CORE FACILITY NEWSLETTER
June 2017

Bioinformatics Infrastructure

Bioinformatics round-table

Recently implemented methods

TRAINING

Dear Customers and Researchers,

To support your research activities in the field of biostatistics and bioinformatics the **Computational Bioanalytics Facility** offers new services and hands-on workshops.

Bioinformatics Infrastructure – Galaxy server

Recently our team member Marija Durdevic visited a Galaxy High-Throughput-Sequencing (HTS) data analysis workshop in Freiburg. The Freiburg Galaxy Team is led by one of the main Galaxy developers, Dr. Björn Grüning. The workshop provided an opportunity to exchange experiences about data analysis over Galaxy and best practices in Galaxy Server administration.

Our Galaxy server will be upgraded to a new version in July to allow Galaxy users to explore new powerful visualisation options and fast data analysis processing. For more information, please follow our Galaxy web page: https://galaxy.medunigraz.at.

If you are interested to learn more about data analysis with Galaxy, please apply for the free Galaxy training we organize once per month. Next one will take a place on 26th of June at 1pm, ZMF seminar room ground floor EG-087.

Bioinformatics round-table

CF-CB again organized the regular Bioinformatics round table at the Medical University Graz on the 28th of March. A new pipeline *TIminer,* tested and implemented at
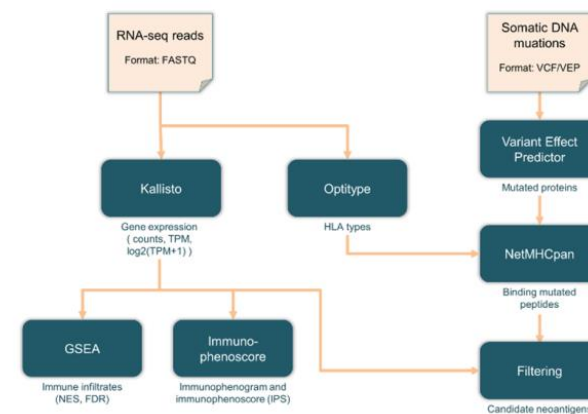

our core facility, was presented. This highly integrated workflow was developed in cooperation with our partner Univ.-Prof. Dr. Zlatko Trajanoski (Division of Bioinformatics at the Medical University of Innsbruck). *TIminer* is a standalone pipeline enclosing a selection of state-of-the-art tools for the investigation of tumour-immune cell interactions from genomic data. *TIminer* allows the following analyses: Gene Expression, Immune infiltrates, Tumor immunogenicity, HLA typing and Neoantigens.

Next Bioinformatics round-table will take place by the end of June. You are cordially invited to join.

Recently implemented methods @ Core Facility Computational Bioanalytics

Machine Learning for Microbiome Data Analysis

Recent advances in next-generation sequencing have enabled high-throughput determination of biological sequences in microbial communities. The large volume of data presents the challenge of how to extract knowledge, recognize patterns, find similarities and relationships from a complex mixtures of microbes.
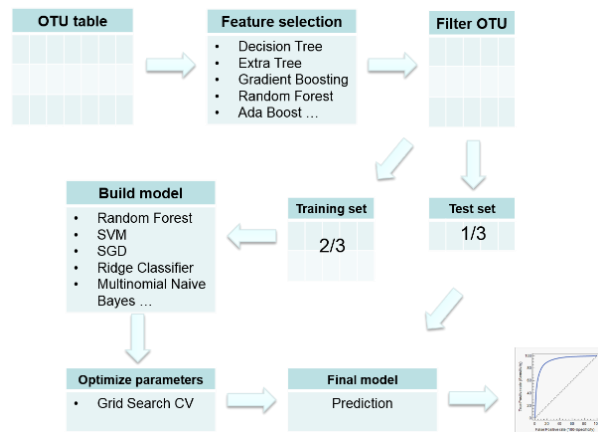
Owing to the complexity and variability of metagenomics studies, we investigated different machine learning techniques for feature selection and classification, to select the most relevant OTUs for discriminating between phenotypes. In the first stage we applied more than 15 different Machine Learning algorithms to select the most promising OTUs. Based on selected microbial signature we built a model based on 2/3 randomly selected sample subset. The predictive power of microbial signature is ascertained by AUROC analysis on the remaining 1/3 samples.

The main strength of such an approach is the ability to take into account the complex and interactional nature of the microbiome by simultaneous consideration of several bacterial features in a combined model.

T-Cell Receptors Profiling

High-throughput sequencing is gaining importance in adaptive immunity studies, demanding efficient software solutions for immunoglobulin (IG) and T-cell receptor profiling. After some research in this area and careful consideration about optimal solution we selected *MiXCR* software to provide this tool to MUG researchers working in this filed.

MiXCR is a universal framework that processes big immunome data from raw sequences to quantitated clonotypes. *MiXCR* efficiently handles paired and single-end reads, considers sequence quality, corrects PCR errors and identifies germline hypermutations. The software supports both partial and full-length profiling and employs all available RNA or DNA information, including sequences upstream of V and downstream of J gene segments.

Bolotin D et al. MiXCR: software for comprehensive adaptive immunity profiling. Nature methods 12, no. 5 (2015): 380-381. doi:10.1038/nmeth.3364
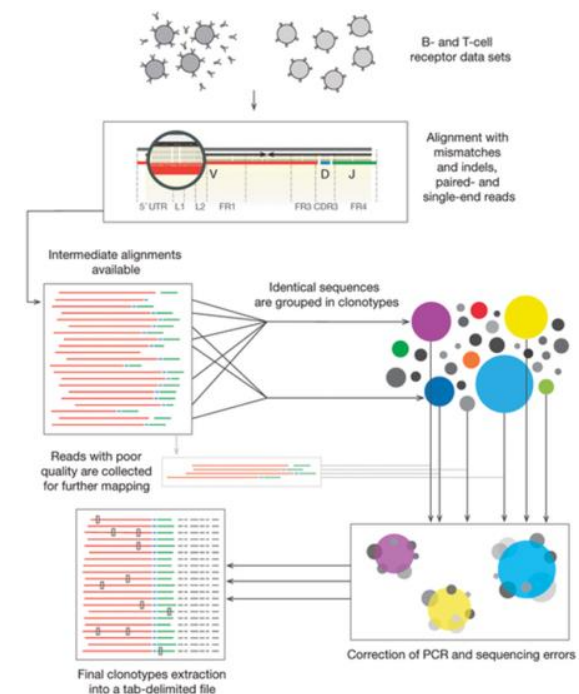
TRAINING

Courses of the ZMF academy in winter term 2017

October

Date	Title
October, 2nd 2017	Introduction into R for Life Science Researchers
October, 9th 2017	Statistical data analysis with SPSS, Day 1
October, 10th 2017	Statistical data analysis with SPSS, Day 2
October, 18th 2017	Microbiome data analysis with R
October, 23rd 2017	Statistical data analysis with SPSS, Day 3
October, 24th 2017	Statistical data analysis with SPSS, Day 4

November

November, 06th 2017	Introduction into NGS data analysis
November, 15th 2017	Advanced R for Life Sciences
November, 17th 2017	Statistical Errors and Pitfalls
November, 20th 2017	Introduction into Python for Life Science Researchers
November, 21st 2017	Getting started with Python in Statistics

December

December, 4th 2017	Statistical data analysis for qPCR

NEW Training

TBA	How to perform and analyze cell based assays? More information coming soon!

Monthly

	Introduction into Galaxy for Life Science Researchers

For course registration please contact: zmf-sekretariat@medunigraz.at

For more information click on the interactive course links and do not hesitate to visit us at the **Core Facility office** or send us a message: comp.bioanalytics@medunigraz.at

Yours sincerely

Andrea Groselj-Strele

Managing Director
Core Facility Computational Bioanalytics
Center for Medical Research
Stiftingtalstraße 24 (Room-Nr: EG089)
8010 Graz
Phone: +43 316 385 73012
Email: andrea.groselj-strele@medunigraz.at

ZMF
Medizinische Universität Graz