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Target and Biomarker Identification Platform to Design New Drugs against Aging and Age-Related Diseases

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Abstract : We studied fundamental aspects of aging to develop a mathematical model of gene regulatory network. We show that aging manifests itself as an inherent instability of gene network leading to exponential accumulation of regulatory errors with age. To validate our approach we studied age-dependent omic data such as transcriptomes, metabolomes etc. of different model organisms and humans. We build a computational platform based on our model to identify the targets and biomarkers of aging to design new drugs against aging and age-related diseases. As biomarkers of aging, we choose the rate of aging and the biological age since they completely determine the state of the organism. Since rate of aging rapidly changes in response to an external stress, this kind of biomarker can be useful as a tool for quantitative efficacy assessment of drugs, their combinations, dose optimization, chronic toxicity estimate, personalized therapies selection, clinical endpoints achievement (within clinical research), and death risk assessments. According to our model, we propose a method for targets identification for further interventions against aging and age-related diseases. Being a biotech company, we offer a complete pipeline to develop an anti-aging drug-candidate.

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