

Poster presentation

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Implementation of a Hidden Markov Model in a photoreceptor cell by the biochemical mechanisms of phototransduction

Audrey Houillon*¹, Pierre Bessi re² and Jacques Droulez¹

Address: ¹Laboratoire de Physiologie de la Perception et de l'Action-CNRS/Coll ge de France, Paris, 75015, France and ²Laboratoire d'Informatique de Grenoble-CNRS/Grenoble Universit s, Grenoble, 38041, France

Email: Audrey Houillon* - audrey.houillon@college-de-france.fr

* Corresponding author

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Introduction

Probabilistic perceptive and behavioral models have received a growing interest lately, as they account for the ability to reason with incomplete knowledge about the external world. In this study, we consider how the probability distributions that need to be estimated in these models could be represented and processed at the single cell level by the underlying biochemical mechanisms, in particular in a photoreceptor cell. We consider how the molecular interactions in a photoreceptor cell can compute a probabilistic inference in the case of a binary Hidden Markov Model (HMM). The HMM is of interest since it is one of the simplest form of time-dependent probabilistic models, and is widely used in cognitive probabilistic modeling, as the base for more complex models. We show that the cell estimates the current state probability distribution by means of the biochemical mechanisms of phototransduction.

The interactions between the different molecular messengers, ions, enzymes and channel proteins within the photoreceptor cell are described by a set of nonlinear coupled differential equations [1], whereas the HMM is described by a discrete recurrence equation. In the first model, we derived, under steady-state conditions, a formal equivalence between the HMM inference and some of the biochemical mechanisms involved in phototransduction. We can then point out the similarity of the solutions and find

the relations between the parameters of both systems if the intracellular calcium concentration encodes the posterior probability ratio. We performed numerical simulations to extend the results to the dynamic case. We then derived a second model under the more general case of a constant input, under which conditions we find a general solution for the binary HMM, as well as for the biochemical system. As in the first model, we can find new relations between both systems and simulate the dynamic case.

Results

For both models we compared the temporal evolution of the intracellular calcium concentration with the posterior probability ratio inferred by the HMM. For the dynamical case, we considered different time-varying light intensities as the input. We finally compared the performance of both models.

Discussion

We have showed how simple biochemical interactions can implement simple probabilistic reasoning. Furthermore, we discuss the possibility to extend the temporal calcium concentration to a spatio-temporal variable by involving the cell structure and diffusion mechanisms and how it could permit us to enhance the probabilistic models to a continuous state variable.

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References

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