11th Conference on Dynamical Systems Applied
to Biology and Natural Sciences DSABNS 2020
Trento, Italy, February 4-7, 2020

HOW MANY GENES FROM Wnt-CASCADE IDENTIFY *tnbc*-PATIENTS?

Elena A. Martynova*, Alena A. Feller

V. F. Voino-Yasenetsky Krasnoyarsk
State Medical University, Russia

martynova_alena@inbox.ru (*corresponding author),
felleraa96@mail.ru

Burst cancer is widely spread pathology, worldwide. Some types of cancer are hard to detect and cure, *tnbc* is among them. Molecular genetics methodology may contribute a lot in the problem. We studied the Wnt-cascade gene expression database of three types of patients: *tnbc* (118 entries), *non-tnbc* (852 entries) and healthy women (112 entries). The database was provided by Prof. Vladimir Katanaev from Geneva University. Due to database inconsistency, few genes have been removed from the consideration, so that we dealt with 68 genes. Standard techniques of statistical analysis fail to distinguish properly *non-tnbc* from *tnbc* patients [1].

We used elastic map technique that provides almost perfect clustering for *non-tnbc*, *tnbc* and healthy patients. It has been found that an incomplete set of genes provides similar (or even the same) clustering, as the full set of them does. Hence, we tried to identify the minimal set of genes still providing the clustering with high resolution of *non-tnbc*, *tnbc* and healthy patients. Obviously, such minimal subset could be ambiguous.

To figure out the minimal subset of genes still yielding the reasonable clustering with good determination of those three groups of patients, we generated a series of subsets of various abundance of the genes involved into the clustering implementation. Each series comprises as many, as 50 different samplings from the original database. The number of genes included into the samplings varied from 68 (a single set of genes) through 34, 16, 8 and 4.

It was found that three sets of 8 genes yield the clusterings with minor deviations from that one provided over the complete set of genes. Other subsets of this capacity failed to provide a proper clustering. This fact means that the set of genes of Wnt-cascade is redundant, from the point of view of revealing the pathology standing behind the difference in genes expression. Obviously, the cascade set may not be claimed as redundant, from the point of view of functioning of the network. Apparently, this duality conspires the good identification of *tnbc* patients with linear statistics techniques.

References

[1] Koval, A., & Katanaev, V. L. (2018). *Dramatic dysbalancing of the Wnt pathway in breast cancers*. Scientific reports, 8(1), 7329. https://doi.org/10.1038/s41598-018-25672-6

 ISBN: 978-989-98750-7-4