# About

## What Bioinformatics means to us

Bioinformatics consists of an applied and an algorithmic branch. The algorithmic one aims to develop and improve solutions to generic problems at the intersection of biology and compuer science. Applied bioinformatics draws from the existing algorithmic solutions; adopts and applies them to specific problems in biology.

**We believe that our work should facilitate medical and biological research.**

To achieve that end we either directly support data analysis in collaboration with experimentalists, and/or develop new algorithms/workflows for complex tasks that have no existing solution.

We have a young and aspiring team tackling different areas in bioinformatics and about 200 dedicated computer cores to support their work in three different areas of bioinformatics.

### Genomics

Most work performed in this area is support for other groups like genome and transcriptome assembly, and annotation. However, we have also compared de novo assembly tools, developed an algorithm for ab initio detection of adapters and showed that some published work contained some deficiencies in the next generation sequence analysis workflow.

<img genomcis group picture>

### Transcriptomics

Differential expression analysis is a task we mostly perform for colleagues in collaboration, but we have used it for microRNA expression in Toxoplasma gondii for our own research. Most interesting for us is miRNA detection using machine learning approaches. Currently, we focus on miRNA target detection and the establishment of miRNA regulatory networks and their interesection with gene regulatory networks and known pathways.

<img transcriptomics groupt picture>

### Proteomics

In our opinion proteomics sways on a shaky foundation where even peptide and protein identification is not a very well established methodology. Therefore, one of our current focus is fixing this problem. Despite these limits, we support protein identification at the state-of-the-art and develop workflows allowing protein quantitation and facilitating proteogenomics.

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