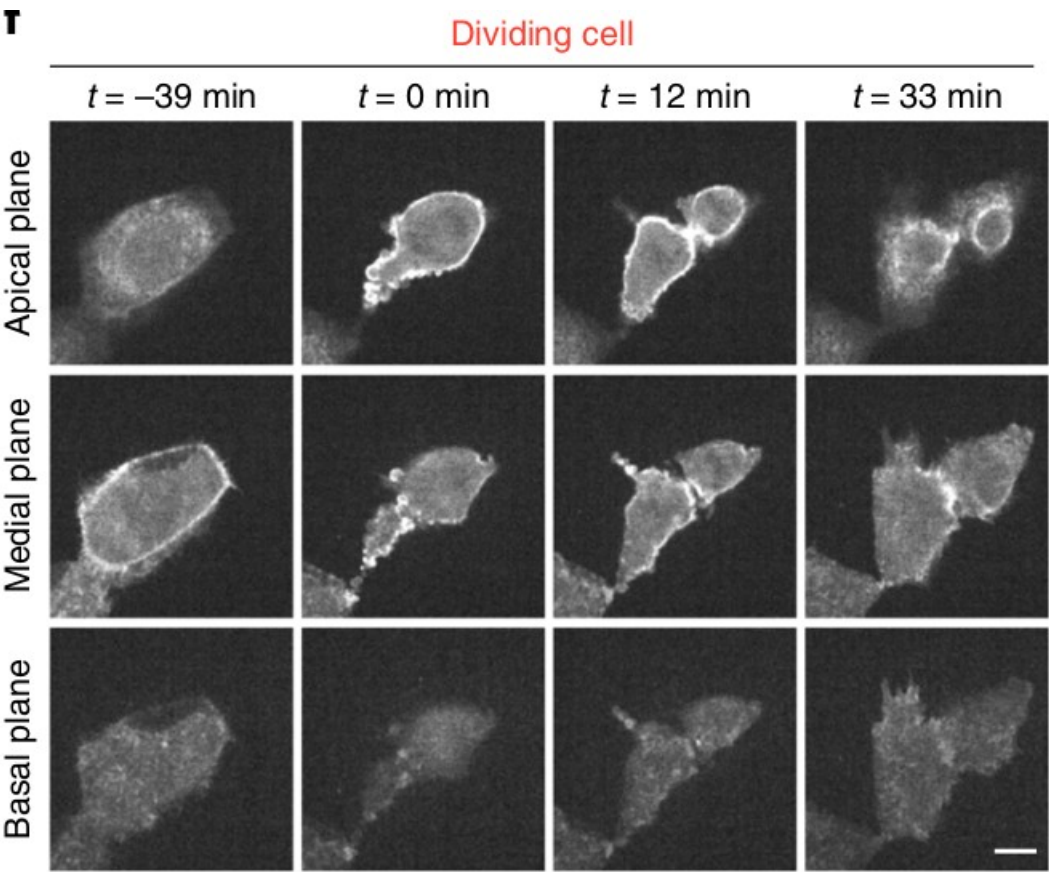


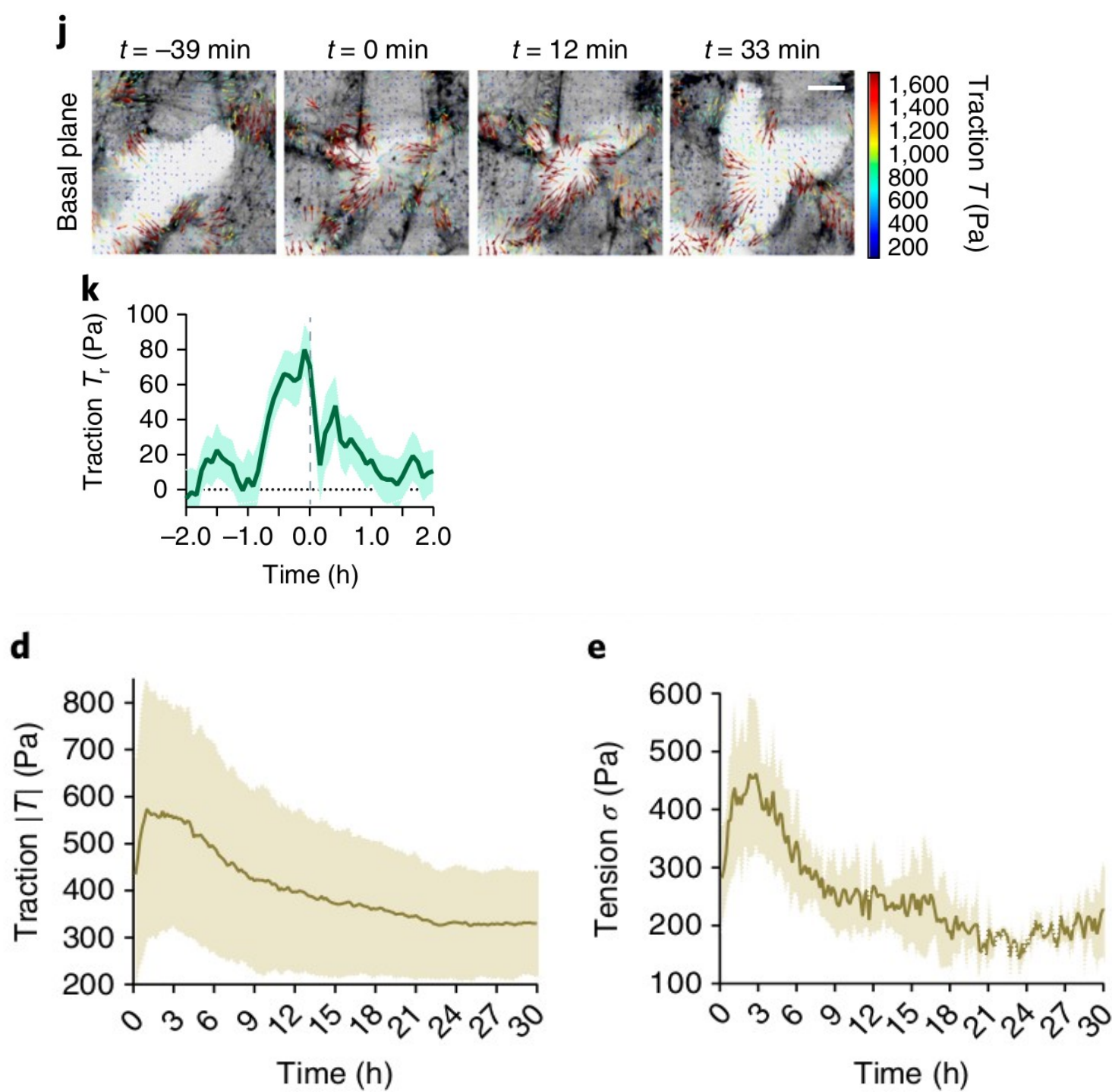
Regulation of cell cycle progression by cell–cell and cell–matrix forces

Marina Uroz¹, Sabrina Wistorf¹, Xavier Serra-Picamal¹, Vito Conte¹, Marta Sales-Pardo², Pere Roca-Cusachs^{1,3}, Roger Guimerà^{2,4} and Xavier Trepat^{1,3,4,5*}







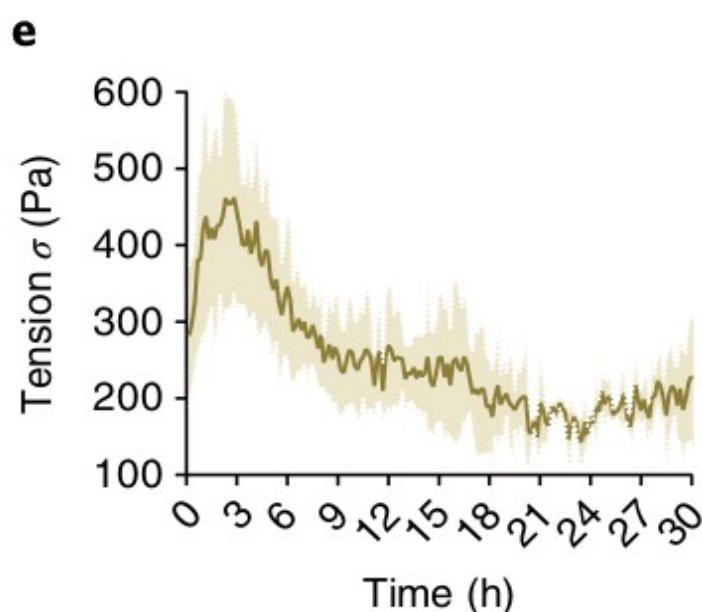
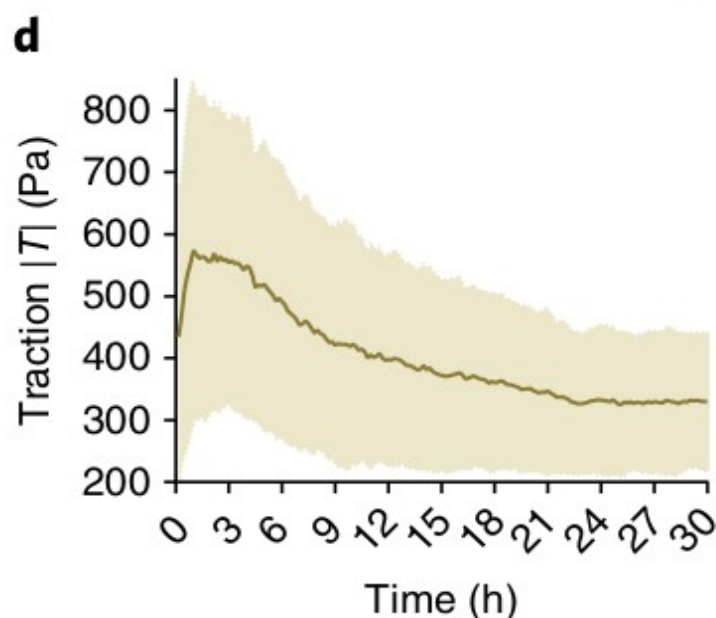


Methods

Linear model selection analysis. To establish which properties are more predictive of the duration of the G1 and the S–G2–M phases, we carried out a systematic model comparison. In particular, we considered all models that are linear in one of the measured properties or in a product between two properties. We also explored all models that are multilinear on any pairwise combination of single properties and property products. To estimate the plausibility of each model, the BIC was used³⁴. All models were compared to the most plausible one (that is, the model with the lowest BIC) using the Bayes factor, which is given by³³:

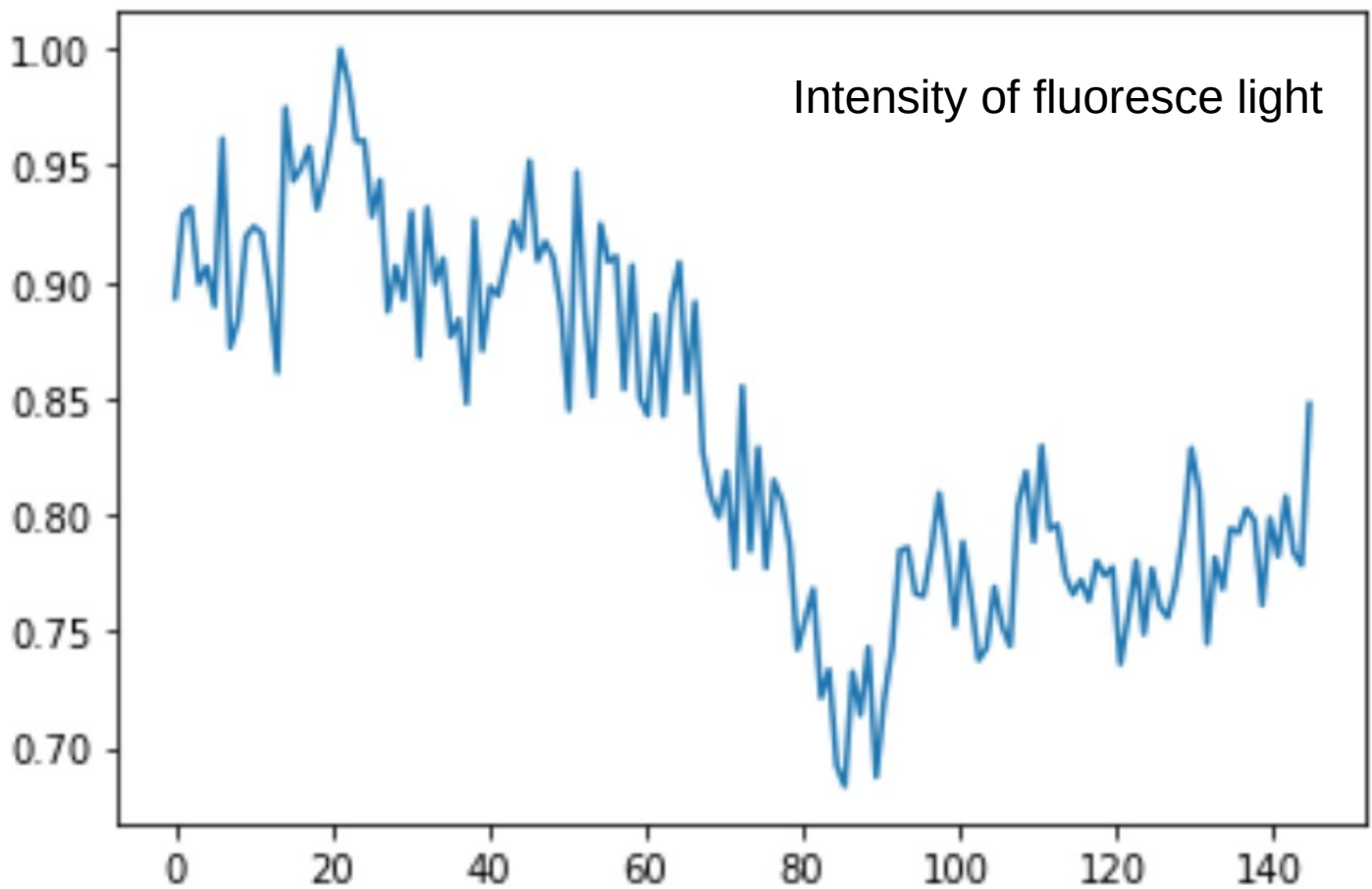
$$\text{BF}(A, B) = p(D|A)/p(D|B) \approx \exp[(\text{BIC}(B) - \text{BIC}(A)) / 2],$$

where $p(D|A)$ is the probability of the observed data given model A. Thus, the Bayes factor (BF) gives the ratio between model plausibility (when all models are considered a priori equally plausible). For example, if the Bayes factor of a model B with respect to the most plausible model A is 10, this means that model A is 10-times more likely than model B.

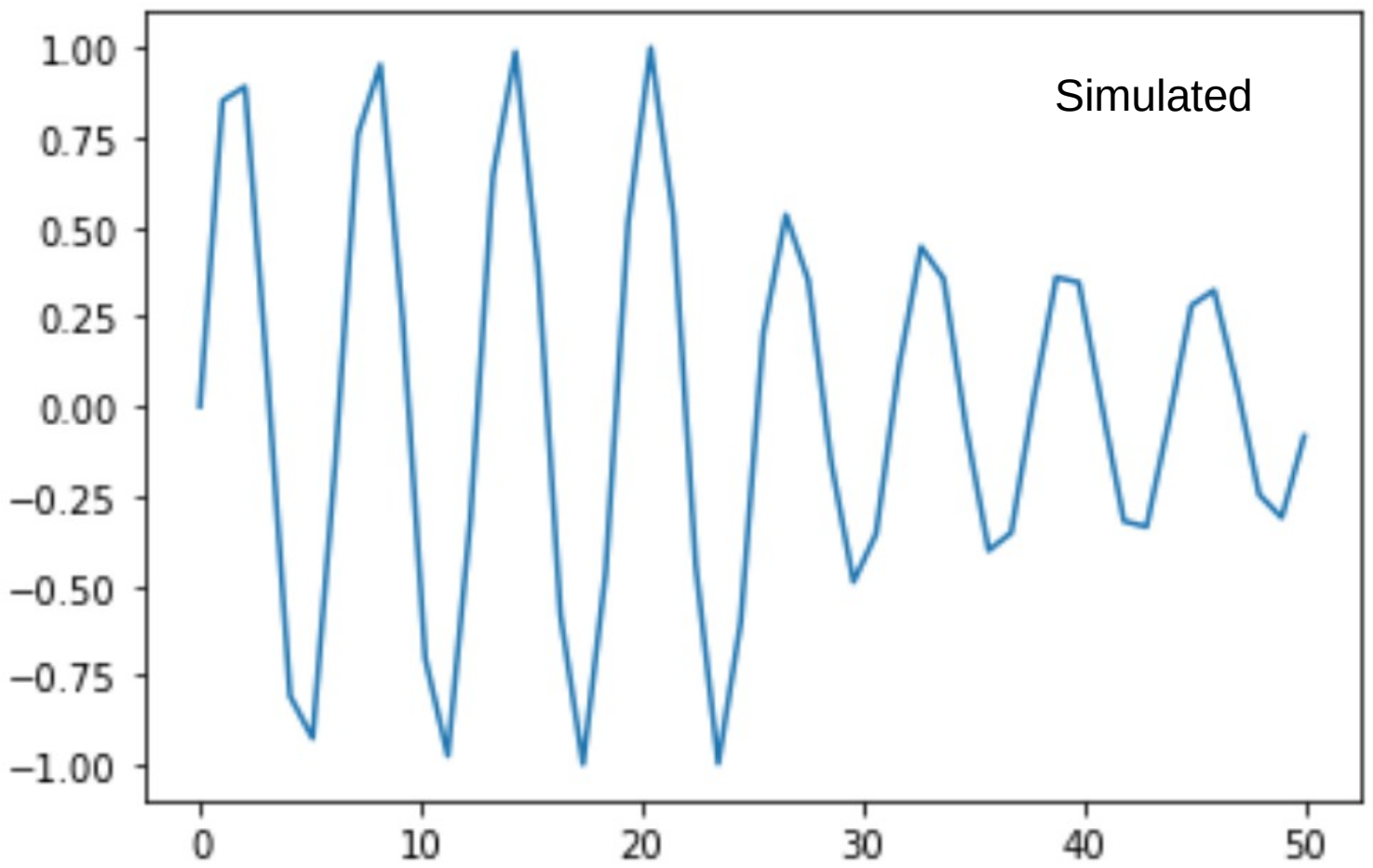


Our approach

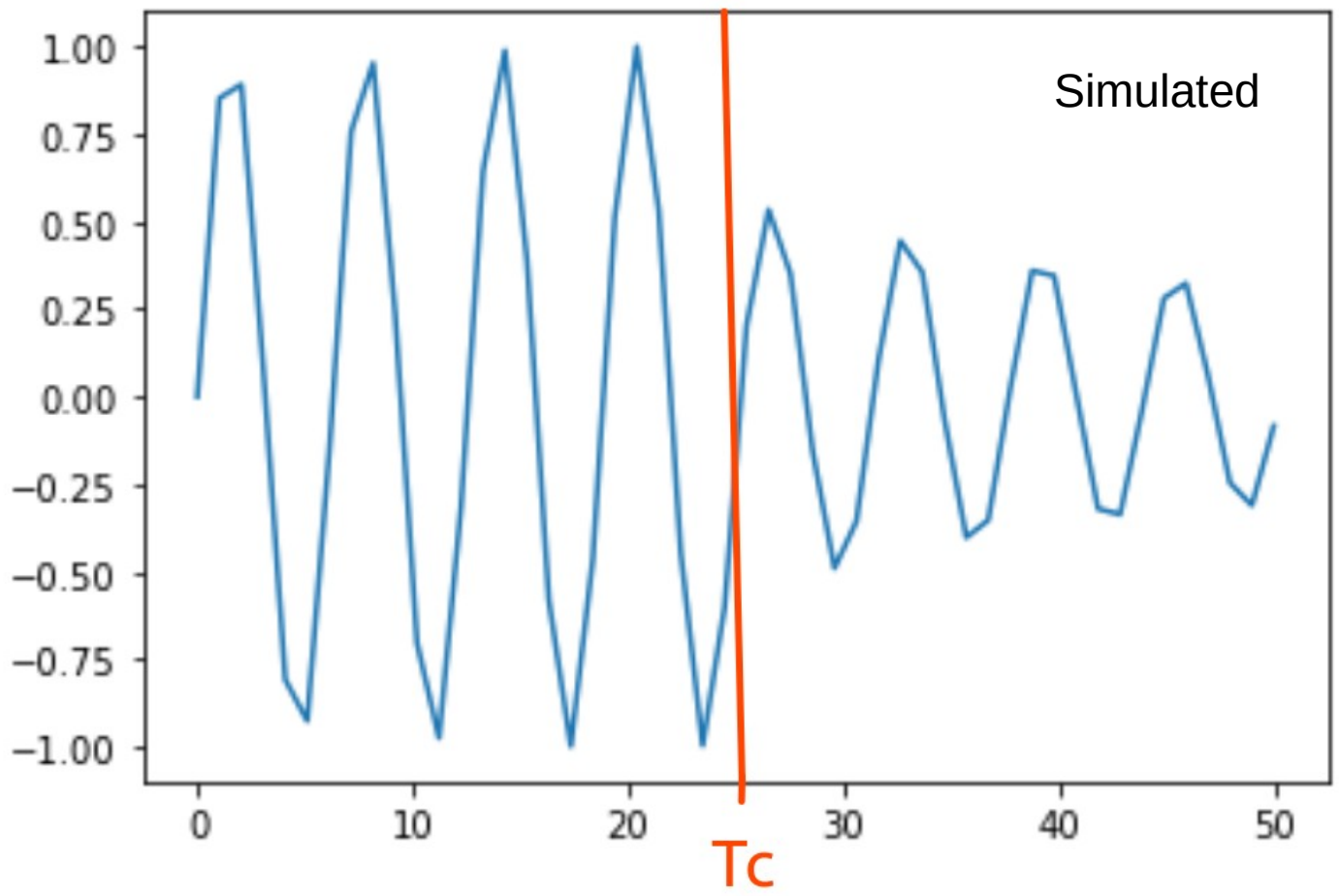
We are trying to identify, where the luminous signal change



Our approach



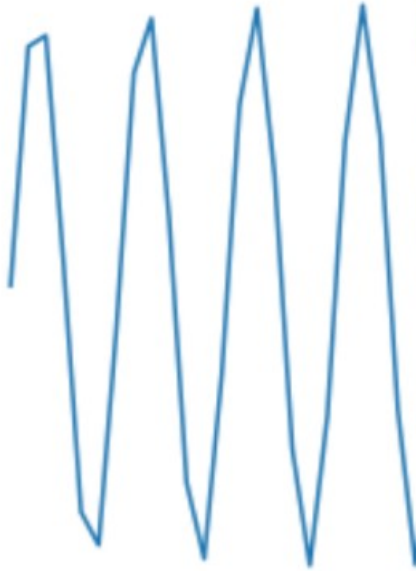
Our approach



Our approach

Best separation:

$\sin(t)$

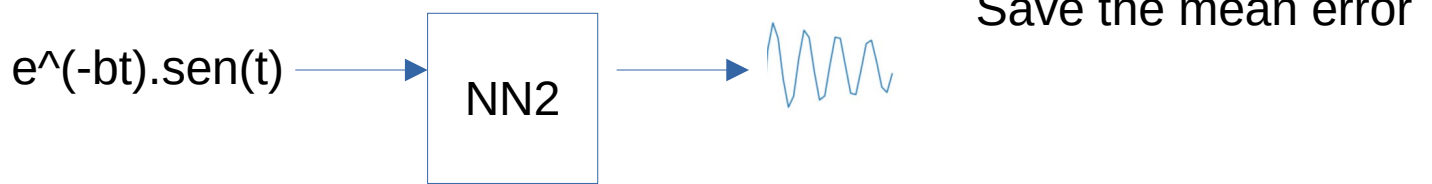
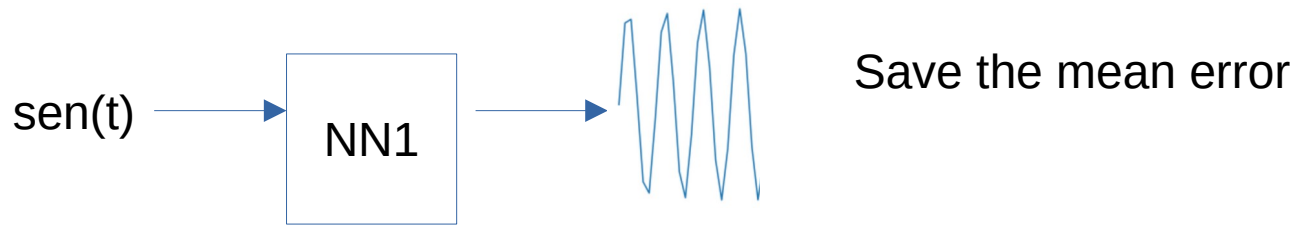


$e^{-bt} \cdot \sin(t)$



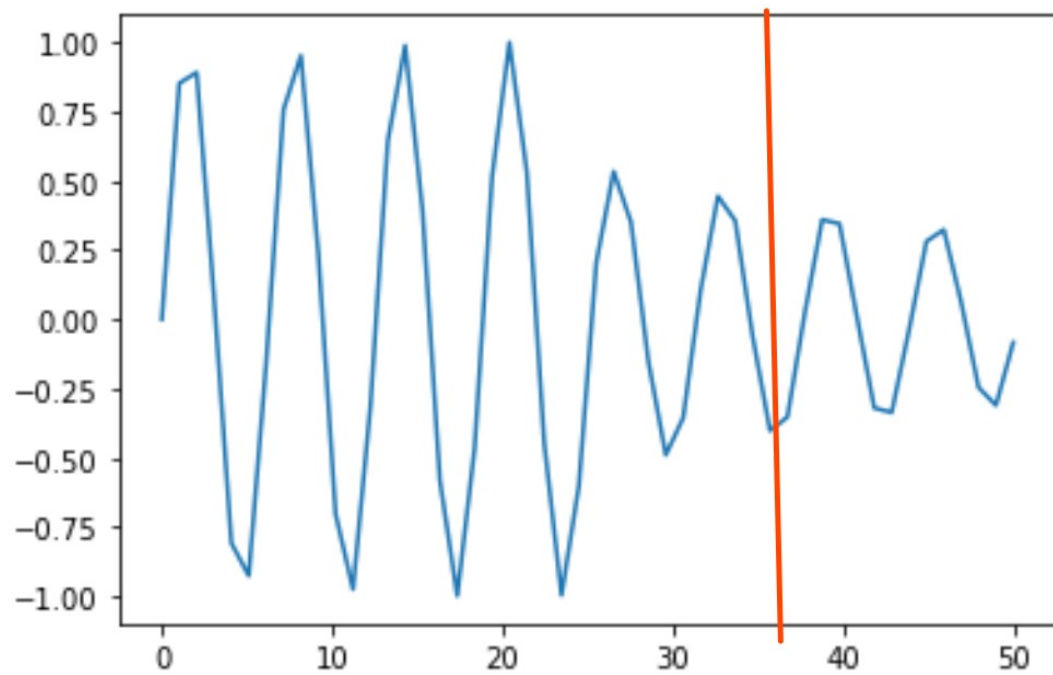
Our approach

Best separation:



Our approach

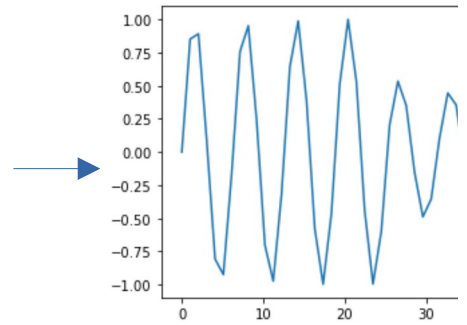
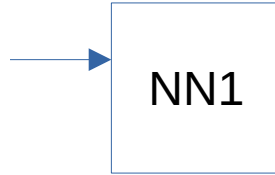
Bad separation:



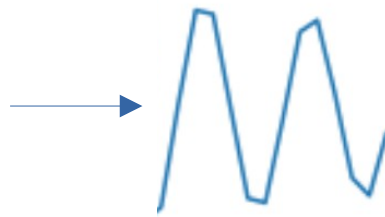
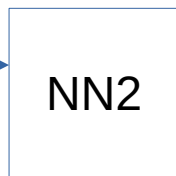
Our approach

Bad separation:

$$F1 = \begin{cases} \sin(t) & ; \quad t < sep \\ e^{-bt} \sin(t) & ; \quad t \geq sep \end{cases}$$



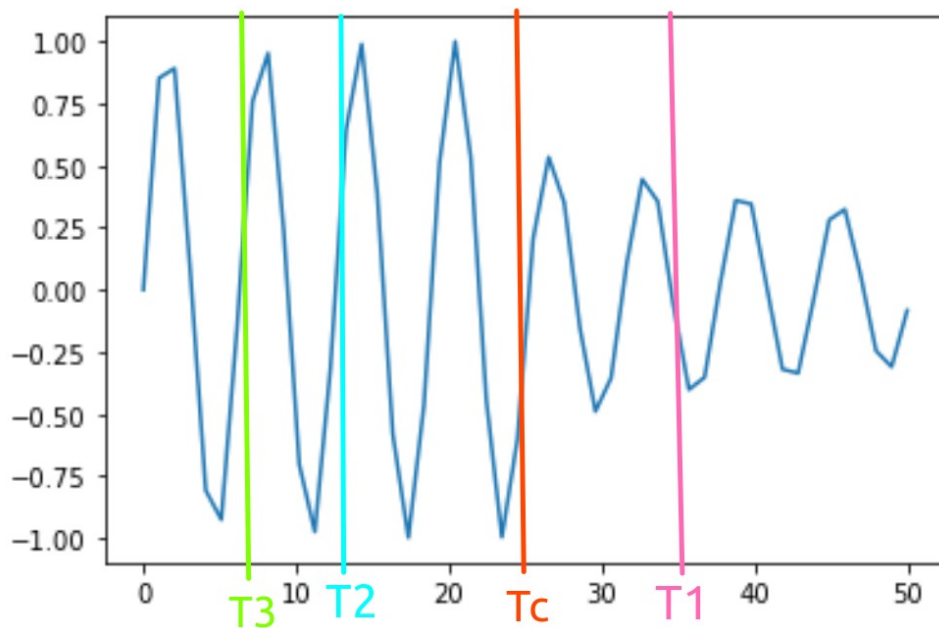
$$e^{-bt} \sin(t)$$



Save the mean error

Our approach

In our method is randomly chose the interval of separation and used it to train two models. The two models with lesser errors, occurs when the simpler functions are used to train. So we use this error information to seek the interval of separation of this two functions.



Conclusion

We are hopeful with this new approach, excited to work on contributions to better understand the cell divisions. We start to work on this approach few days ago and we have no answers if this method will work well. To see future results you can follow this project on github's page:

https://github.com/SchultzVV/Biology/tree/main/method_prove