

NEVER WORRY ABOUT BIOINFORMATICS AGAIN

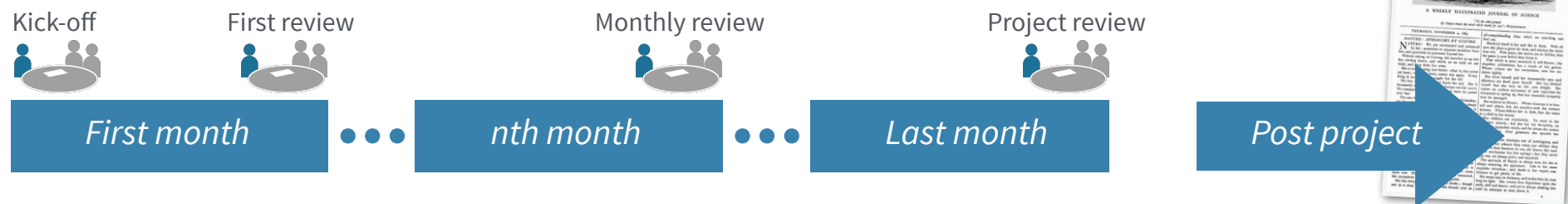
High-throughput molecular measurements have opened up an exciting world of new possibilities for researchers like you. To ensure a seamless process from planning such experiments to having the data analyzed and published, you deserve bioinformatics support that adapts to your unique needs. That is what we call Bioinformatics as a Service.

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BIOINFORMATICS AS A SERVICE



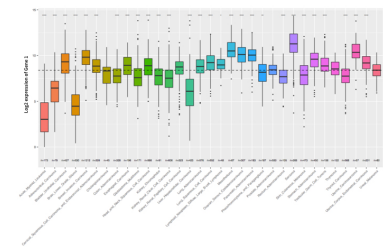
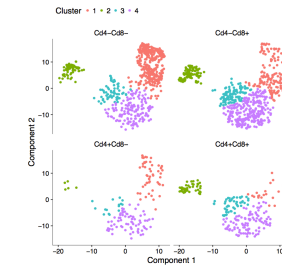
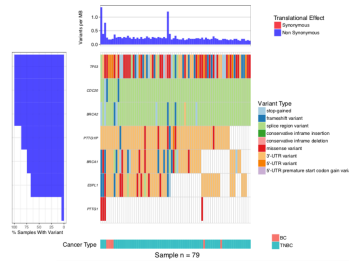
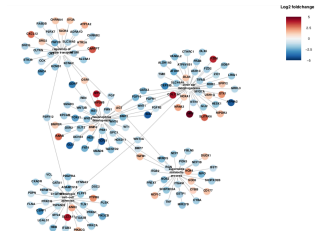
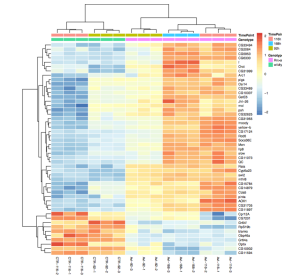
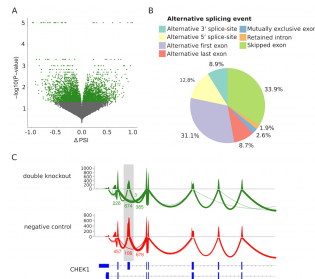
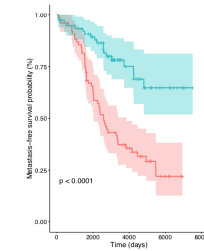
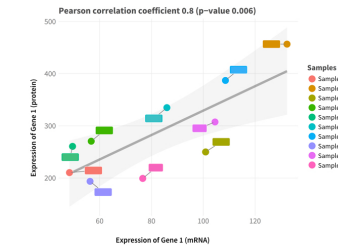
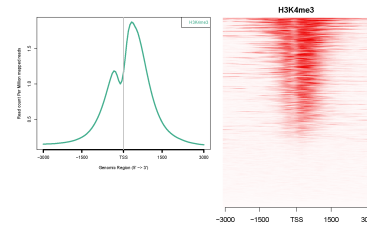
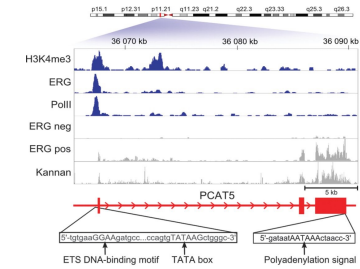
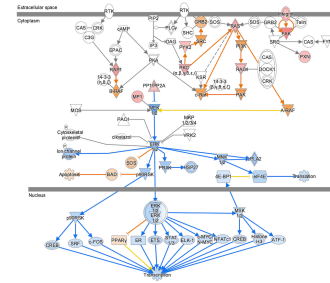
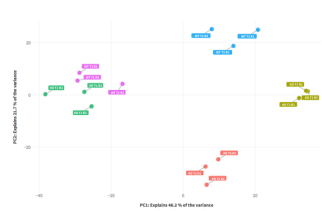
- ✓ Fast and easy communication with a dedicated PhD-level project manager
- ✓ Access to the expertise of a full bioinformatics team
- ✓ Just the right amount of work allocated each month
- ✓ Full satisfaction guarantee for each month of service
- ✓ Analysis fully customized to your data and research questions
- ✓ Access to our computing servers, pipelines and software
- ✓ All results presented and discussed in a teleconference
- ✓ Publication-ready figures and method descriptions
- ✓ Free post-project support to help you in publishing the findings

Amount of contracted work (min. 3 months)	Standard rate	Academic/startup rate (discounted -25%)
Working time: 5 days/month	5 290 EUR/month	3 968 EUR/month
Working time: 10 days/month	9 990 EUR/month	7 493 EUR/month
Working time: 15 days/month	13 990 EUR/month	10 493 EUR/month

Additional requests	Benefit	Price
Pre-payment of the project (min. 3 months)	+10 % working time	—
Expedited delivery	Project starts next business day	1 900 EUR

ANALYSIS TAILORED TO YOUR NEEDS

- Expression and pathway analysis with transcriptomic and proteomic data
- Single-cell expression analysis to study tissue heterogeneity and differentiation
- Identification of germline and somatic variants and associating them to phenotype
- *De novo* assembly of genomes and transcriptomes
- Identification of splice variants, fusion genes and novel transcripts from RNA-seq data
- Identification of epigenetic events and associating them to gene expression and phenotypes
- Predicting clinical endpoints from high-throughput patient data
- ...and much more!



FREQUENTLY ASKED QUESTIONS

Do I have to define the analysis in detail to receive a quote?

You do not have to be able to define the contracted bioinformatics work in detail. We just have to understand how the data was generated, and what are your research questions. Then, we plan the workflow accordingly.

Do you have experience working with researchers in my specific field?

It is likely. Our scientists come from a range of backgrounds, and our customers throughout the years span almost every corner of the academic and industrial life sciences. While every project is unique as a whole, we have probably dealt with data sets, analyses and research questions similar to yours.

Can I change the project contents after you have begun the work?

Absolutely! We will keep you up-to-date on the progress, and will discuss intermediary results with you in order to decide with you on the next batch of deliverables and their schedule. We are happy to adapt to your changing requirements; your dedicated project manager is always there to hear your wishes.

I didn't see a mention of the type of analysis I need.

Does it mean you do not provide it? Our flexible service model enables us to help you in nearly any bioinformatics-related questions. As far as the analysis lists go, there are so many different possibilities that it would be impossible to list everything we we can do. The easiest way to find out is to call or email us!

What if there are data quality issues? We perform a thorough computational quality control before moving on to downstream analyses. If there are any quality concerns, we will decide together on how to deal with them. If you wish to re-run the experiments, we can put the project on hold.

How do I deliver the data to you?

You may share the data files using any preferred file sharing service, or just send them on an external hard drive to our office (Mr Klaus Breitholtz, Genevia Technologies Oy, Hämeenkatu 14 C 33, 33100 Tampere, Finland). Just make sure you have local copies of the files as a backup before sending the data!

Will you help me interpret the results? Yes, we really want to make sure that you understand the results and that you have everything you need for further research or a publication. We will present and discuss all the findings with you before composing a final project report.

Do you require authorship in resulting publications?

No. Our customers sometimes ask us to coauthor, and we have been happy to do so, but authorship is never required. It is, however, a good practice to mention us in the acknowledgements or contributions section.

What exactly is the post-project support? It means that we will review the bioinformatics part of an ensuing manuscript, and help in replying to any bioinformatics-related reviewer comments. This service is free of charge for up to three years after the project.

If you analyze the data, will I learn anything in the process?

Yes, we are happy to help you not only to understand what we do, but also to analyze the data on your own if you are interested in learning a specific analysis yourself. This happens through personalized training via teleconferences and by providing analysis scripts to use on your future data sets.

How does the satisfaction guarantee work? If, during any month of the service, you feel that our model is not optimal for you, we may conclude the project immediately and you will not be invoiced the current or any following months. If this happens during the first month, you will never pay anything for the service.

This all sounds very interesting! How do I get this started? Just send us a message and let's schedule a meeting to discuss your needs!

