To „see” or not to „see”?

Is AI able to detect external world?

NICOLAUS COPERNICUS UNIVERSITY IN TORUŃ
Faculty of Physics, Astronomy and Informatics

W. Łachmański, J. Rydzewski, W. Nowak

[a] Institute of Physics, Faculty of Physics, Astronomy and Informatics, Nicolaus Copernicus University, Grudziadzka 5, 87-100 Torun, Poland

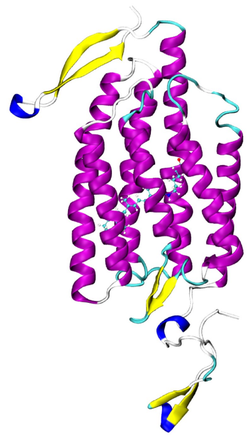
I Background

Optogenetics is a quite new field of biotechnology that allows us to control living tissues by light. The most promising application of this technique is supervision over neuronal activity. Everything started from photon-sensitive protein called channelrhodopsin and still it is the most significant system at optogenetics service.

We have performed molecular dynamics simulation of channelrhodopsin, imitating continuous light excitation of retinal (flip-flop between trans-cis states) in 2 ns rate. The aim of the work is to create cluster analysis of trajectory, check if we can use artificial intelligence to recognize state of the system and if so – what are foremost elements of this recognition.

II Channelrhodopsin

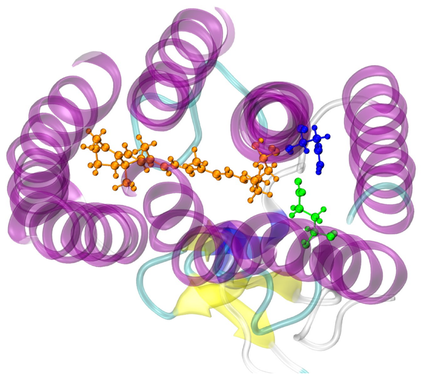
Channelrhodopsin is transmembrane ion channel, consisting of seven alpha-helices and light-sensitive retinal. Immediately after photon absorption retinal changes conformation from all-trans to 13-cis, leading a cascade of events in protein structure that final product is an open-state of the ion channel.



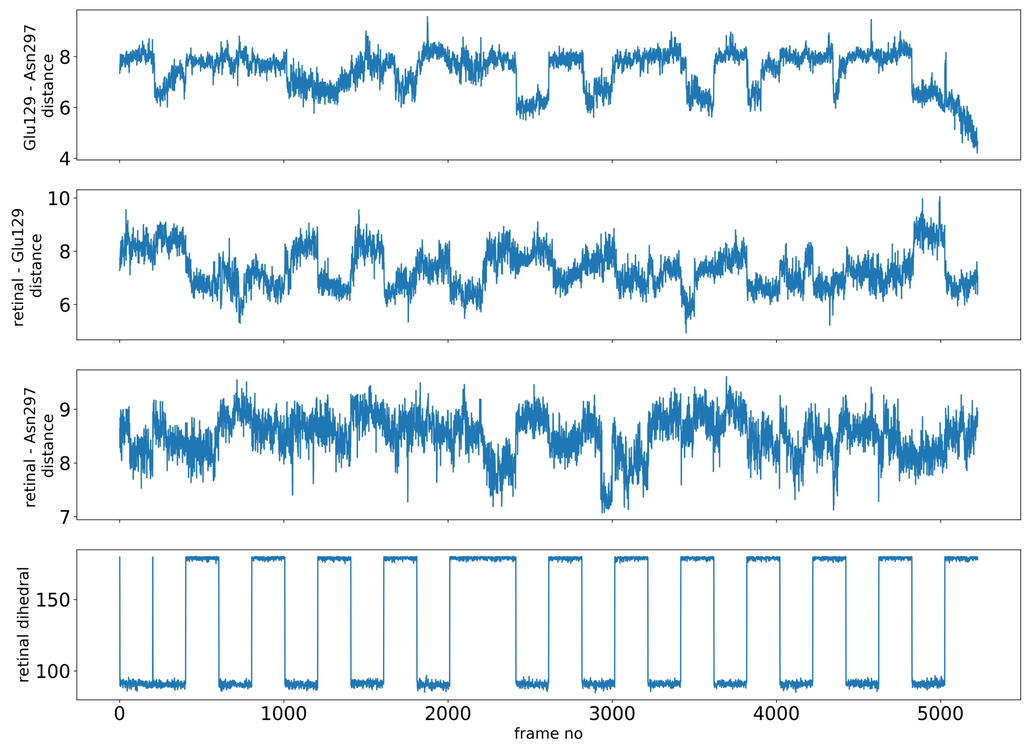
III Dark—light states

It has been shown [1] [2] that the most important changes induced by retinal excitation involve two amino acids—Glu129 (green) and Asn297 (blue).

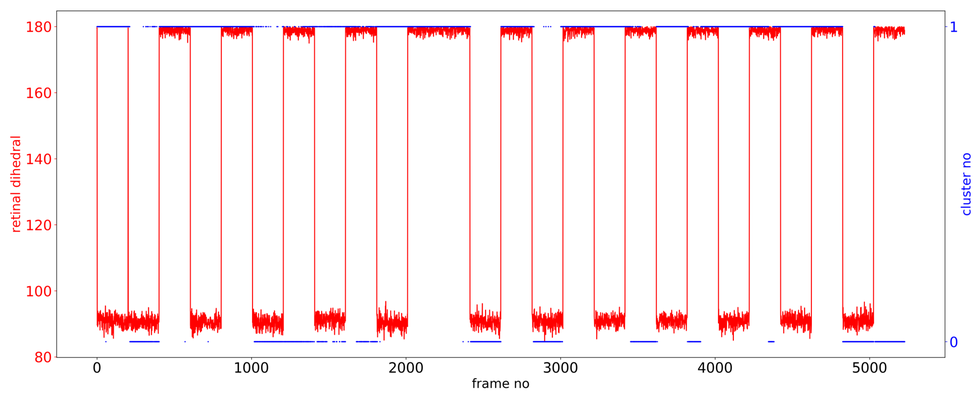
These residues together with retinal connected to Lys296 (orange) form “the gate” of ion channel.



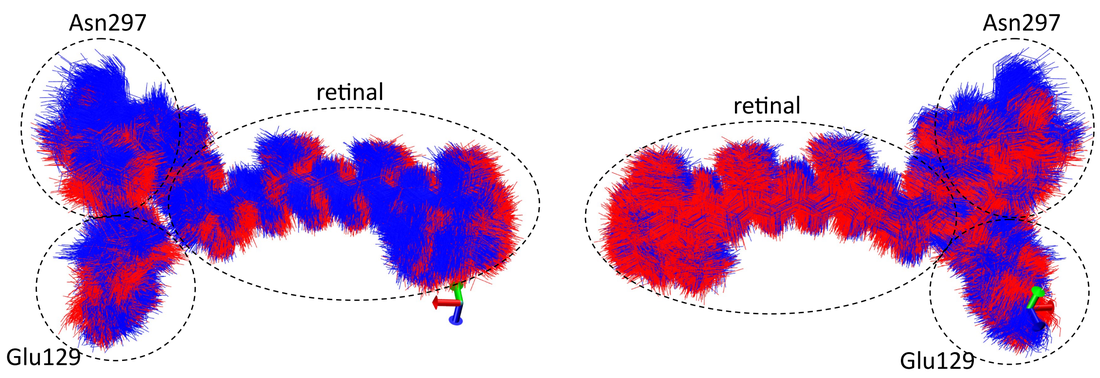
IV MD results



V Clustering



Clustering over Glu129-Asn297, retinal-Glu129 and retinal-Asn297 distances using k-means algorithm. There are 32% of frames in cluster 0 (open state) and 68% of frames in cluster 1 (close state).



Blue—frames of cluster 0 (open state)
Red—frames of cluster 1 (close state)

VI Conclusions

For sure 2ns rate of dark-light state changes seems to be too fast in terms of channelrhodopsin inertia. This can be clearly noticed after analysis of MD results. Not only the nearby environment of retinal sometimes loses open-close cycle but even retinal itself can have problem to switch from all-trans to 13-cis. Perhaps diminution of frequency in which system is excited can give better results. Clustering such MD results has given inconclusive outcome. On the one hand geometric distribution of open state frames is more extensive in space. On the other hand clustering poorly follows retinal cis-trans changes. Nonetheless there is some spatial shift between these two classes of frames. One side is dominated by “blue” frames, the other by “red” frames. For sure it is necessary to increase time between cis-trans switches to give protein more time for relaxation in given state.

VII References

[1] J. Wietek *et al.,* Conversion of channelrhodopsin into a light-gated chloride channel, *Science*, 334 (2015)
[2] J. Kuhne *et al.,* (2016), Early formation of the Ion-Conducting Pore in Channelrhodopsin 2, *Ang. Chem.*, 54 (2014)