

Comparing Two Different Models.

The comparison of two different models of the Central Regulatory Circuit of *Drosophila*.

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Abstract

We established and observed two different models of Central Regulatory Circuit of *Drosophila* (CRC) from different articles and compared them. The models describe the Central Regulatory Circuit which acts in the early stage of the *Drosophila melanogaster* mechanoreceptors morphogenesis. The main component of the Central Regulatory Circuit is the complex of *Achaete-Scute* genes.

Abbreviations

CRC : Central Regulatory Circuit

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Introduction

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Methods

Two different models have been searched for. Both models deal with the CRC circuit, but they use different models. First, both models are constructed, with all parameters and values and such. The model has been created with the `dede` function of the `deSolve` package. These models are visualised with the `plot` function of `r`.

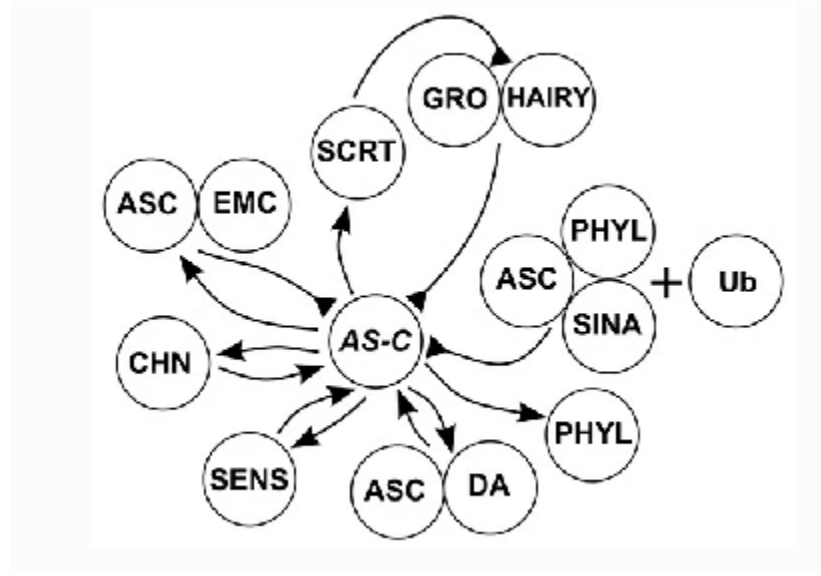


Figure 1: The CRC of the gene networks of the morphogenesis system of Drosophila mechanoreceptors.

This model has been created by the first article [1]. This is the differential equation of this model:

$$\begin{aligned}\frac{dx}{dt} &= k_x \frac{\sigma_1(Dx) + \sigma_3(z) + \sigma_5(w)}{(1+Gy)(1+Ex)} - (1 + p(t - \Delta t)US)m_x x \\ \frac{dy}{dt} &= k_y \frac{C}{d1+u^m r} \\ \frac{dz}{dt} &= k_z s_3(Dx) - m_s z \\ \frac{du}{dt} &= k_u s_4(Dx) - m_u u \\ \frac{dw}{dt} &= k_w s_5(Dx) - m_w w \\ \frac{dp}{dt} &= k_p \frac{s_6(Dx)h(t-\Delta t)(t-\Delta t^2)}{L+h(t-\Delta t)(t-\Delta t)^2}\end{aligned}$$

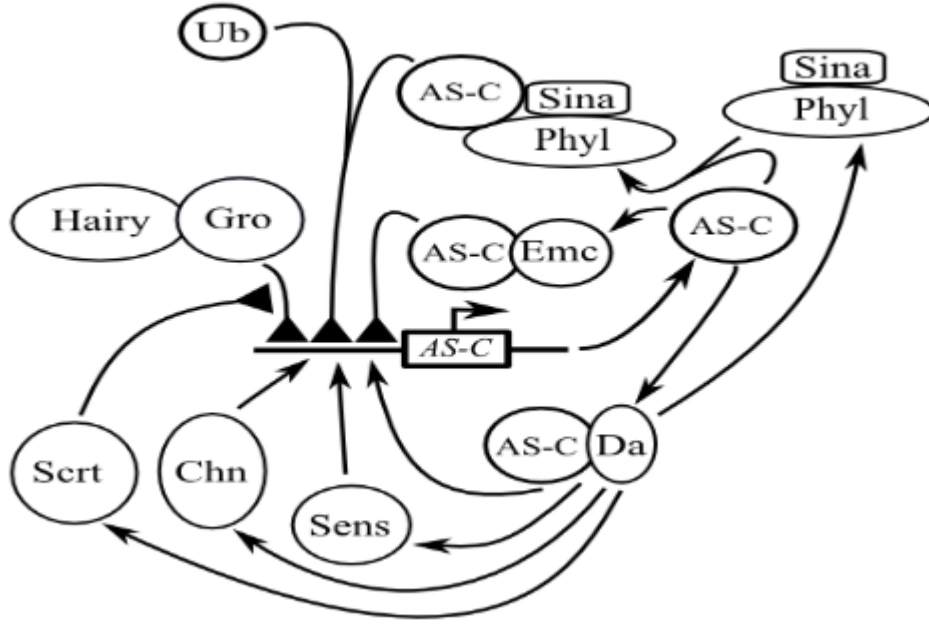


Figure 2: The other CRC of the gene networks of the morphogenesis system of Drosophila mechanoreceptors.

This is the other model that has been created by the second article [2]. This is the differential equation used by the article:

$$\begin{aligned}
 \frac{dx}{dt} &= \frac{\sigma_1(Dx) + \sigma_3(z) + \sigma_5(w)}{(1+Gy)(1+Ex)} - k_x(1 + p(t - \Delta t)US)x \\
 \frac{dy}{dt} &= \frac{C}{d1+u} - k_y y \\
 \frac{dz}{dt} &= s_3(Dx) - k_z z \\
 \frac{du}{dt} &= s_4(Dx) - k_u u \\
 \frac{dw}{dt} &= s_5(Dx) - k_w w \\
 \frac{dp}{dt} &= \frac{s_6(Dx)h(t-\Delta t)(t-\Delta t^2)}{1+(t-\Delta t)^2} - k_p p
 \end{aligned}$$

Result

The result of this research papers are two graphs showing the models and the difference.

Models

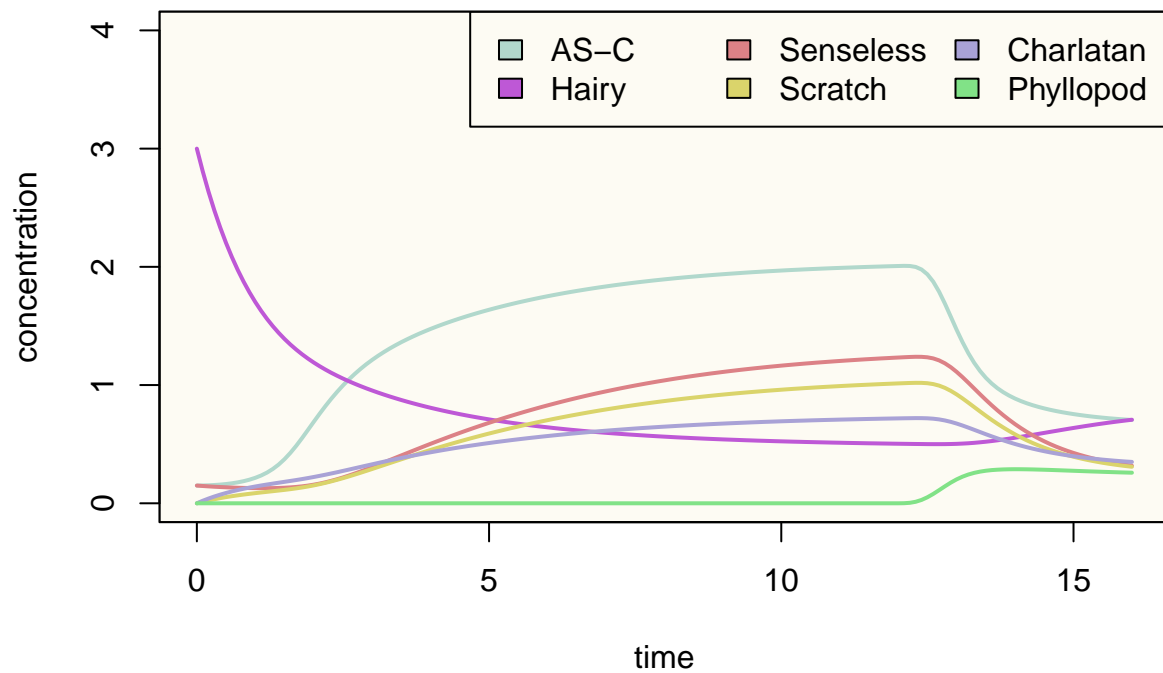


Figure 3: The CRC model of the first article

The *AS-C* curve increases immediately and reached a steady state, after a while it decreases to about a concentration of below 1. The curve of *Hairy* goes steadily down until *AS-C* decreases. Then the concentration went up.

The other curves *Senseless*, *Scratch* and *Charlatan* all followed the same curve just with a lower value, and it steady went down at the same timepoint as *AS-C*.

Phyllopod stays the whole time around 0, untill all the others one decreases/increases.

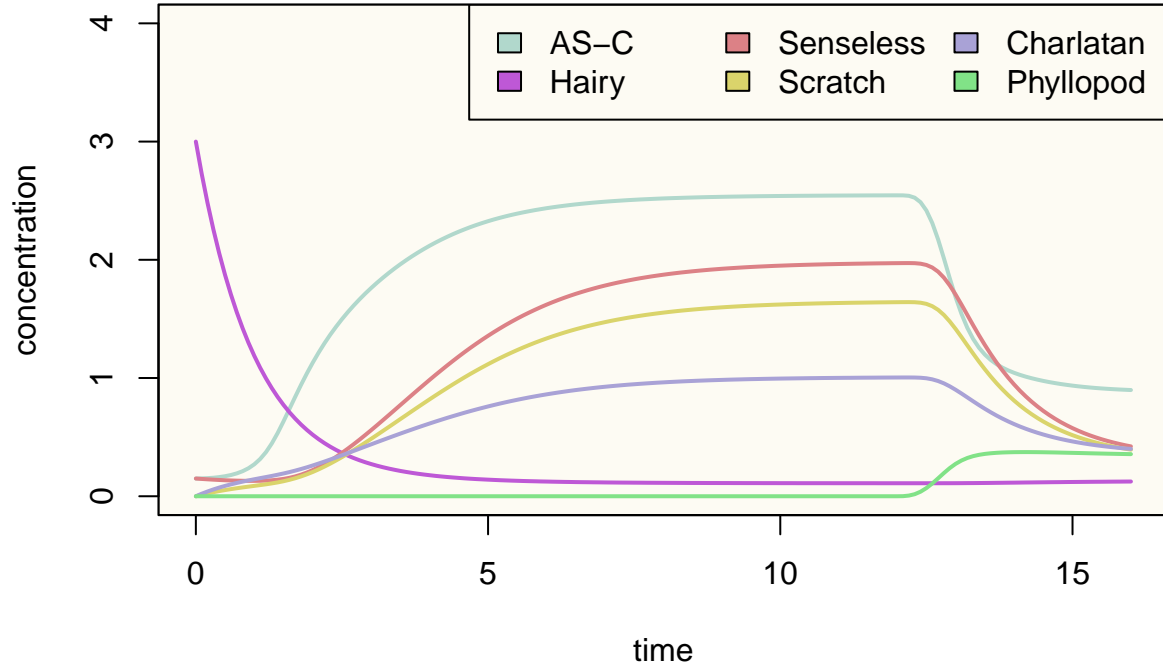


Figure 4: The CRC model of the second article

The curve of *Hairy* goes steadily down until it reached a steady state. *AS-C* curve reaches a steady state pretty quick, after a while it nose dives to about a concentration of 1.

At the same time, other curves *Senseless*, *Scratch* and *Charlatan* all followed the same curve just with a lower value, and it steady went down at the same timepoint as *AS-C*.

Phyllopod stays the whole time around 0, untill all the others one, except *hairy*, reduce.

Discussion

We have encountered problems in this papers. There is no concrete experimental data. There is a site, FlyAtlas, but you cannot actually use it. Firstly, there is nothing about *AS-C*. And secondly, it is not clear which data we should use.

In the second article, they give other parameter values, but if you go to the site mentioned in the article. You get a graph with the same values as the first article, so we used these values. And we have not played with the parameters values to see what happens. But the first article did changed the values and their outcome was this: 'From the biological point of view, this means a ban on the formation of a mechanoreceptor' [1].

We now have two graphs, but we still do not really know which model uses the best differential equation.

Conclusion

Our goal was to compare two different models of the CRC of *Drosophila*. The conclusion we draw is that we compared the different models. But we lack the experimental data to see which is good.

We now have two graphs with two different CRC models, but as mentioned earlier, there is simply no/little experimental data. When more data emerges, we can really compare which model is the best. Or how we can then adjust it so that the model becomes even better.

References

- [1] = Bukharina, T.A., Akinshin, A.A., Golubyatnikov, V.P., (2020) ‘Mathematical and Numerical Models of the Central Regulatory Circuit of the Morphogenesis System of *Drosophila*’ *Springer* <https://link.springer.com/article/10.1134/S1990478920020040> **24-05-22**
- [2] = Ayupova, N.B., Demidenko, G.V., Matveeva, I.I., Fadeev, S.I., Zhubr , A.V. (2018) ‘MATHEMATICAL AND NUMERICAL MODELS OF TWO ASYMMETRIC GENE NETWORKS’ *nsc* <http://semr.math.nsc.ru/v15/p1271-1283.pdf> **24-05-22**