DEVELOPMENT OF BIOMEDICAL EDUCATIONAL PROGRAMS

Yuriy L. Orlov[1,2*], *I.A.Volkov*[1], *S.Y.Simonenko*[1], *Anastasia A. Anashkina*[1,3]

[1] The Digital Health Institute, I.M.Sechenov First Moscow State Medical University (Sechenov University), Trubetskaya 8-2, 119991 Moscow, Russia
[2] Novosibirsk State University, Pirogova, 1, 630090 Novosibirsk, Russia
[3] Engelhardt Institute of Molecular Biology RAS, Vavilova, 32, 199991 Moscow, Russia

Development of computer programs for drug discovery needs qualified scientific staff, not only software development and technical support. Growth of biomedical data volume and availability of new experimental technologies give solid background for complex computer modeling limiting rather by human resources than hardware. Bioinformatics education faces new challenges related to changing educational standards, distant education on online meeting formats.

Way2Drug
Understanding Chemical-Biological Interactions

XXVIII Symposium on Bioinformatics and Computer-Aided Drug Discovery

Moscow (Virtual), 26/05/2022

COVID-19 changed research and development directions in 2020-2021.
We still have consequences (distal conferences and disrupted contacts)

Professor of Sechenov University

Minister of Health of the Russian Federation Mikhail Murashko

Rector Prof., Acad. P.V.Glybochko

Importance of the digital solutions for medicine was strengthen by COVID-19 and related lockdowns

At the forefront of health care

Monument to the feat of medical workers in the fight against COVID-19 (монумент «Подвигу медицинских работников в борьбе с COVID-19») (open 17.09.2021 in campus of Sechenov University in Moscow

New challenges in digital medicine and education

Scientific challenges in connection with the coronavirus pandemic have raised research and educational problems, changes in the methodology for mastering scientific disciplines.

Medical universities use new E-health technologies, one of the global areas of which is telemedicine. Medical teleconsultations make it possible to increase the availability of medical care for the population of remote areas, elderly and inactive patients, which is especially relevant for monitoring the spread of coronavirus infection.

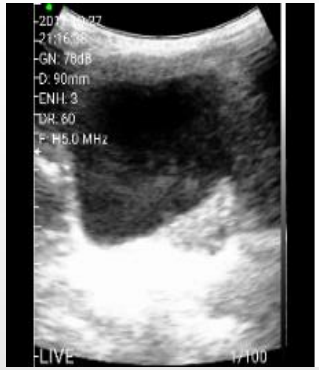
The First Moscow State Medical University of the Ministry of Health of Russia (Sechenov University) and the Institute of Digital Medicine deal with the problems of digitalization of medicine, provide a platform for discussing existing issues in the development of medical technologies, online conferences, and new educational programs.

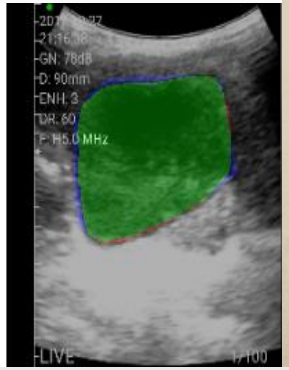
Publication activity - The Russian Journal of Telemedicine and E-Health continues series of publication on this topic (https://jtelemed.ru/). We have arranged series of international journal issues on gene expression regulation as well.

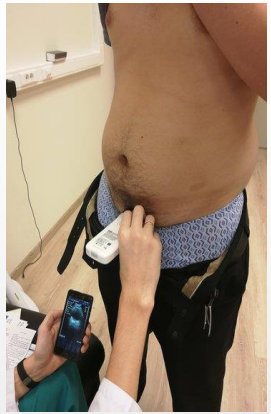
РОССИЙСКИЙ ЖУРНАЛ ТЕЛЕМЕДИЦИНЫ И ЭЛЕКТРОННОГО ЗДРАВООХРАНЕНИЯ
ISSN print 2712-9217 ISSN online 2712-9225 DOI: 10.29188/2712-9217

Machine learning tasks - analysis of bioimages, microscopy data

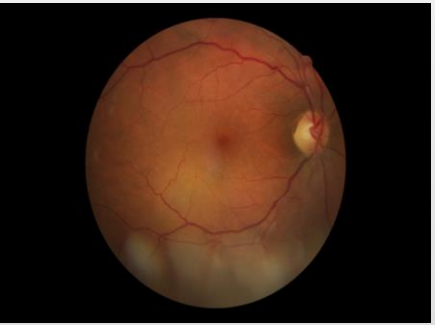
Training a neural network to recognize bladder malady



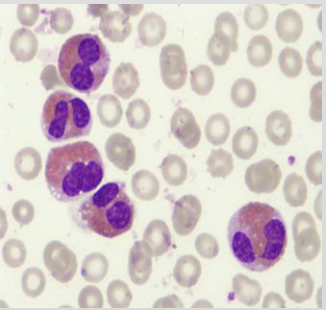




Dr. I.A.Shaderkin
Laboratory of electronic healthcare, Sechenov University



Fundus pictures



Peripheral and bone marrow smear images

3D positioning

Approaches at Sechenov University

- Teaching on informatics, IoT, Machine Leaning courses
- Master-classes for students
- Specialized Russian journal on telemedicine (RSCI - РИНЦ)

РОССИЙСКИЙ ЖУРНАЛ ТЕЛЕМЕДИЦИНЫ И ЭЛЕКТРОННОГО ЗДРАВООХРАНЕНИЯ
ISSN print 2712-9217 ISSN online 2712-9225 DOI: 10.29188/2712-9217

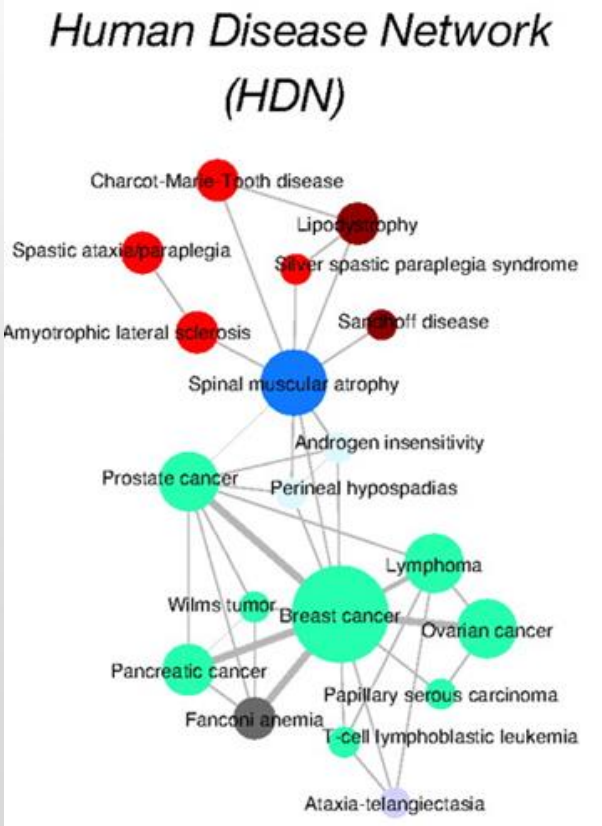
Network medicine conception – extension of gene network, drug-disease network, genotype-phenotype network terms

Network medicine: a network-based approach to human disease

Albert-László Barabási, Natali Gulbahce & Joseph Loscalzo

Nature Reviews Genetics **12**, 56–68(2011) | Cite this article

4557 Accesses | **2032** Citations | **68** Altmetric | Metrics

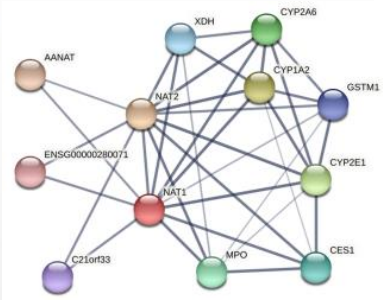


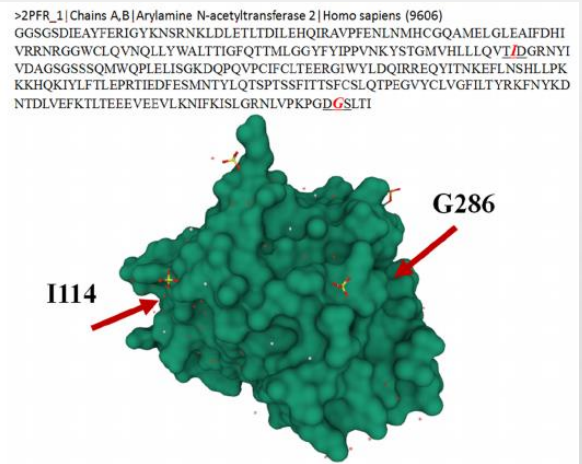
The idea is to compare diseases by comparing the functions of genes, symptoms, drug compounds - **the network approach**.

Analysis of genes associated with a disease, assessment of their place in the gene network (connectivity) allows us to evaluate them as target genes for drug effects

Standard for students' diploma and course works at Sechenov University on gene networks for complex human diseases – cancers, metabolic syndrome, Parkinson's disease

Work on gene network of **metabolic syndrome** with students





N-ACETYLTRANSFERASE (*NAT2*) GENE POLYMORPHISM AND GENE NETWORK ANALYSIS

R.P. Tiis[1,2], L.P. Osipova[1,2], E.R. Galieva[2], D.V. Lichman[1,2], E.N. Voronina[2,3], A.V. Melikhova[4], Y.L. Orlov[1,2,4]*, M.L. Filipenko[2,3]

[1]Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, 10 Lavrentyeva str., Novosibirsk, 630090 Russia; *e-mail: orlov@d-health.institute
[2]Novosibirsk State University, 2 Pirogova str., Novosibirsk, 630090 Russia
[3]Institute of Chemical Biology and Fundamental Medicine, Siberian Branch of the Russian Academy of Sciences, 8 Lavrentyeva str., Novosibirsk, 630090 Russia
[4]Sechenov First Moscow State Medical University of the Russian Ministry of Health (Sechenov University), 2-4 Bolshaya Pirogovskaya str., Moscow, 119991 Russia

To search for new targets of therapy, it is necessary to reconstruct the gene network of the disease, and identify the interaction of genes, proteins, and drug compounds. Using the online bioinformatics tools we have analyzed the current data set related to the metabolism of xenobiotics, mediated by the N-acetyltransferase 2 (*NAT2*) gene. The study of allelic polymorphism of the NAT2 gene has a prognostic value, allowing to determine the risk of a number of oncological diseases, the degree of increased risk due to smoking and exposure to chemical carcinogens, including drugs. The aim of this study was to determine the frequencies of two important "slow" variants of the *NAT2* gene (*NAT2*5*, rs1801280 and *NAT2*7*, rs1799931), which significantly affected the rate of xenobiotic acetylation among the indigenous Nenets population of Northern Siberia. The obtained frequencies of polymorphic variants among the Nenets occupy an intermediate value between those for Europeans and Asians, which might indicate specific features of adaptation. We present a model of the distribution of two polymorphic variants of the *NAT2* gene involved in the biotransformation of xenobiotics to study the characteristics of their metabolism in the indigenous inhabitants of Yamal.

Key words: xenobiotics; N-acetyltransferase 2; gene polymorphism; Nenets; bioinformatics; gene networks reconstruction

Funding. The work was supported by the Russian Science Foundation (project no. 19-15-00219).

Received: 23.04.2021, revised: 05.05.2021, accepted: 11.05.2021.

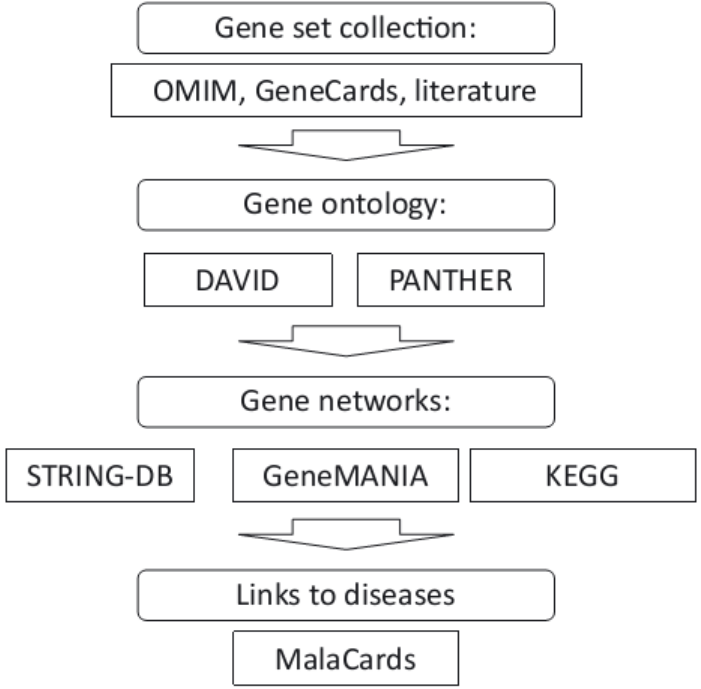
Tiis, R. P., Osipova, L. P., Galieva, E. R., Lichman, D. V., Voronina, E. N., Melikhova, A. V., Orlov, Y. L., Filipenko, M. L. (2021). N-acetyltransferase (NAT2) gene polymorphism and gene network analysis. *Biomeditsinskaya khimiya*, 67(3), 213-221.

DOI: 10.18097/PBMC20216703213

Presented at previous "Way2drug" conference in 2021

Publication on bioinformatics in co-authorship with the students (*Journal of Integrative Bioinformatics*, Q1)

Due to distant education format in Moscow in 2020-2021 we set priority for online bioinformatics tools



Computer pipeline – using only online tools – appropriate for students and distal education format

DE GRUYTER Journal of Integrative Bioinformatics 2021; 20210031

Natalya V. Gubanova, Nina G. Orlova, Arthur I. Dergilev, Nina Y. Oparina and Yuriy L. Orlov*

Glioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools

https://doi.org/10.1515/jib-2021-0031
Received August 31, 2021; accepted October 18, 2021; published online November 16, 2021

Table 5: Diseases found by prioritization of shared genes to glioblastoma.

No.	Description	Category	Score
1	Glioma	1.882×10^{-25}	9.333×10^{-22}
2	Pilocytic astrocytoma	3.147×10^{-25}	1.561×10^{-21}
3–4	Adult pilocytic astrocytoma/childhood pilocytic astrocytoma	1.829×10^{-22}	9.069×10^{-19}
5	Malignant glioma	3.741×10^{-21}	1.855×10^{-17}
6	Mixed gliomas	3.741×10^{-21}	1.855×10^{-17}
7	Neurofibromatosis 1	6.750×10^{-21}	3.348×10^{-17}
8	Malignant neoplasm of soft tissue	2.560×10^{-20}	1.270×10^{-16}
9	Ganglioglioma	4.231×10^{-20}	2.098×10^{-16}
10–11	Childhood oligodendroglioma/adult oligodendroglioma	4.616×10^{-20}	2.290×10^{-16}
12	Sarcoma	2.272×10^{-19}	1.127×10^{-15}

The research interest in the study of **Parkinson's disease** is due to the fact that this disease is a medical and economic problem for society and at the moment there are no treatments that can stop or reverse the neurodegenerative process accompanying this disease.

The growth in the volume of genetic data provides a basis for searching for associations with diseases, which is reflected in the replenishment of such databases as OMIM (https://omim.org/), GeneCards (https://www.genecards.org/).The development of experimental sequencing technologies leads to an increase in transcriptomic data, which allows the reconstruction of gene networks / signal transduction pathways based on co-expression. Existing online bioinformatics tools allow solving many practical tasks for the reconstruction of gene networks without using additional software (used in the training course for students of the Sechenov University - First Moscow State Medical University of the Ministry of Health of the Russian Federation named after I.M.Sechenov).

Figures are from
http://griza.nevrologica.ru/parkinson

DAVID

PANTHER

Сеченовский Университет

http://www.pantherdb.org/

LOGIN REGISTER CONTACT US HELP

Home | Browse | Genes and orthologs | Trees and HMMs | Pathways | Ontologies | Tools | Workspace

Quick links

- Whole genome function views
- Gene expression tools
- cSNP tools
- Upload multiple gene IDs
- Community Curation
- My Workspace
- HMM scoring
- Downloads
- Genome statistics
- Site map

Newsletter subscription

Enter your Email:

Subscribe

KEYWORD SEARCH

All Go

SEQUENCE SEARCH

Enter a protein sequence:

Sequence query limits: Protein - 50kb

Submit

The PANTHER (**P**rotein **AN**alysis **TH**rough **E**volutionary **R**elationships) Classification System is a unique resource that **classifies genes by their functions**, using published scientific experimental evidence and evolutionary relationships to predict function even in the absence of direct experimental evidence. Proteins are **classified by expert biologists** according to:

- Gene families and subfamilies, including annotated phylogenetic trees
- Gene Ontology classes: molecular function, biological process, cellular component
- PANTHER Protein Classes
- Pathways, including diagrams

PANTHER is part of the Gene Ontology Reference Genome Project.

PANTHER is supported by a research grant from the National Institute of General Medical Sciences [grant GM081084] and maintained by the Thomas lab at the University of Southern California.

What can I do on the PANTHER site?
Guide to getting started

News

(December 12, 2011)

PANTHER tools are now supporting all 48 organisms.

Click for additional info.

Publications

How to cite PANTHER

"PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium." Mi, et al.

"Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools." Thomas, et al.

"PANTHER: a library of protein families and subfamilies indexed by function." Thomas, et al.

Online tools for gene ontology analysis based on gene list

https://david.ncifcrf.gov/

DAVID Bioinformatics Resources 6.8
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

Home | Start Analysis | Shortcut to DAVID Tools | Technical Center | Downloads & APIs | Term of Service | Why DAVID? | About Us

*** Welcome to DAVID 6.8 ***
*** If you are looking for DAVID 6.7, please visit our development site. ***

Shortcut to DAVID Tools

Functional Annotation
Gene-annotation enrichment analysis, functional annotation clustering , BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and more

Gene Functional Classification
Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. More

Gene ID Conversion
Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically. More

Gene Name Batch Viewer
Display gene names for a given gene list; Search functionally related genes within your list or not in your list; Deep links to enriched detailed information. More

Recommending: A paper published in *Nature Protocols* describes step-by-step procedure to use DAVID!

Welcome to DAVID 6.8

2003 - 2019

The Database for Annotation, Visualization and Integrated Discovery (**DAVID**) v6.8 comprises a full Knowledgebase update to the sixth version of our original web-accessible programs. DAVID now provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:

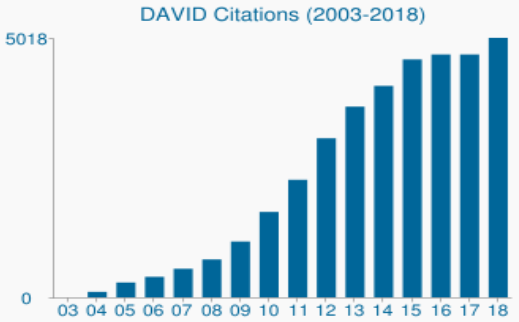
- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Cluster redundant annotation terms
- Visualize genes on BioCarta & KEGG pathway maps
- Display related many-genes-to-many-terms on 2-D view.
- Search for other functionally related genes not in the list
- List interacting proteins
- Explore gene names in batch
- Link gene-disease associations
- Highlight protein functional domains and motifs
- Redirect to related literatures
- Convert gene identifiers from one type to another

Search

What's Important in DAVID?

- Cite DAVID
- IDs of Affy Exon and Gene arrays supported
- Novel Classification Algorithms
- Pre-built Affymetrix and Illumina backgrounds
- User's customized gene background
- Enhanced calculating speed

Statistics of DAVID



- > 38,000 Citations

The tool for gene list manipulations and gene ontology analysis

Сеченовский Университет

Preparation of the list of genes associated with the disease

OMIM®

Online Mendelian Inheritance in Man®

An Online Catalog of Human Genes and Genetic Disorders

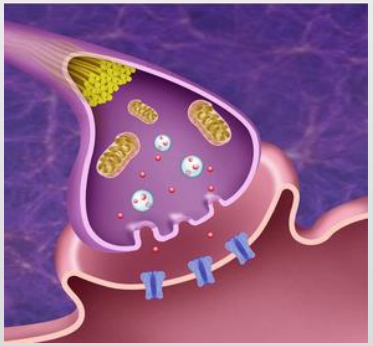
The Internet resource OMIM (Online Mendelian Inheritance in Man) (https://omim.org/) was used to search for genes of susceptibility to the disease. A list of 229 genes was found, and the categories and analysis of gene ontologies were calculated using the PANTHER resource (Protein ANalysis THrough Evolutionary Relationships) (http://pantherdb.org/) (Mi et al., 2013).
Of the 229 original genes, 170 identifiers were recognized, 59 identifiers were not recognized or could not be unambiguously mapped. In total, 20851 genes were used in the PANTHER reference genome. With the help of PANTHER, we built a table of ontologies for categories of biological processes, in order to obtain the most informative results, the p-values were limited to E-20.

The most significant categories for the genes of Parkinson's disease are general regulation of cell death, regulation of cell death of neurons, regulation of apoptosis and programmed cell death, negative regulation of cell death, which confirms the etiology of the disease - death of substantia nigra neurons.

These data confirm the key etiological features of the disease, among which the central aspect of the pathophysiology of Parkinson's disease is the progressive death of dopamine neurons in the midbrain and their axonal projections.
(Published recently at “Biomedical chemistry” (2021))

Some findings on gene ontologies for Parkinson's disease using these tools

GO molecular functions	Number of genes	P-value (corrected)
enzyme binding	59	2,48E-12
protein binding	150	2,22E-11
ubiquitin protein ligase binding	22	7,08E-11
ubiquitin-like protein ligase binding	22	1,94E-10
signaling receptor binding	46	2,15E-09
heatshock protein binding	15	2,41E-09
binding	164	2,80E-08
identical protein binding	46	9,35E-08
tau protein binding	9	1,69E-06
kinase binding	26	4,88E-06
protein domain specific binding	25	6,55E-06
catalytic activity	86	1,38E-05
protein kinase binding	22	1,99E-04



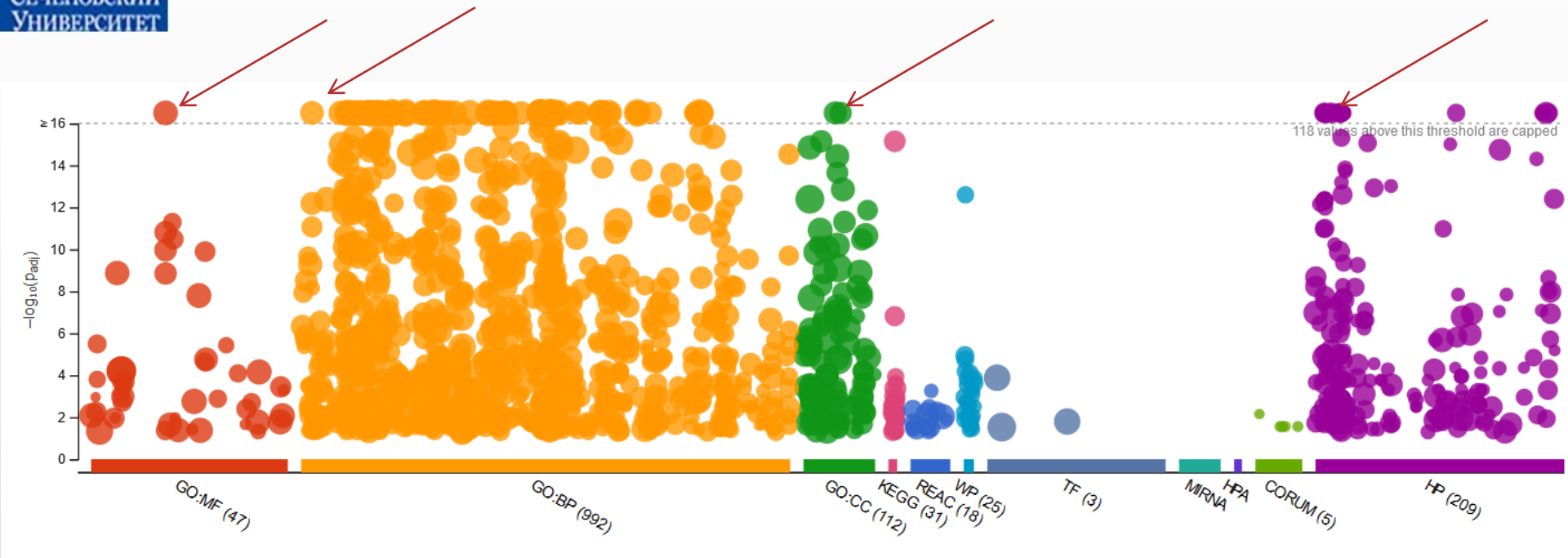
The most significant are the categories of enzyme binding, protein binding, binding of ubiquitin ligase and ubiquitin-like proteins, and binding of signaling proteins and heat shock proteins.

Autophagy is one of the main pathways for intracellular degradation of α-synuclein, and current research shows that dysfunctional autophagy in Parkinson's disease is one of the main risk factors for the development of the disease (Hale et al. 2016).

Сеченовский Университет

Plot of pointwise values of the categories of gene ontologies of Parkinson's disease genes, calculated using the GOSt program for a list of 293 genes.

g:Profiler



Findings on gene ontologies for Parkinson's disease using these tools

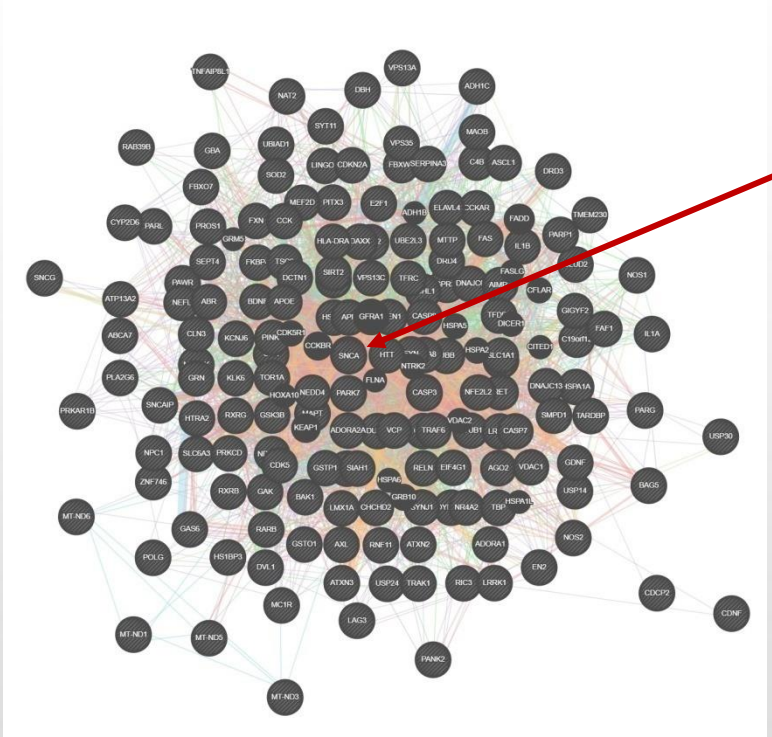
The most significant categories of this list of genes include the death of neurons, Lewy bodies, regulation of cell death, and the somatodendritic compartment.

http://biit.cs.ut.ee/gprofiler/gost

Сеченовский Университет

GeneMANIA and STRING-DB resources were used to reconstruct the gene network of interactions between Parkinson's disease genes.The figure shows a gene network of 187 genes for Parkinson's disease, reconstructed using GeneMANIA.

Gene network reconstruction for Parkinson’s disease using same gene list



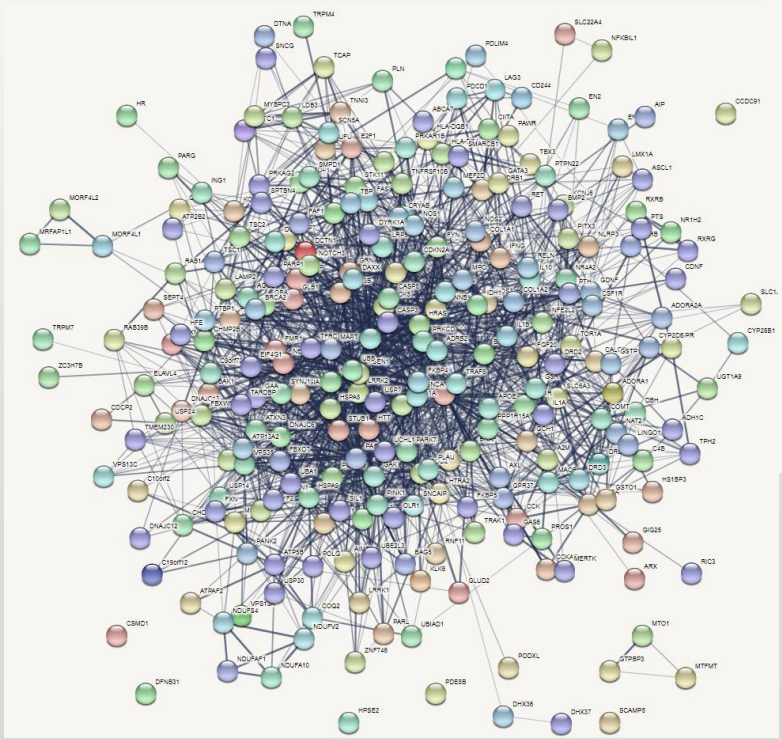
To date, it is known that the SNCA gene encoding α-synuclein is pleiomorphic, and any, both rare mutations and common, variations in this locus change the risk of developing the disease.

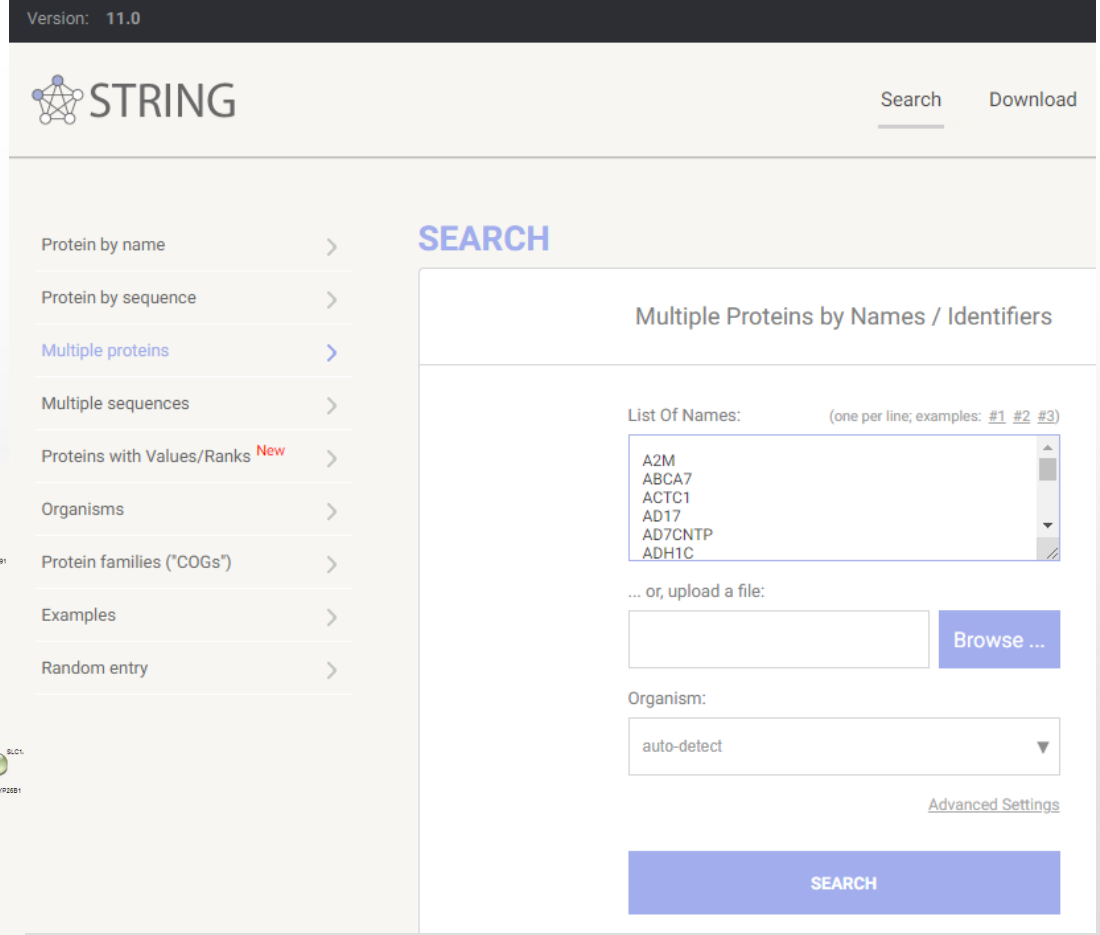
In the center of the constructed network are genes (proteins) that have a large number of connections with other elements - **SNCA, CASP3, GFRA1, HTT, PARK7.**
This trend is supported by current studies of candidate gene associations (Billingsley *et al.* 2018), in which the most statistically significant signals associated with Parkinson's disease are common variants located close to SNCA, LRRK2 and MAPT, as well as low-frequency coding variants in GBA.

Сеченовский Университет

https://string-db.org/

Gene network for the same disease reconstructed using STRING-DB





number of nodes:	268	
number of edges:	2079	
average node degree:	15.5	
avg. local clustering coefficient:		0.428
expected number of edges:		942
PPI enrichment p-value:	< 1.0e-16	

Integrative database tool – GeneCards.org

According to the GeneCards resource, the following 10 genes are the most significant for Parkinson's disease

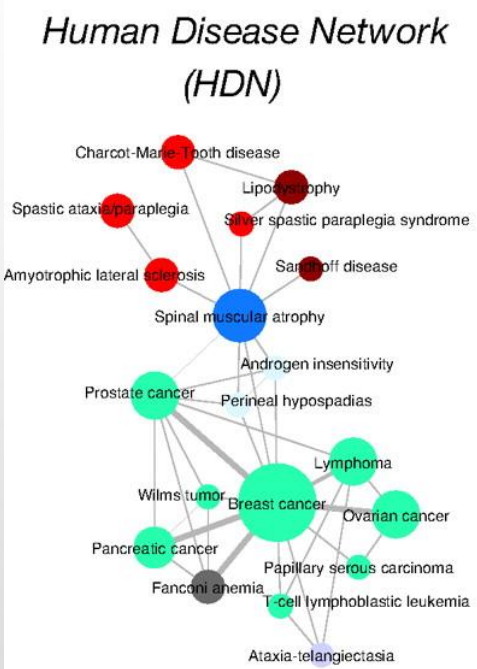
	Gene	Full name	Score
1	SNCA	Synuclein Alpha	157.73
2	LRRK2	Leucine Rich Repeat Kinase 2	151.68
3	PRKN	Parkin RBR E3 Ubiquitin Protein Ligase	142.61
4	PARK7	Parkinsonism Associated Deglycase	119.70
5	PINK1	PTEN Induced Kinase 1	114.13
6	MAPT	Microtubule Associated Protein Tau	106.49
7	ATP13A2	ATPase Cation Transporting 13A2	104.18
8	GBA	Glucosylceramidase Beta	103.77
9	APOE	Apolipoprotein E	94.18
10	APP	Amyloid Beta Precursor Protein	85.19

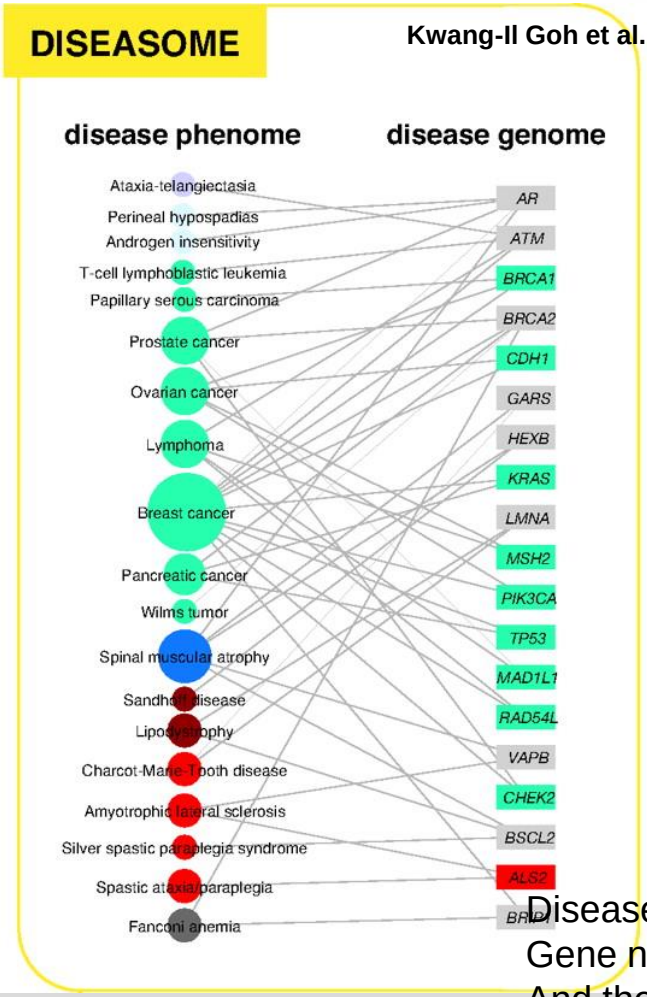
The first place in this hierarchical list is occupied by the *SNCA* gene encoding the alpha-synuclein protein, mutations in this gene lead to the development of autosomal dominant forms of the disease, the severity of the disease correlates with the number of copies of the *SNCA* gene. Mutations in the *LRRK2* gene have been identified as the causes of the autosomal dominant nature of Parkinson's disease as the most common monogenic form of the disease identified to date (Paisán-Ruíz *et al*., 2004; Zimprich *et al*., 2004). Genetic variants in *LRRK2* are associated with most of all known inherited manifestations of Parkinson's disease.

Approach for Diseases network reconstruction by genes and back - diseasome bipartite network

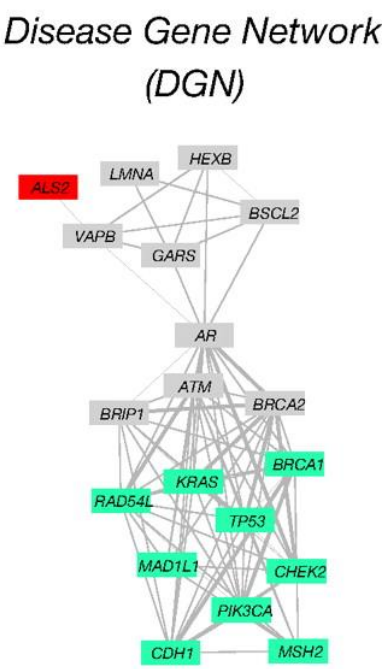
Generating human disease–drug networks

Online tools (some not free)
GeneGO (www.genego.com), Ingenuity (www.ingenuity.com) and Biocarta (www.biocarta.com).





Kwang-Il Goh et al. PNAS 2007;104:21:8685-8690



The human disease network
Kwang-Il Goh, M.E. Cusick, D.Valle, B.Childs, M.Vidal, A.-L. Barabási
PNAS, 2007 104 (21) 8685-8690;
https://doi.org/10.1073/pnas.0701361104

Disease Network (left panel)
Gene network (right)
And the link between diseases through genes (center).

Reconstruction of gene networks associated with Parkinson's disease leads to the identification of network structures. Such a discovery of functional connections opens the way to the creation of new drugs. The same network modeling approach is applied to series on complex diseases.

Acknowledgements

Sechenov University, Novosibirsk State University

Students:

A.G.Galieva
E.N.Ivanova
N.A.Makarov
A.I.Dergilev
Y.A.Mozyleva
R.R.Shakirova
A.V.Korobeinikova
M.A.Elistratova

The development of education programs using online bioinformatics tools was supported in 2022 by Potanin Foundation (grant **ГК22-000797**) :

Natalya V. Gubanova, Nina G. Orlova, Arthur I. Dergilev, Nina Y. Oparina, Yuriy L. Orlov. Glioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools. *Journal of Integrative Bioinformatics*.2021.Vol. 18, pp. 20210031.

Орлов Ю.Л., Галиева А.Г., Орлова Н.Г., Иванова Е.Н., Мозылева Ю.А., Анашкина А.А. (2021) Реконструкция генной сети болезни Паркинсона для поиска генов-мишеней. *Биомедицинская химия*, 2021, том 67, выпуск 3, с. 222-230 doi: 10.18097/PBMC20216703222

Тийс Р.П., Осипова Л.П., Галиева Э.Р., Личман Д.В., Воронина Е.Н., Мелихова А.В., Орлов Ю.Л., Филипенко М.Л. Полиморфизм вариантов гена N-ацетилтрансферазы 2 (*NAT2*) и анализ генной сети. *Биомедицинская химия*, 2021, 67(3): 213-221 doi:10.18097/PBMC20216703213

Yuriy L. Orlov, Ayya G. Galieva, Anton N. Luzin, Anastasia A. Anashkina (2021). Reconstruction of Gene Networks Associated with Complex Disorders on Example of Parkinson Disease //In: *Biologia Serbica* Vol. 43 - No. 1 Special Edition. Book of Abstracts Belgrade BioInformatics Conference 2021, 21-25 June 2021, Vinča, Serbia, P.62.

Orlova N.G., Orlov Y.L. (2022) Problems of developing online training courses for students in digital disciplines using bioinformatics as an example // In: *Proceedings of the International Conference "Scientific research of the SCO countries: synergy and integration".* Part 3 - Reports in English. March 31, 2022. Beijing, PRC). Scientific publishing house Infinity P. 58-65

Advertisements

Сеченовский Университет

MDPI Journals Topics Information Author Services Initiatives About Sign In / Sign Up Submit

Search for Articles: Title / Keyword Author / Affiliation International Journal ... All Article Types Search Advanced

Journals / IJMS / Special Issues / Medical Genetics, Genomics and Bioinformatics—2022

IMPACT FACTOR 5.924 Covered in: PubMed

International Journal of *Molecular Sciences*

Submit to Special Issue

Submit Abstract to Special Issue

Special Issue "Medical Genetics, Genomics and Bioinformatics—2022"

Special Issue Editors

Prof. Dr. Yuriy L. Orlov E-Mail Website1 Website2
Guest Editor
The Digital Health Institute, I.M. Sechenov First Moscow State Medical University of the Ministry of Health of the Russian Federation (Sechenov University), Moscow, Russia
Interests: medical genomics; e-Health; bioinformatics; systems biology
Special Issues, Collections and Topics in MDPI journals

Prof. Dr. Vadim Klimontov E-Mail Website
Guest Editor
Laboratory of Endocrinology, Research Institute of Clinical and Experimental Lymphology – Branch of the Federal Research Center Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Interests: diabetes; obesity; chronic kidney disease; metabolism; biomedicine; e-health
Special Issues, Collections and Topics in MDPI journals

Prof. Dr. Marina I. Sekacheva E-Mail Website
Guest Editor
Institute of Personalized Oncology, I.M. Sechenov First Moscow State Medical University of the Ministry of Health of the Russian Federation (Sechenov University), Moscow, Russia
Interests: oncology; medicine; medical genetics; genomics

Special journal issue – ***MPDI International Journal of Molecular Sciences***

For the conference participants!

https://www.mdpi.com/journal/ijms/special_issues/Medical_Genetics_2022

Сеченовский Университет

Post-conference publication is a way to connect fix the conference results, present the work for wider audience

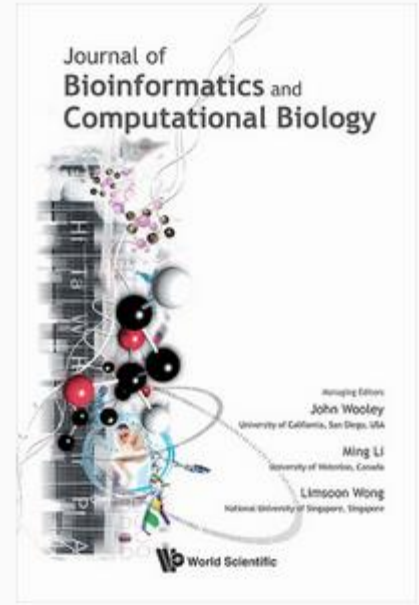
Special journal issues help in faster publications and free publications as well

Free journals (in English)

Vavilov Journal of Genetics and Breeding is a Platinum Open Access peer-reviewed scholarly journal, which does not charge author fees.

The journal has been published since 1997 (until 2011, as The Herald of Vavilov Society for Geneticists and Breeding Scientists) eight issues per year.

The journal publishes works on all fields of genetics, breeding, and related sciences. The scope of the journal includes: plant genetics, animal genetics, plant breeding, animal breeding, human genetics, medical genetics, neurogenetics, paleogenetics, microbial genetics and breeding, symbiogenetics,



Journal of Integrative Bioinformatics

Open Access

ISSN: 1613-4516

First published: January 1, 2017

Editors-in-chief: Falk Schreiber, Ralf Hofestädt

Edited by: Jan Baumbach, Ming Chen, Yuriy Orlov, Jens Allmer

Managing Editor: Björn Sommer

Editorial Board: Alejandro Giorgetti, Andrew Harrison, Aleksey Kochetov, Jens Krüger, Qi Ma, Hiroshi Matsuno, Chanchal K. Mitra, Josch K. Pauling, Chris Rawlings, Florentino Fdez-Riverola, Paolo Romano, Richard Röttger, Alban Shoshi, Siomar de Castro Soares, Jan Taubert, Andreas Tauch, Malik Yousef, Stephan Weise, Keywan Hassani-Pak

Publications in Russian journals (free)

Сеченовский Университет

РОССИЙСКИЙ ЖУРНАЛ ТЕЛЕМЕДИЦИНЫ И ЭЛЕКТРОННОГО ЗДРАВООХРАНЕНИЯ

ISSN print 2712-9217 ISSN online 2712-9225 DOI: 10.29188/2712-9217

SECHENOV UNIVERSITY
LIFE SCIENCES

Sechenov Medical Journal

https://www.sechenovmedj.com/jour/index

Vavilov Journal of Genetics and Breeding is a Platinum Open Access peer-reviewed scholarly journal, which does not charge author fees.

The journal has been published since 1997 (until 2011, as The Herald of Vavilov Society for Geneticists and Breeding Scientists) eight issues per year.

The journal publishes works on all fields of genetics, breeding, and related sciences. The scope of the journal includes: plant genetics, animal genetics, plant breeding, animal breeding, human genetics, medical genetics, neurogenetics, paleogenetics, microbial genetics and breeding, symbiogenetics,

https://vavilov.elpub.ru/jour

Сетевое издание *Основано в 2015 году*

Письма в ВАВИЛОВСКИЙ ЖУРНАЛ ГЕНЕТИКИ И СЕЛЕКЦИИ

http://pismavavilov.ru/

Сеченовский Университет

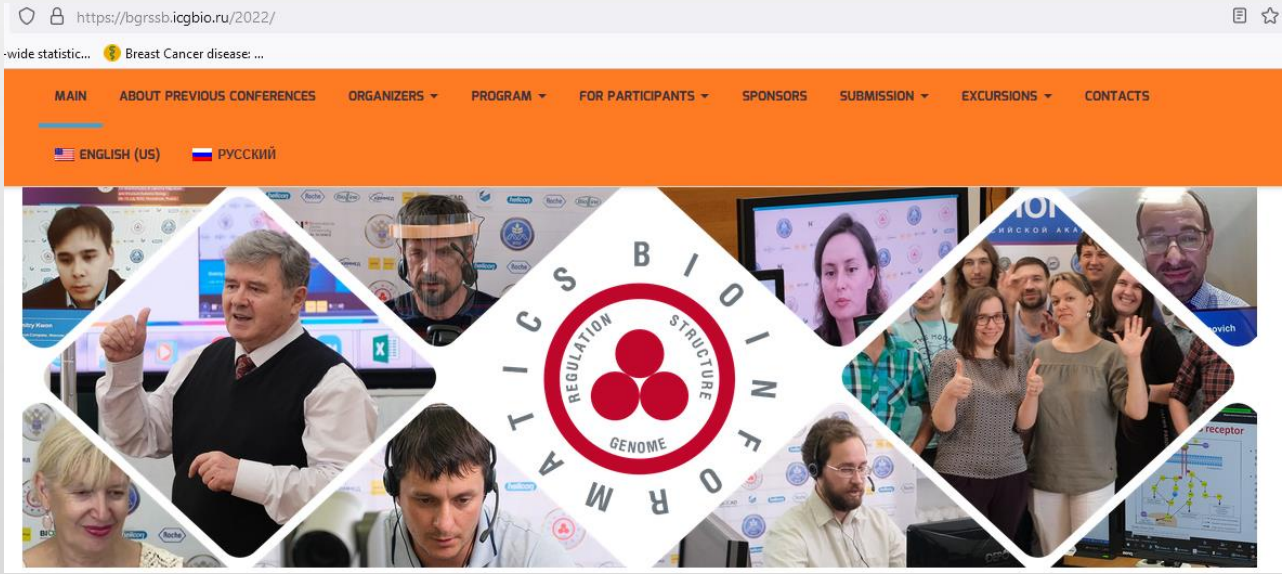
Welcome to the conference in live format – BGRS-2022 (Bioinformatics of Genome Regulation and Structure)

Novosibirsk, Russia

4-8 July 2022

XXVIII Symposium on Bioinformatics and Computer-Aided Drug Discovery

https://bgrssb.icgbio.ru/2022/



Longest conference series on bioinformatics in Russia, in Novosibirsk (biannually since 1998)

26/05/2022