



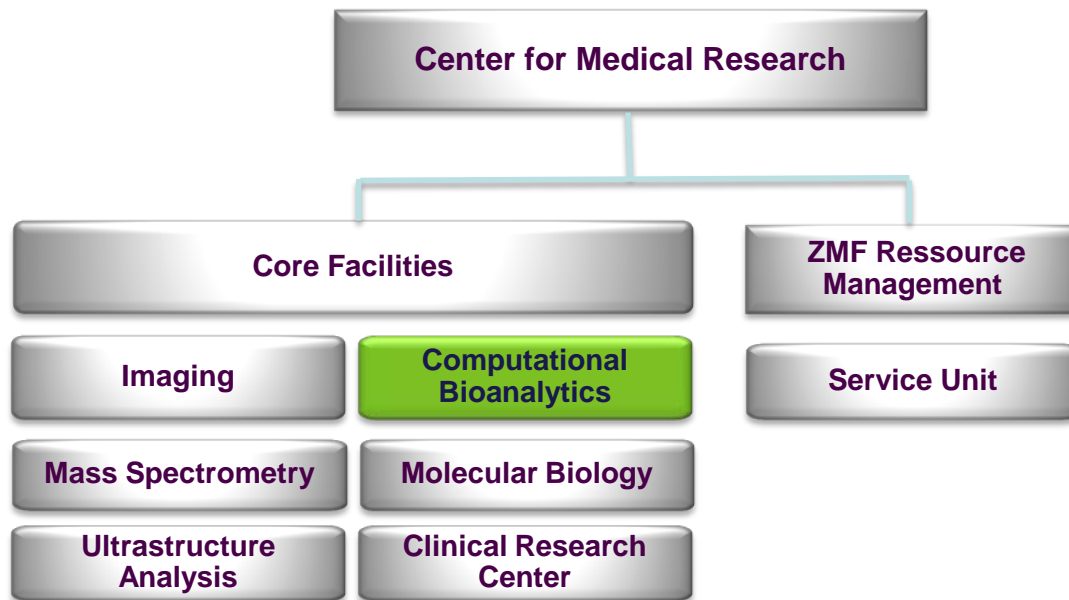
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# Core Facility Computational Bioanalytics



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# Institutional information



## ►► Biostatistics and Bioinformatics services for:

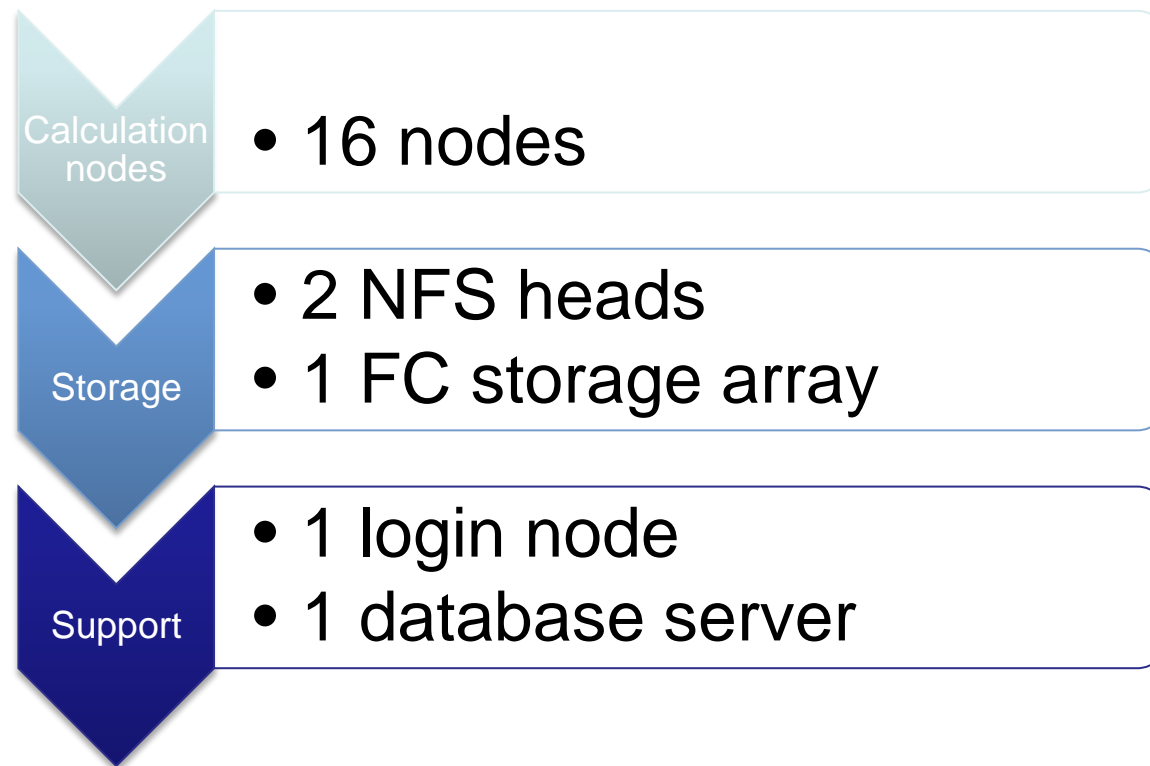
- Data analysis
- Consulting
- Training and Coaching

# Hardware



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- ▶▶ Current situation: small cluster with storage and 4 computing nodes
- ▶▶ Future perspective for 2016:



# Personnel setup

**Katharina Eberhard**  
BIOSTATISTICS



**Marija Durdevic**  
BIOINFORMATICS



**Andrea Groselj-Strele**  
HEAD OF CORE  
FACILITY



**Slave Trajanoski**  
BIOINFORMATICS

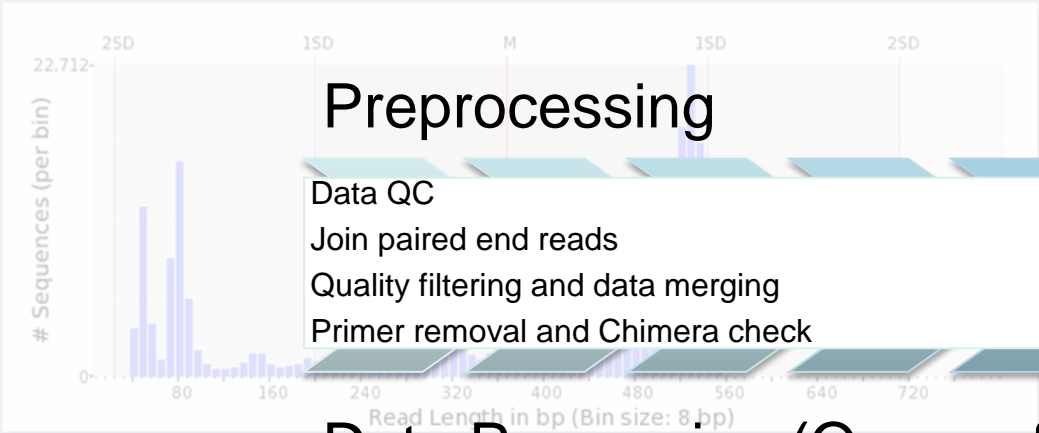


# 16s Microbiota analysis with Galaxy-Workflow



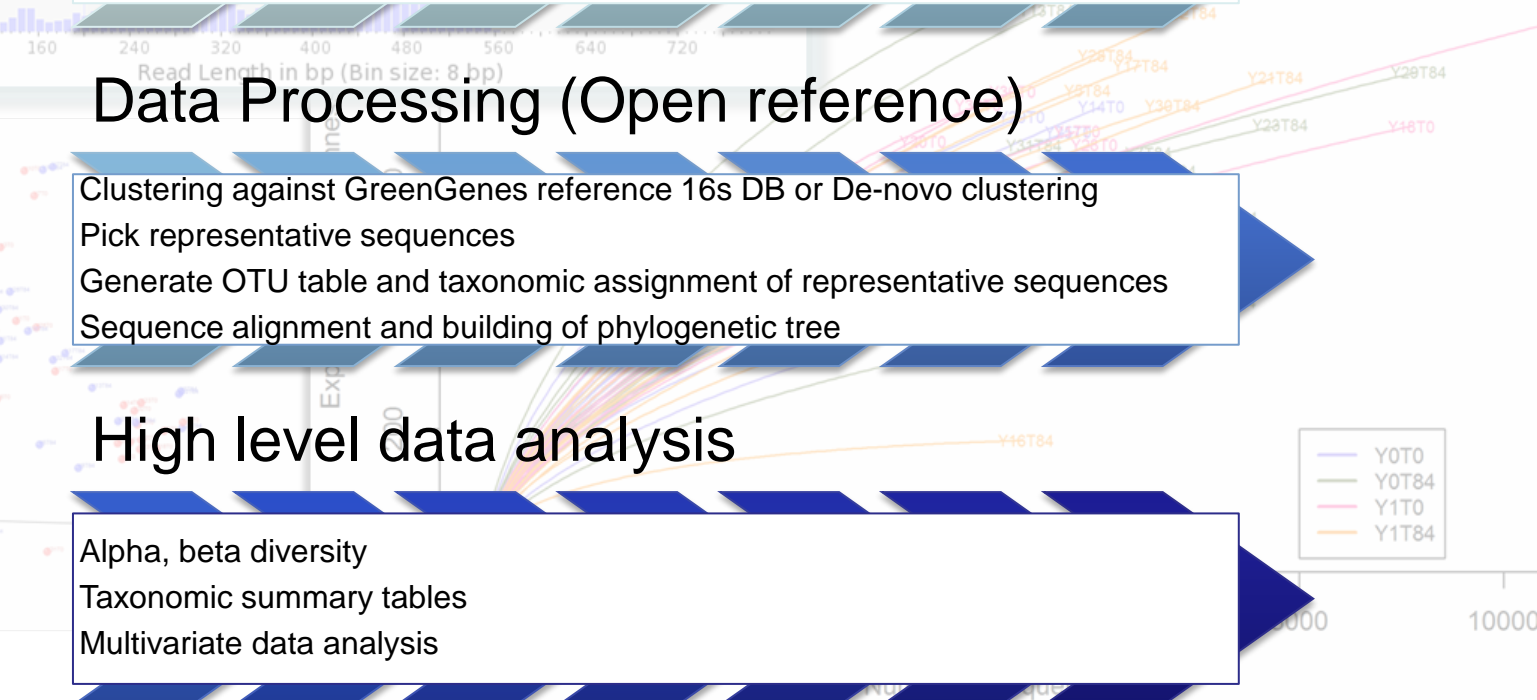
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## Preprocessing



- Data QC
- Join paired end reads
- Quality filtering and data merging
- Primer removal and Chimera check

## Data Processing (Open reference)



- Clustering against GreenGenes reference 16s DB or De-novo clustering
- Pick representative sequences
- Generate OTU table and taxonomic assignment of representative sequences
- Sequence alignment and building of phylogenetic tree

## High level data analysis

- Alpha, beta diversity
- Taxonomic summary tables
- Multivariate data analysis

# Thoughts and comments



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- ▶▶ Sustainable financing of computer infrastructure should enable state-of-the-art computing over a long period.
- ▶▶ Data analysis for large projects cannot be fulfilled with local resources at universities.
- ▶▶ Challenge to manage central HPC infrastructure with possibility to offer many different tools and databases to be used and regularly updated.
- ▶▶ Information and knowledge exchange is necessary and provides faster progress and development of bioinformatics in Austria.
- ▶▶ Networking and close cooperation of bioinformatics groups can strengthen our position and provide better financial support from government in Austria.



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# Thank you for your attention!



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