



We specialize in bioinformatic service and consulting by delivering integrated solutions for life science projects.

Welcome

Our vision is to enable the most real reconstruction of genomic landscape of factors responsible for phenotypic differences.

We believe that it can be achieved by combining different omics methods including linear and structural de-novo genome reconstruction, expression profiling of RNAs, epigenetic marks information and TFBS data - but not limited to. As the published genome assemblies can sometimes substantially differ in the information content, we specialize in providing researchers with reference genome sequence specific for their project - as the foundation of further comparative omics studies.

About us

Our main role is to support researchers achieving their scientific goals.

Main idea of this support is helping in planning of experiments for the project, coordinating activities between Researchers and Sequencing Service providers as well as in providing professional bioinformatics analysis service - this 'Triangle' of cooperation leads to the full success of the scientific project.

For the scientific research project, the most important is the researcher's idea. Realization of the most complicated tasks in the project, especially these requiring new technologies, can be outsourced to specialized service providers.

Finally to facilitate and fasten the project accomplishment, bioinformatic analysis can be commissioned to professional bioinformatics companies.

We work with researchers with over 20 years of experience in different fields of Biotechnology and with over 10 years of experience in Bioinformatics with the use of new sequencing technologies (NGS). Our specialists have several years of postdoctoral experience at international Universities (Canada, Poland, Switzerland, USA) as well as working at genomics divisions of international companies.

We have experience in the wide range of genomics and transcriptomics methods on the wide range of models from prokaryotic bacterias through simple and higher eukaryotic organisms like plants and animals to cancer cell lines and human tissues affected by diseases.



Experience

Our experience includes but is not limited to:

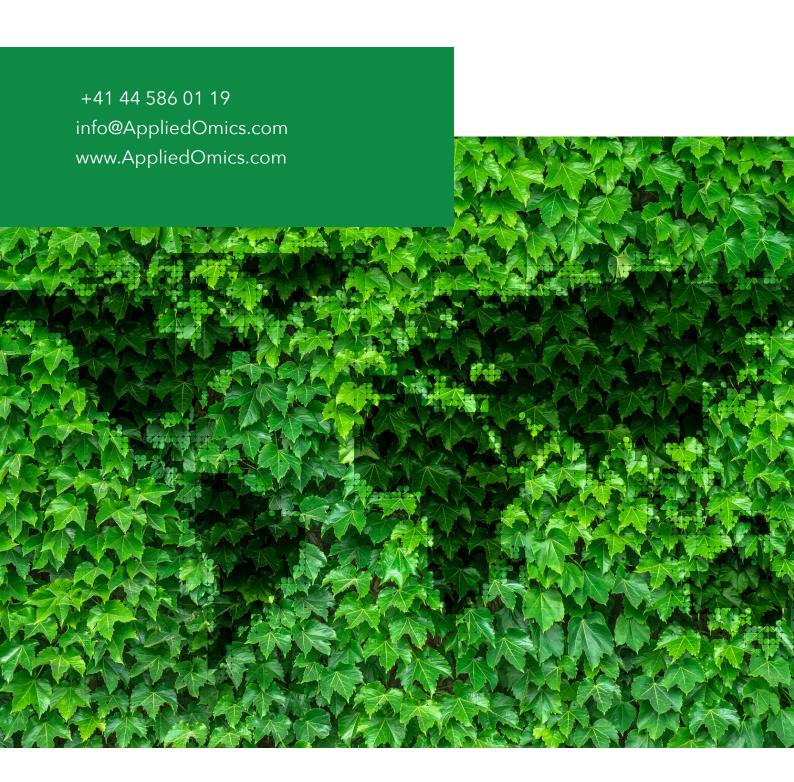
- de-novo genome assembly using variety of NGS technologies
- analysis of data after NGS and microarrays
- variants calling
- genome resequencing
- transcriptome assembly
- expression profiling of RNAs
- epigenetic marks profiling

- structural and functional annotation of genes
- comparative genomics focusing also on structural differences between genomes
- metabolic pathways analysis
- TFBS analysis
- repeat sequences analysis
- single cell genomics

What we offer

We would like to offer you our expertise in:

- planning the project, the experiments, having in mind the goals and the necessary bioinformatic analysis
- choosing optimal omics methods to extract relevant biological information for the specific scientific goals
- choosing the most effective service providers to extract the correspondent cellular information
- bioinformatic analysis, e.g. assembly, annotation, expression profiling, comparative genomics but not limited to
- bioinformatics training including linux and scripting courses
- Having other needs and ideas? Do not hesitate to contact us!



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Applied Omics Wóycicki

science for better life, nauka dla rozwoju