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► **To cite this version:**

Selma Souihel, Bruno Cessac. Motion processing in the retina. GDR multielectrodes , Nov 2017, Strasbourg, France. hal-01638105

**HAL Id: hal-01638105**

**<https://inria.hal.science/hal-01638105>**

Submitted on 19 Nov 2017

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# Motion processing in the retina

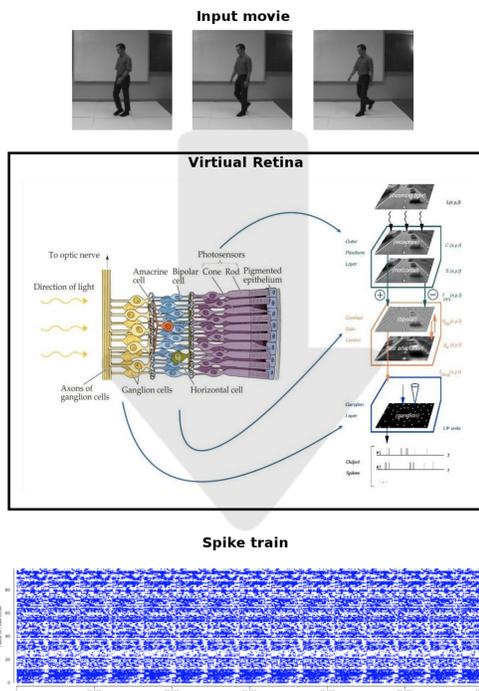
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## Introduction

- The visual system uses motion anticipation to compensate the delays in retino-cortical transmission.
- Recent experimental and modelling studies on simple stimuli (moving bars) ([1], [2]) show that a notable preprocessing of visual motion is made by the retina.
- They emphasized the role of the gain control occurring at the level of bipolar and ganglion cells (RGCs), in anticipation and other motion features.
- These studies feature independent RGCs while these are, in reality, connected (via amacrine cells).
- We want to understand how non linear mechanisms (gain control, spike frequency adaptation and connectivity), act on the anticipation of complex shapes motion.
- For this we have developed a retina simulator, PRANAS [3] emulating the retina spike response to a visual scene.
- We have studied the pairwise correlations between ganglion cells, under the influence of a moving object both, in vivo and in silico.

## I) Retina Simulator

PRANAS [4] is a software able to convert a movie into spike trains similar to those transmitted by the retina to the brain. It uses a three-processing-stage model mimicking photoreceptors, bipolar cells and ganglion cells.



## II) Spike frequency adaptation

Adaptation is commonly defined as a decrease in response to a constant stimulus. In our work, we regard it as all the non-linear phenomena involved in the neuronal response to motion stimuli. We implemented different adaptation mechanisms, ranging from the cascade model by Chen & al. [2] to moving threshold at the level of RGCs. We found that a simple threshold adaptation following the equation:

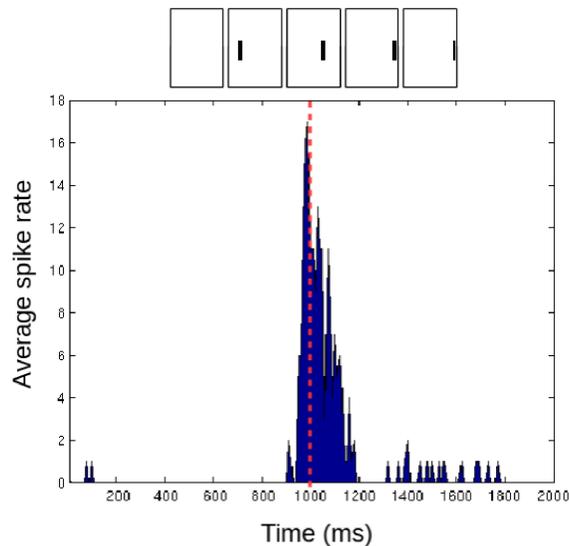
$$\theta(t) = \theta_0 - \gamma |\delta(V_{bip})|$$

where  $\gamma$  a strength coefficient of the timewise bipolar potential variation  $V_{bip}$  and  $\theta_0$  the initial threshold gives fairly good results in terms of anticipation.

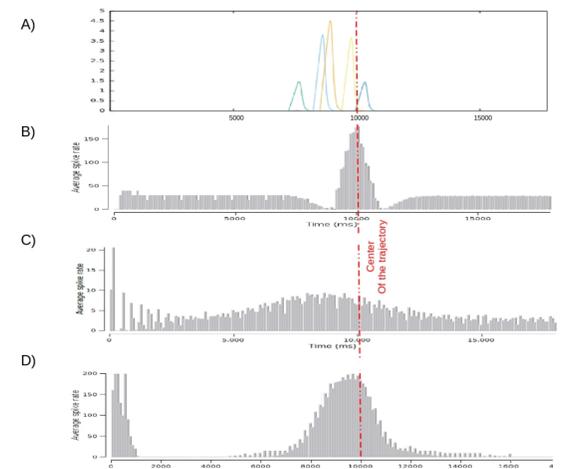
## Acknowledgement

This research is entirely funded by Agence Nationale de la Recherche. We would like to thank our collaborators, Olivier Marre from Institut De la Vision and Frédéric Chavane from Institut des Neurosciences de la Timone for their significant help and their insightful suggestions.

## III) Smooth motion results, in vivo & in silico



In vivo results : RGCs population response to a moving bar  
Courtesy of Olivier Marre.

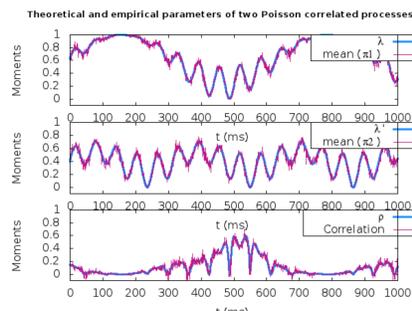


Population response to smooth motion of a translating bar A) The results using direct integration of gain control equations. B) The results using linear spatio-temporal filtering at the level of bipolar cells and a discrete leaky integrate and fire model to produce spikes, with PRANAS. C) The results of the implementation of Chen & al. model in PRANAS. D) The results using threshold adaptation as a function of  $\Delta(V_{bip})$ , and the pooling of bipolar cells by ganglion cells.

## IV) Correlation performance test

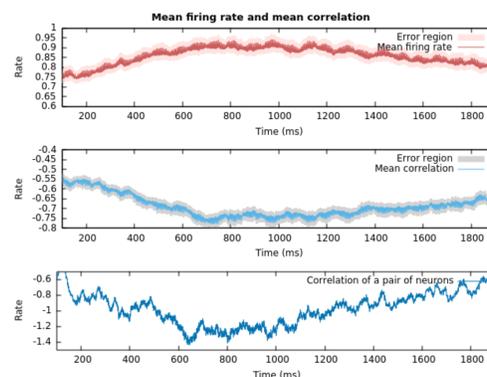
In order to test our correlation algorithm, we generate two correlated Poisson processes following the method :

- X, Y and Z are three independent Poisson variables of rates  $\lambda_1$ ,  $\lambda_2$  and  $\lambda_{12}$ .
- $\Pi_1$  &  $\Pi_2$  are Poisson processes such as :  $\Pi_1 = X \cup Z$  &  $\Pi_2 = Y \cup Z$  with rates  $\lambda$  and  $\lambda'$ .
- The rates are :  $\lambda = \lambda_1 + \lambda_{12}$  &  $\lambda' = \lambda_2 + \lambda_{12}$
- The joint probability of  $\Pi_1$  and  $\Pi_2$  is then given by :  $P = \lambda_1 \lambda_2 + \lambda_{12} - \lambda_1 \lambda_2 \lambda_{12}$
- And finally the correlation is :  $\rho = \frac{P - \lambda \lambda'}{\sqrt{\lambda \lambda'}}$



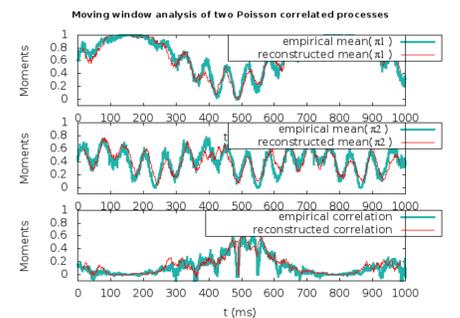
## VI) Experimental data correlation

We compute the mean correlation over 80 recorded salamander retina RGCs, choosing pairs with similar spike rate activity. The stimulus center is at  $t=1000$ ms.

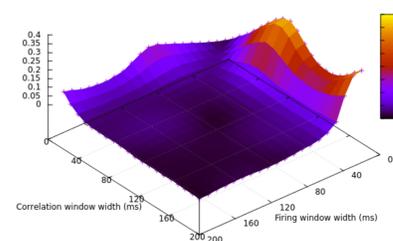


The correlation is negative, which can be explained by lateral inhibition. The minimum is then achieved when the cell responds to the translating bar, showing that lateral inhibition is maybe increased by neurons activity.

## V) Correlation with moving window



The reconstructed firing rates and correlation follow quite good the variation of the empirical measures. The width of the moving window for both computations is taken here equal to 30 ms.



The error is lower when the width of correlation computation window is taken equal to the firing rate window. The window should also be small enough to follow the variations of the firing rate and big enough to retrieve significant statistics.

## References

- [1] Michael J. Berry, Iman H. Brivanlou, Thomas A. Jordan & Markus Meister: *Anticipation of moving stimuli by the retina*, Nature (1999)
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- [4] Adrien Wohrer & Pierre Kornprobst: *Virtual Retina, a biological retina model and simulator*, Journal of Computational Neuroscience(2009)
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## Conclusion & future work

- Our threshold adaptation model enabled us to reproduce anticipation but also other motion features, such as alert response, motion onset and motion reversal.
- In terms of run-time efficiency, the threshold adaptation computation is faster than the cascade model of Chen & al.
- There are biological evidences of adaptation at the level of bipolar and ganglion cells, and amacrine cells seem to play a crucial role.
- Our study of correlation on experimental data recorded from salamander retina shows the effect of neurons activity on lateral inhibition.
- Our future work will be to model amacrine cells in order to mimic a biologically plausible connectivity.