

# Institute of Biomedical Informatics



Leila Taher



Christian Sailer



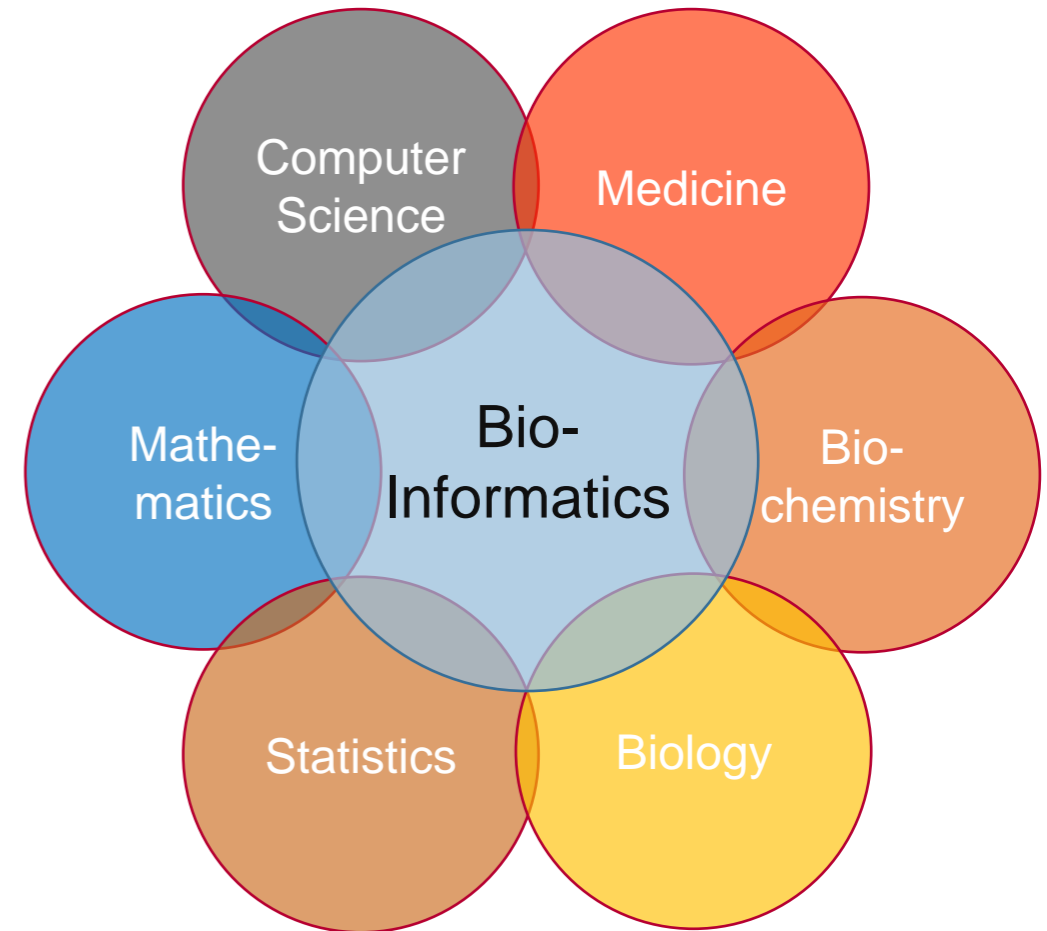
Gerhard Thallinger

# What is „Bioinformatics“

“Ask five bioinformaticians for a definition and you’ll get six different ones”

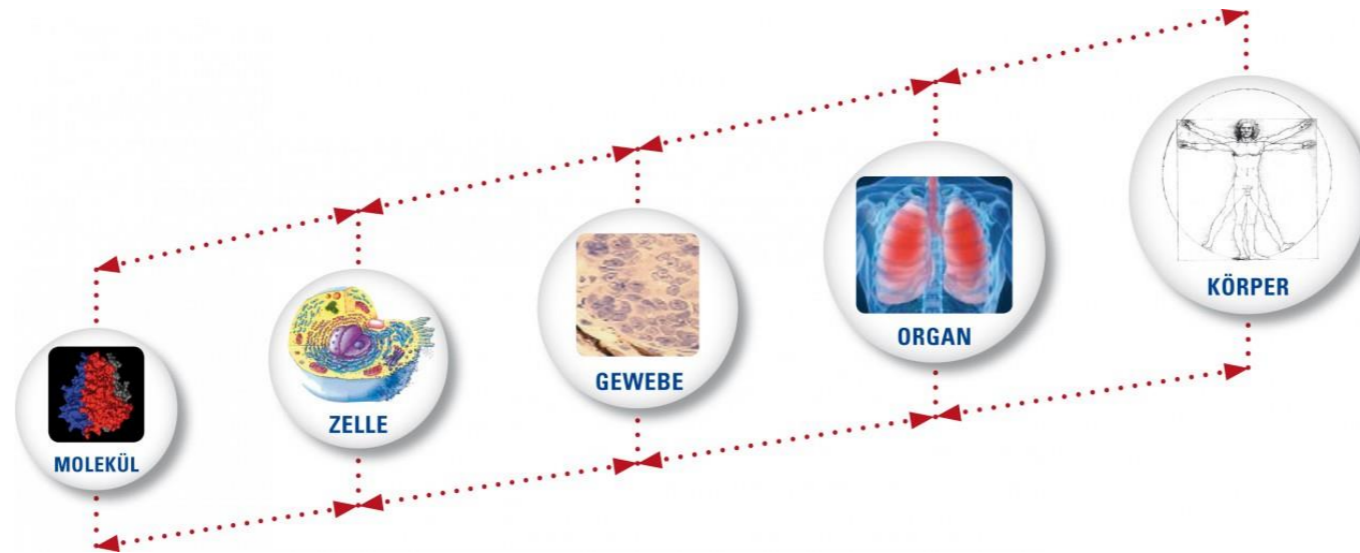
**Biology and Informatics = Bioinformatics**

- Theoretical biology
- Computational biology
- Systems biology
- (Theoretical) ecology
- Biomathematics
- Biostatistics
- Computational omics
- Computational evolutionary biology
- Applied bioinformatics



# What is „Bioinformatics“

Elucidation of biomoleculare relations in organisms at the cell-, tissue- und and organ level ...



... by developing and applying methods from computer science, mathematics and statistics on data generated in the „wet“ lab.

# What is „Bioinformatics“

**“Bioinformatics is the field of science in which biology, computer science, and information technology merge into a single discipline.”\***

\* NCBI,  
<https://www.ncbi.nlm.nih.gov/Class/MLACourse/Modules/MolBioReview/bioinformatics.html>

Algorithms  
and methods

Data analysis  
and interpretation



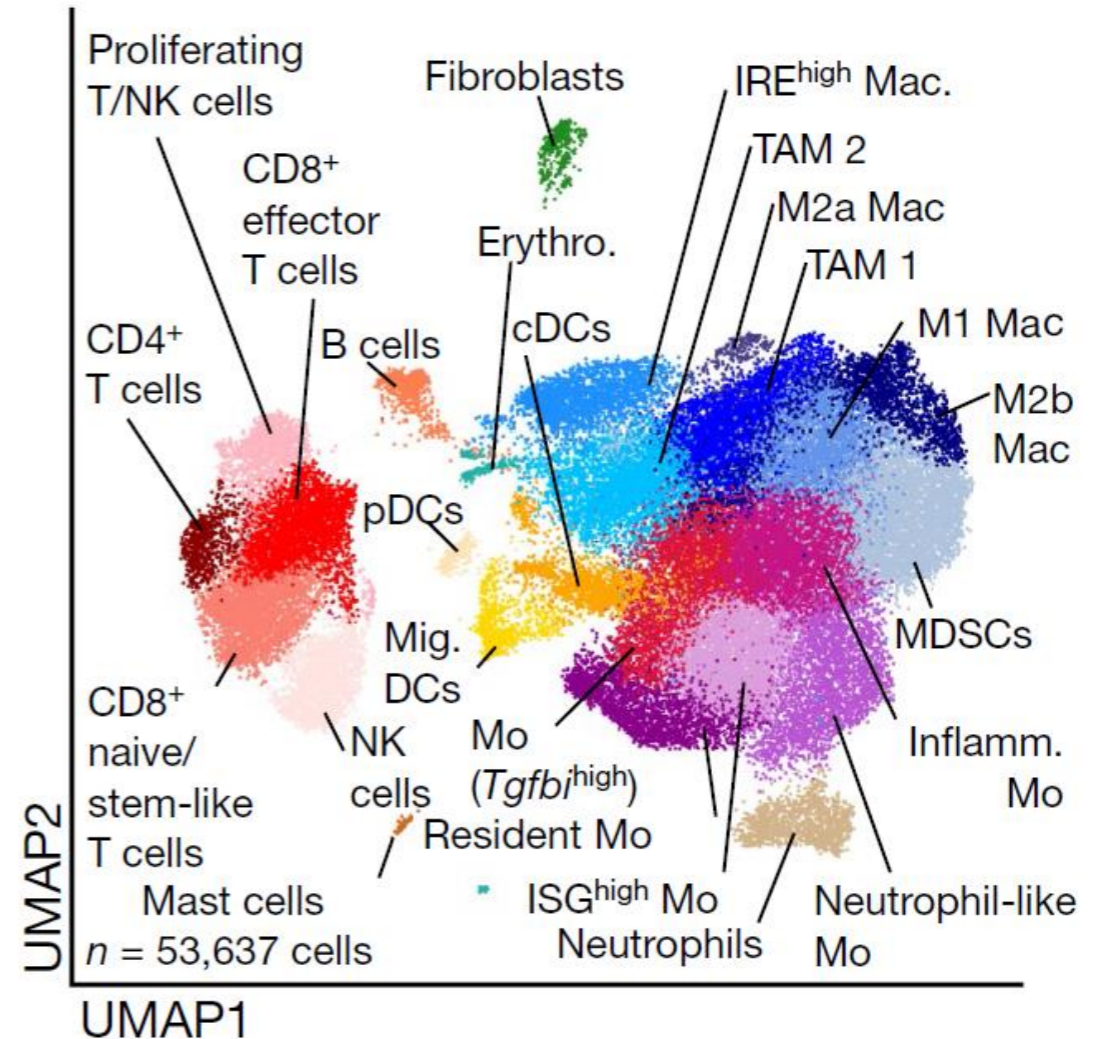
Tools and  
databases

# Bioinformatics applications

## Fight resistance to cancer immunotherapy\*

- Single cell sequencing data analysis
- Flow cytometry data analysis

\*Sun et al. Targeting TBK1 to overcome resistance to cancer immunotherapy, Nature 2023

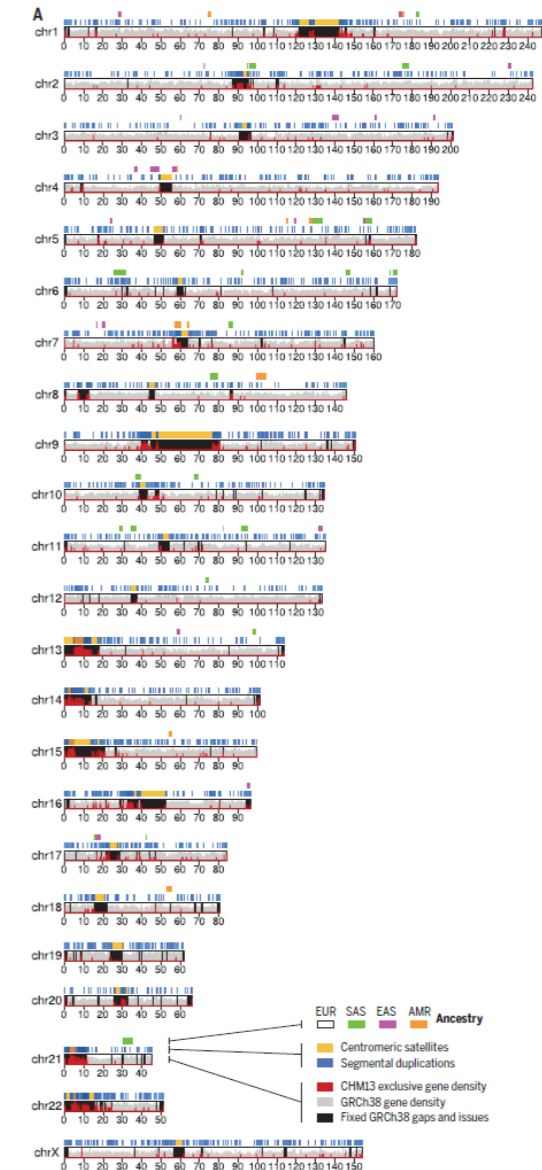


# Bioinformatics applications

## Completion of the human genome\*

- Long-read sequencing
- Genome assembly
- Genome annotation and visualization

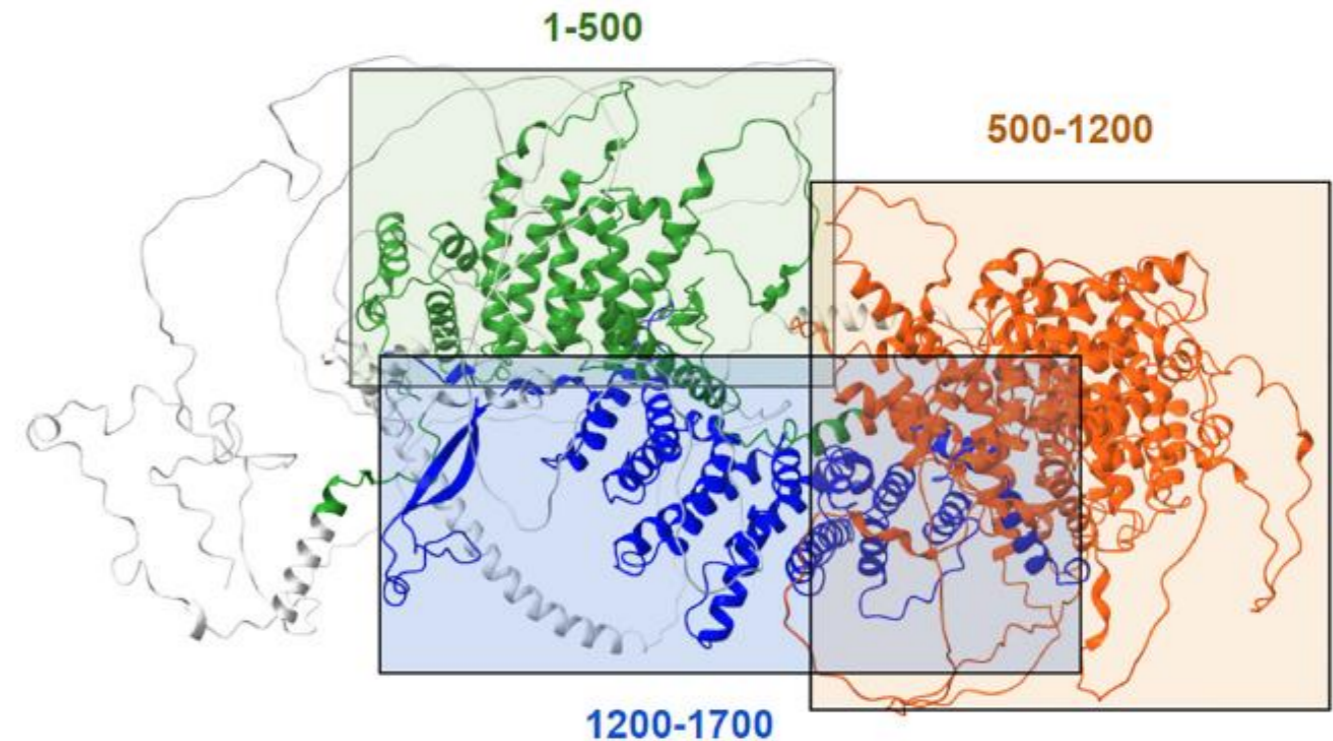
\*Nurk et al. The complete sequence of a human genome, *Science* 2022



# Bioinformatics applications

## 3D Structure database of all known proteins\*

- Deep learning for structure prediction
- Database application
- Web-frontend



**\*Varadi et al. AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models, Nucleic Acids Res 2022**

# Bioinformatics in the BME curriculum I

## Bachelor:

- Grundlagen der Informatik
- Grundlagen der Molekular- und Zellbiologie
- Algorithmen in der Bioinformatik
- Verfassen wissenschaftlicher Arbeiten



# Bioinformatics in the BME curriculum II

## Master:

- Biostatistics and experimental design
- Evolution
- Molecu
- Perl pro
- Statistic
- Systems biology (coming soon!)
- DNA-RNA sequencing

Master's thesis from any major

|        |    | Minors  |   |     |      |      |   |      |   |     |     |     |      |
|--------|----|---|---|-----|------|------|---|------|---|-----|-----|-----|------|
| Majors |    | 1   | 2 | 3   | 4    | 5    | 6 | 7    | 8 | 9   | 10  | 11  | 12   |
|        |    |   |   |     |      |      |   |      |   |     |     |     |      |
|        |    |   |   |     |      |      |   |      |   |     |     |     |      |
|        | c1 | and Simulation                                  |   |     |      |      |   |      |   |     |     |     |      |
|        | c2 | Biomedical Instrumentation and Sensors          |   |     |      |      |   |      |   | (2) |     | (3) |      |
|        | c3 | Biomedical Imaging and Sensing                  |   | (4) |      | (5)  |   |      |   | (8) | (6) | (7) | (9)  |
|        | c4 | Computational Neuroscience                      |   |     |      |      |   | (10) |   |     |     |     | (11) |
|        | c5 | Biomedical Device Design, Safety and Regulation |   |     | (12) | (13) |   |      |   |     |     |     |      |
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# Thesis topics I

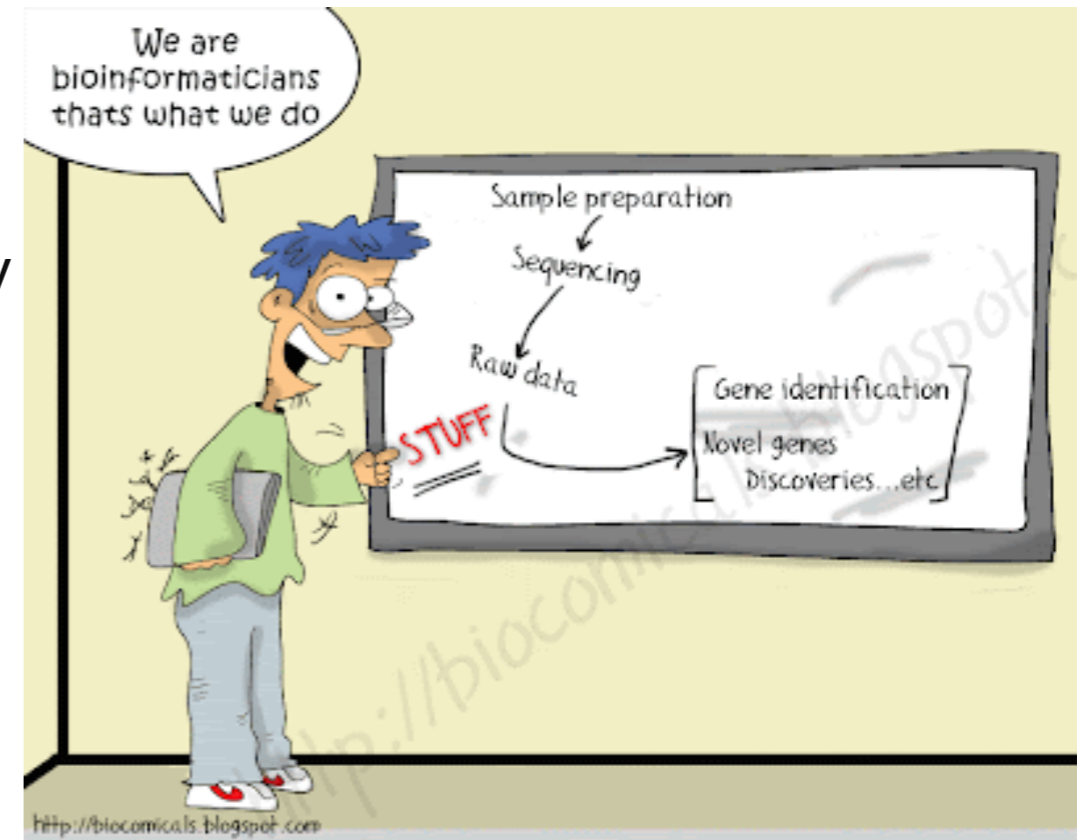
- Characterization of transposons as drivers of genome evolution
- Generation and/or analysis of Oxford Nanopore sequencing data
- Identification of structural variants associated with different cancer types
- Comparative transcriptomic analysis of cancer tumours and derived cell lines
- Implementation of models for simulating different population genetics scenarios
- Investigation of the relationship between enhancer RNA (eRNA) secondary structure and DNA enhancer function
- Application of deep learning in the analysis of omics data
- Long-read transcriptomics (ISO-seq) of fungi

# Thesis topics II

- Genome assembly and annotation
- Summarization of functional enrichment analyses
- Visualization of genome annotation
- Investigation of the lipidome using mass spectrometry
- Integrative analysis of data from different omics technologies with applications in biotechnology
- Characterization of the microbiome
- Comparative genomics of microorganisms
- Expansion of the regulatory network of a yeast
- Analysis of the alterations of the genome and epigenome of mammalian cells during fermentation

# Bioinformatics core skills

- Proficiency in at least one programming language. Perl, Python and/or R knowledge is a plus
- For specific projects you may need to be familiar with other programming languages
- (Good) understanding of molecular cell biology
- Linux (command line)
- Algorithms
- Databases
- Statistics
- Time management
- Readiness for self-study
- Patience



# What you should expect

- No pure literature work (there is always a practical part)!
- Frequent (weekly or biweekly) meetings between you and your supervisor
- Thesis supervision agreement
- Research proposal and short presentation at the beginning of your project
- Final presentation shortly before submitting your thesis
- Regular participation in our weekly lab meetings

# Collaborations

## Collaboration with:

- Harvard Medical School (Boston)
- Sloan Kettering Cancer Center (New York)
- New York University, Department of Medicine (New York)

**=> Stay abroad possible**

## Thesis combined with a FEMtech scholarship:

- Female students only
- 2-6 month scholarship
- Attractive remuneration

# Contact

**Talk to us. If you are interested in a particular bioinformatics topic that is not part of the list, we will do our best to design a project around it!**

<mailto:Bakk-Mas@genome.tugraz.at>



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Christian Sailer



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