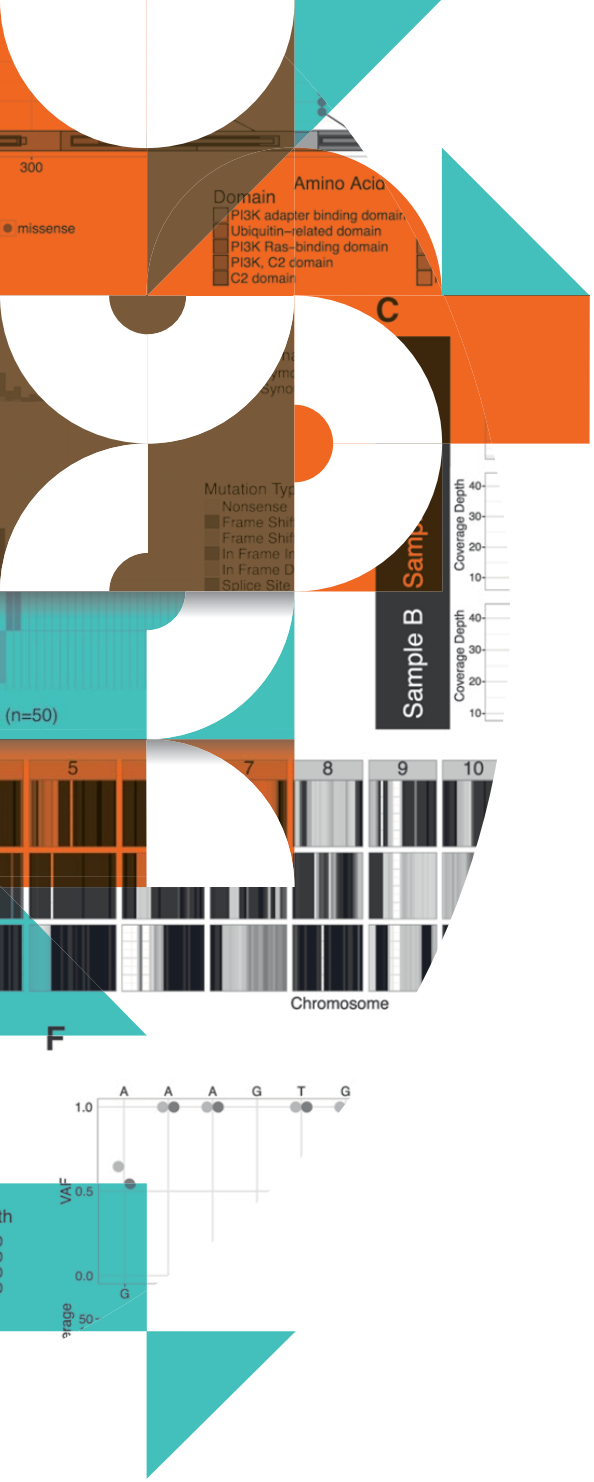


EUROPEAN UNION

RI AT CZ

Interreg
Austria-Czech Republic
European Regional Development Fund

New Generation Sequencing Bioinformatics

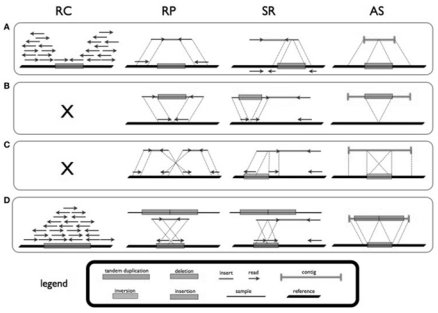
What we do

Our facility offers high-throughput data analysis services to support the research activities. The facility maintains and implements standardized data processing pipelines for the largescale biological data analysis. Our custom-made workflow management system allows us to provide reproducible and scalable data analyses with a quick turnout. Detailed downstream analysis of the results and assistance with the results interpretation can be provided upon individual requests. If your experiment requires a specialized and tailored custom pipeline, we can help with the implementation and development.

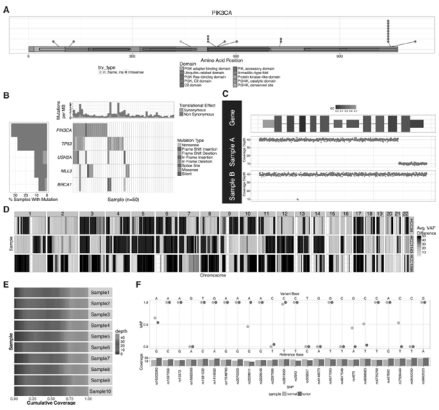
We will meet with you to discuss your needs free of charge. We are able to help you in all the stages of your project: before grant/project submission, after your project was approved before you start the analysis of your data or even if you have already started analyzing your data and need help to troubleshoot any ongoing procedure.

We can provide training for the usage of our standard pipelines in both Linux environment as well as the friendly graphical interface of our Galaxy server. We closely collaborate with PIs, researchers and graduate students on their projects and help them to get the most out of their data.

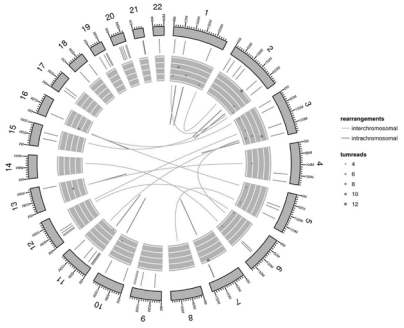
CEITEC
Kamenice 753/5, Brno, 625 00
University Campus Bohunice
Building A35
Czech Republic
www.ceitec.eu/bioinformatics
bioinformatics@ceitec.muni.cz



Stratification of structural variant calling algorithms based on variant type.



Overview of visualisations used for somatic and copy number variant effect estimation.



Circo plot of chromosomal rearrangements identified in sequenced tumor sample.

Services and Methodologies Provided

Our facility provides following data analysis solutions for:

- Gene expression studies (RNA-Seq,smallRNA-Seq)
- DNA variation single-nucleotide variant identification (SNP/InDel), structural variant (SV) and copy-number variation (CNV) analysis
- Protein-DNA/RNA interactions (ChIP-Seq, CLIP-Seq)
- Genome and transcriptome assembly
- Customized and project-tailored workflows and pipelines

In addition, we provide following services:

- Downstream bioinformatics support, statistical analysis and creation of publication-ready visualizations
- Teaching, training and consultation in high-throughput bioinformatics, experimental design and statistics
- Access to bioinformatics software and computational resources

Contact and Location

CEITEC
Kamenice 753/5, Brno, 625 00, Czech Republic
University Campus Bohunice
Building A35
www.ceitec.eu/bioinformatics
bioinformatics@ceitec.muni.cz

MUNI | CEITEC