



ALAPY

Save your time
for your greatest
results

Genetic data processing and analysis takes time which can be used more efficiently

OUR MISSION

We help genetic labs and medical centers to save time and money needed for bioinformatics, IT and data analysis.



We catch your needs on the fly
and create the way to free your
time for your greatest results

Since 2015,
11 experts in:

Genetics

Bioinformatics

Programming

Math modeling

Big data algorithms

OUR VALUE

We integrate data analysis algorithms for big data processing into genetic labs workflow. This allows quick and easy pipeline updates for specific user needs.



We help our clients solve the most difficult problems in data analysis

OUR FOCUS

Bioinformatics

Multifactor analysis with the latest big data innovations applied to genetics.

Mathematics

Automation and optimisation of genome analysis pipeline and its integration into single software tool.

Mathematical statistics

Genome data mass processing and analysis (comparison of several thousand samples).

Industry oriented software development

Genome data upload, download and storage optimization for bcl, fastq, bam, vcf and other files.



We create automated tools and customized solutions

ALAPY Genome Explorer

AGx is a cloud-based service that makes multifactor genome analysis fast, flexible and affordable for any lab, clinic or individual.

ALAPY Compressor

We compress fastq.gz (gzip compressed fastq) files up to 4 times with no data loss restoring exact copy of your original files using highest quality commercial software standards and outperforming gzip, bzip2 and other algorithms.

ALAPY for you

Your tasks are unique and we are here to help you thrive. We automate your tasks and embed them into your working environments or pipelines natively. With us you achieve goals faster and with better results.



WE ROCKET YOUR SCIENCE

Our projects

Client:

Big genetics research institute in Russia.

Project:

Research in TATA-box binding protein (TBP) interactions with promoters.

Our work:

We gathered data on known TATA-boxes that TBP binds, validated data on mutations in promoters that change phenotype, experimental data on physical and chemical interactions of TBP with DNA, data on changes in TBP/DNA binding. We created model of TBP/DNA interaction that estimates well changes in TBP/promoter binding due to mutations and its effect on phenotype. Hundreds of promoter mutations in humans, animals and plants were analysed with that model. Stability of genes promoters to mutations was assessed and correlation with population structure and phenotypes. Alternative promoters were found as well as promoters of pseudogenes that are triggered on and off by mutations. Dozens of inherited diseases like different types of anemia were found to be explained by TBP/promoter binding model as well as predisposition to malaria, different types of cancer and many other health issues.

Project results:

Our model was experimentally tested. This model as well as the collection of data we gathered is used in products developed by client. Based on methods and using our model and data client's employees developed new models, wrote dozens of peer-reviewed papers and dissertations. Scientific papers published during the project are well cited by international science community.



Our projects

Client:

Global leader in palm oil research.

Project:

Bioinformatics support of client's projects and training of client's employees.

Our work:

We did oil palm genome annotations including regulatory regions, analysis of mutations, methylation, histone modifications, gene expression, protein 3d structure modeling and analysis. Client's employees got training and experience from us on these and other bioinformatics topics. We provided consulting on computational biology for client's employees on their projects. We analysed quality of different oil palm genomes, detected and removed bacterial contamination, predicted genes and regulatory regions, selected high quality set of gene models, promoters and other regulatory regions, estimated effects of mutations and their distribution in populations, compared different oil palms between each other and with other species like rice, including epigenetics.

Project results:

Genome annotation, bioinformatics analysis and knowledge obtained from us by client during the project is used by it in many of its projects and products as well as in science publications. Client assembled bioinformatics group, that gather experience and knowledge from us sufficient to perform analysis themselves.



ALAPY

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