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## Sano Computational Medicine Seminars

Monday, 14 December 2020, 14:00-15:30 (CEST)

Join us via Zoom: <https://seminar.sano.science/>

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### The Communication System in Living Organism

#### Abstract

The communication system is part of strategies employed by living organisms on a molecular level. The information storage and management is of high importance in keeping the steady state called homeostasis. The information consumption to achieve the required effect has been solved by evolution for random actions as well as for highly specific processes. The probability of achieving the goal "P" with very low probability "p" of reaching the goal in elementary event increases together with number of attempts. The increase of the number of attempts requires high energy consumption. The increase of probability "P" using the increase of "p" – probability of elementary event is also possible. All processes acting according to this strategy is simply called "specific". However this way of achievement requires information. The molecules carrying large amount of information represent the complex structures. The more complex is the structure the more information is coded in it. Complexity of these structures carries the accumulation of information and they play a role of discrimination control. Only complete set of parts of the complex structure allows the action to be undertaken. The examples of two solutions for reaching the goal in macro-life as well as in nature and on molecular level in human organism will be presented.

**Prof. Dr. Irena Roterman-Konieczna** - head of Department of Bioinformatics and Telemedicine at Jagiellonian University – Medical College 2000-2020. IR-K educated in theoretical chemistry is involved in bioinformatics – structure and protein folding and systems biology. She is the author of the fuzzy oil drop model for protein folding simulation taking into account the active participation of water environment. This model appears to be able to identify the biological activity of protein as well as the recognition of the mechanism of amyloidosis [From globular proteins to amyloids – Ed IR-K, Elsevier 2020]. The proposal to treat the negative feed-back system as the functional-structural unit to construct the proteome to keep the homeostasis is expressed in Systems Biology – Ed. Leszek Konieczny, IR-K Springer 2012. IR-K is the author of educational program addressed to medical students in "Simulation in Medicine" – two volumes: Ed IR-K Walter de Gruyter 2015 and 2020. IR-K is also the Chief Editor of the journal "Bio-Algorithms and Med-Systems" published since 2000. The journal is focused on implementation of programming in medicine for the whole spectrum from basic research to practical medicine.

[1] Fabian P, Banach M, Stapor K, Konieczny L, Ptak-Kaczor M, Roterman I. The Structure of Amyloid Versus the Structure of Globular Proteins Int. J. Mol. Sci. 2020, 21(13), 4683; <https://doi.org/10.3390/ijms21134683>

[2] Banach M, Konieczny L, Roterman I. The Amyloid as a Ribbon-Like Micelle in Contrast to Spherical Micelles Represented by Globular Proteins Molecules 2019, 24(23), 4395; <https://doi.org/10.3390/molecules24234395>