



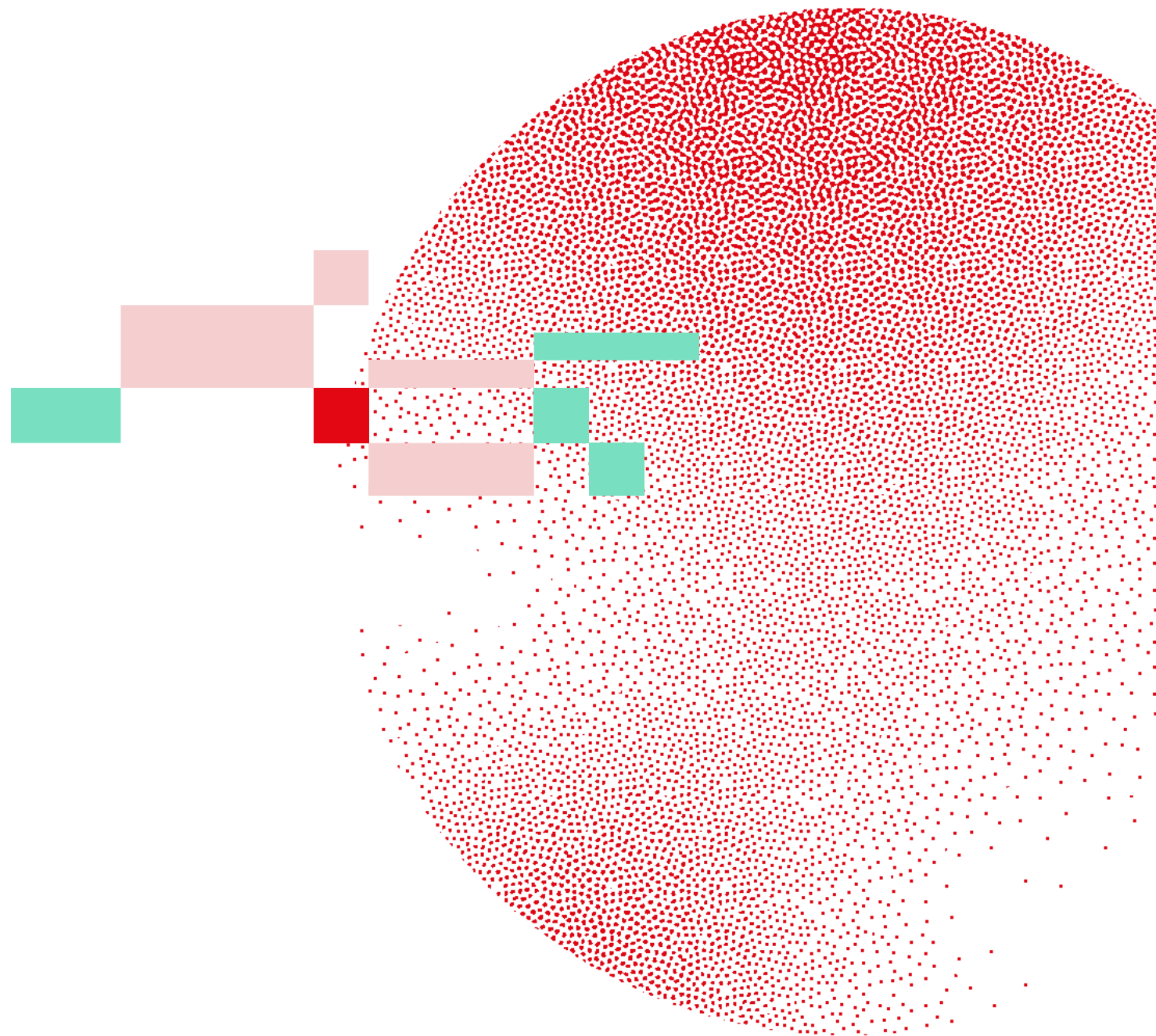
Swiss Institute of
Bioinformatics

SINGLE-CELL TRANSCRIPTOMICS WITH R

Introduction

Luciano Cascione

November 12-14, 2025



Trainers/ organisers/ helpers

- »» **Luciano Cascione:** Head of Bioinformatics Core Unit, IOR & SIB
- »» **Deepak Tanwar:** Trainer at SIB & Bioinformatics Specialist at UZH
- »» **Serena Zambarbieri:** Bioinformatician at IOR
- »» **Gregoire Rossier:** Training Project Manager at SIB
- »» **Patricia Palagi:** Training Group Leader at SIB

Learning outcomes

- » Explain the **characteristics** of the most-used **methods** to scRNA-seq data
- » Perform **quality control** at different steps of the analysis
- » Use **dimensionality reduction** (PCA, t-SNE, UMAP)
- » Apply **best practices** for **translating** single cell transcriptomic data into **biological knowledge**

Learning experiences

- » Lectures
- » Quizzes
- » Exercises

Quiz: 1-4

Communication

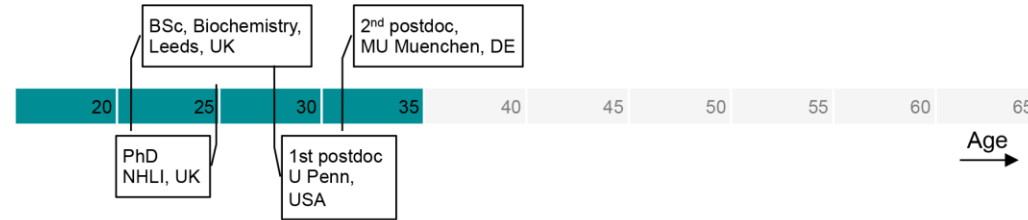
- » Course website: <https://sib-swiss.github.io/single-cell-r-training>
- » Shared document
 - » General links for the course
 - » Please write your name for the exam

Leon (bioinformatics user)

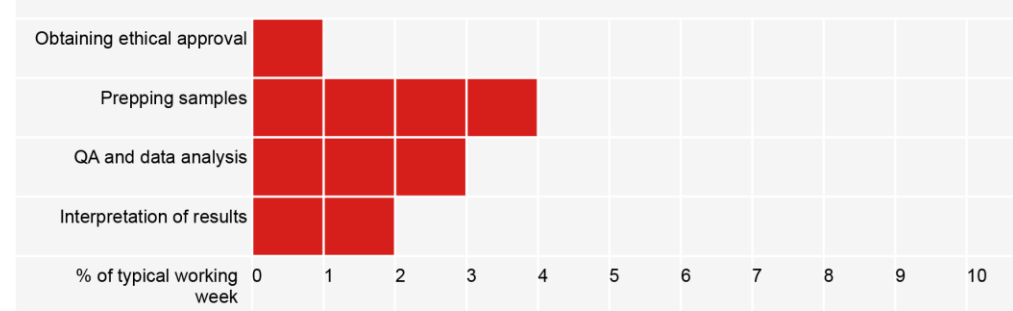
Leon is on his second postdoctoral fellowship, working on quorum sensing in bacteria. "I'm using a combination of transcriptomics, proteomics and metabolomics to understand these pathogenic changes better" he explains. "I end up with big spreadsheets of protein or gene IDs and I'm trying to piece together which signaling pathways are involved in flipping to the pathogenic state". He has been on an introductory Unix course but is much more comfortable with GUIs than with the command line. "I just have a visual brain", he says.



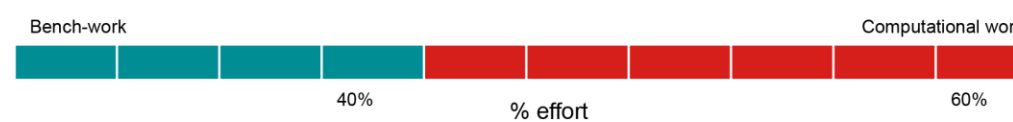
Career timeline



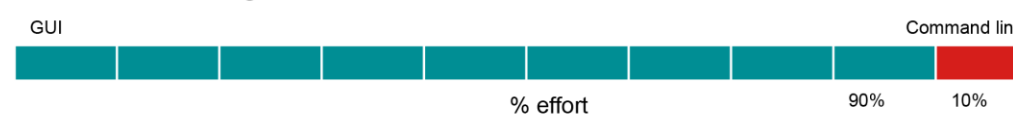
Typical activities



Distribution of time between bench-work and computational work



Preference for using GUI vs command line



Drivers

- Understanding what makes a usually harmless bacterium pathogenic in the lungs of people with cystic fibrosis

Goals

- QA of -omics data
- Statistical analysis of data
- Data integration and pathway analysis

Pain points

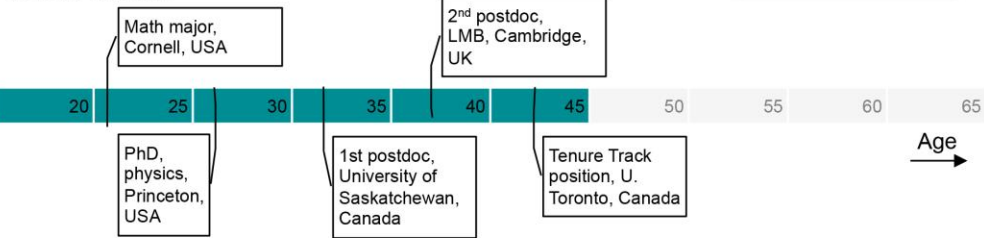
- Lack of access to departmental compute farm
- Sporadic to non-existent access to bioinformatics support

Martha (bioinformatics scientist)

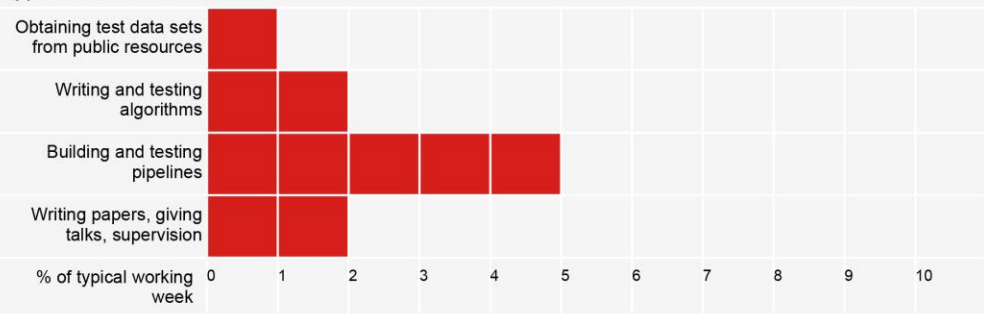
Martha is a senior bioinformatician in an international structural genomics consortium. Her biggest project is on predicting the functions of proteins whose structures have just been solved; she's building a structure-to-function prediction pipeline for the project. This is funded partly by the NIH and partly through industrial funding. She also has a fascination for predicting structure and usually has a student or two working on structural prediction projects.



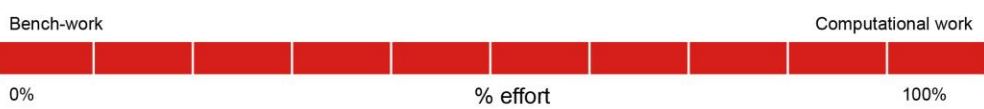
Career timeline



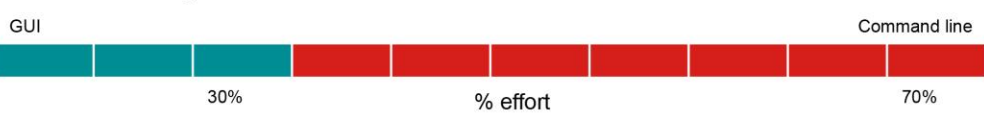
Typical activities



Distribution of time between bench work and computational work



Preference using for GUI vs command line



Drivers

- Understanding the relationship between sequence, structure and function
- Application to target discovery and validation

Goals

- Create a structure-to-function pipeline for molecular biologists
- Predict structures de novo from models of similar, solved structures

Pain points

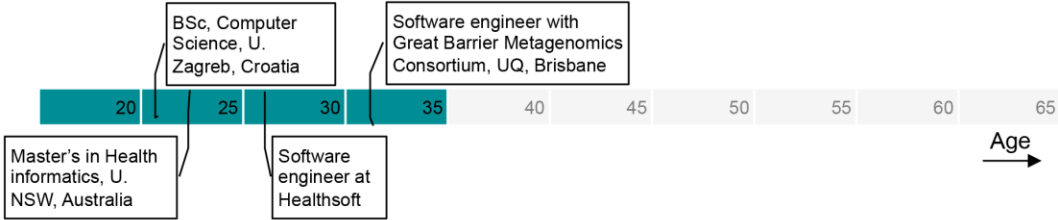
- Sometimes the guys in the lab expect her to fix their computers for them
- Finding students and more senior staff with adequate math

Ivan (bioinformatics engineer)

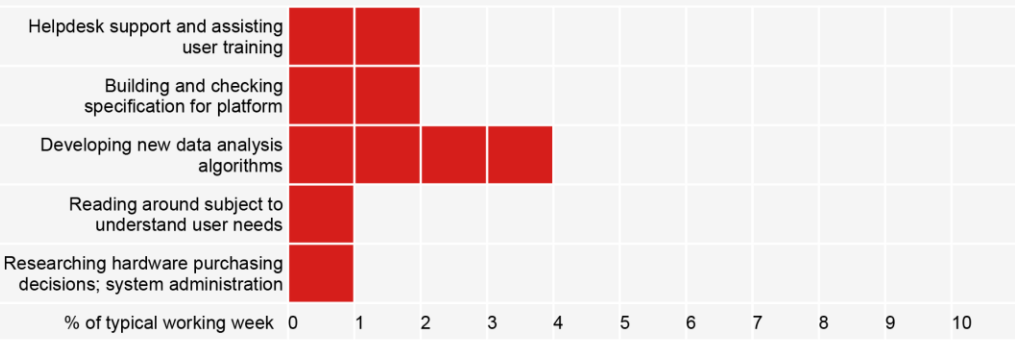
Ivan has just started a new support role in a bioinformatics core facility after working for an electronic health records company for four years. His main project is to develop a major new data integration platform for metagenomics data from coral reefs, but he also has to take his share of helpdesk queries on other projects. “I come from a computer science background, so talking the same language as the guys analysing the data is a bit of a challenge,” he says. “I also didn’t really figure that I’d be working on the GUI as well as the code – in my last job we had design folks to take care of that”.



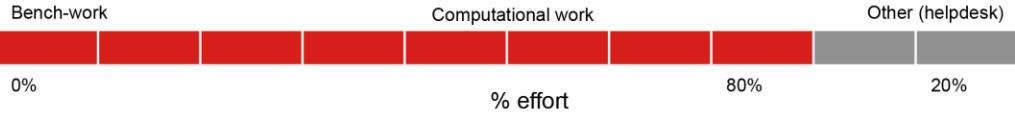
Career timeline



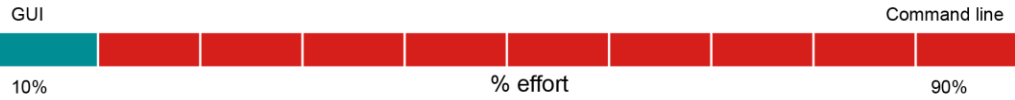
Typical activities



Distribution of time between bench-work and computational work



Preference for using GUI vs command line



Drivers

- Writing algorithms and developing a platform to support novel research
- Supporting other research projects in a busy academic department

Goals

- Define a spec that meets the needs of his users
- Prototype and build part of the platform
- Make sure his part of the project complements others

Pain points

- Has to work with another software engineer who isn't a team player
- Sometimes struggles to interpret what his users want



About me – Luciano Cascione



Bike-aholic, married, two kids



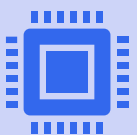
Background in computational science and cancer biology and genomics



Research focus: B-cell lymphomas, RNA-Seq & single-cell omics



Passionate about teaching, reproducible and impactful data analysis



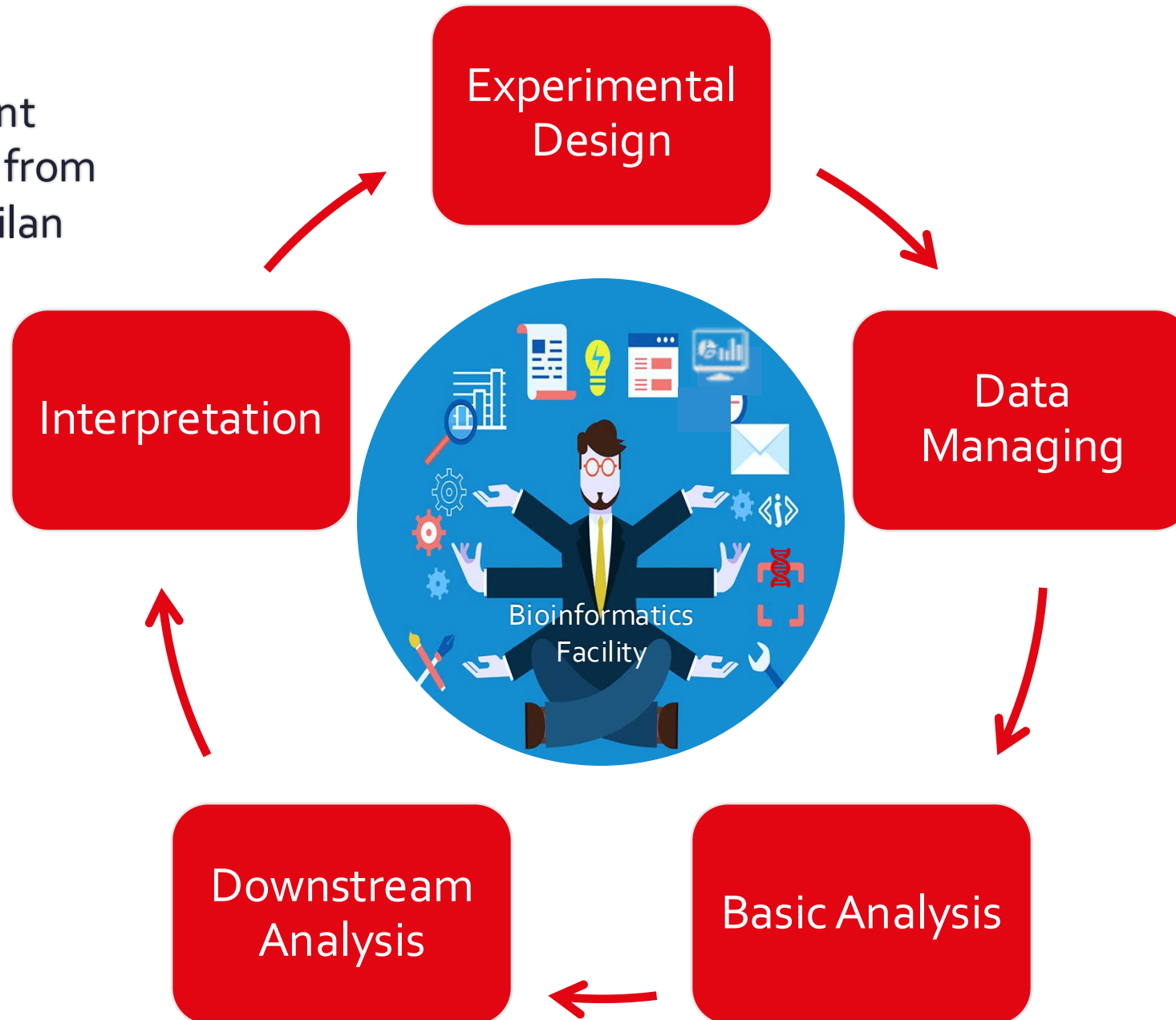
Developer of bioinformatics tools (e.g., EasyCircR for circRNA analysis)



Co-Head of the Bioinformatics Core, Institute of Oncology Research (IOR)

Supporting throughout the project

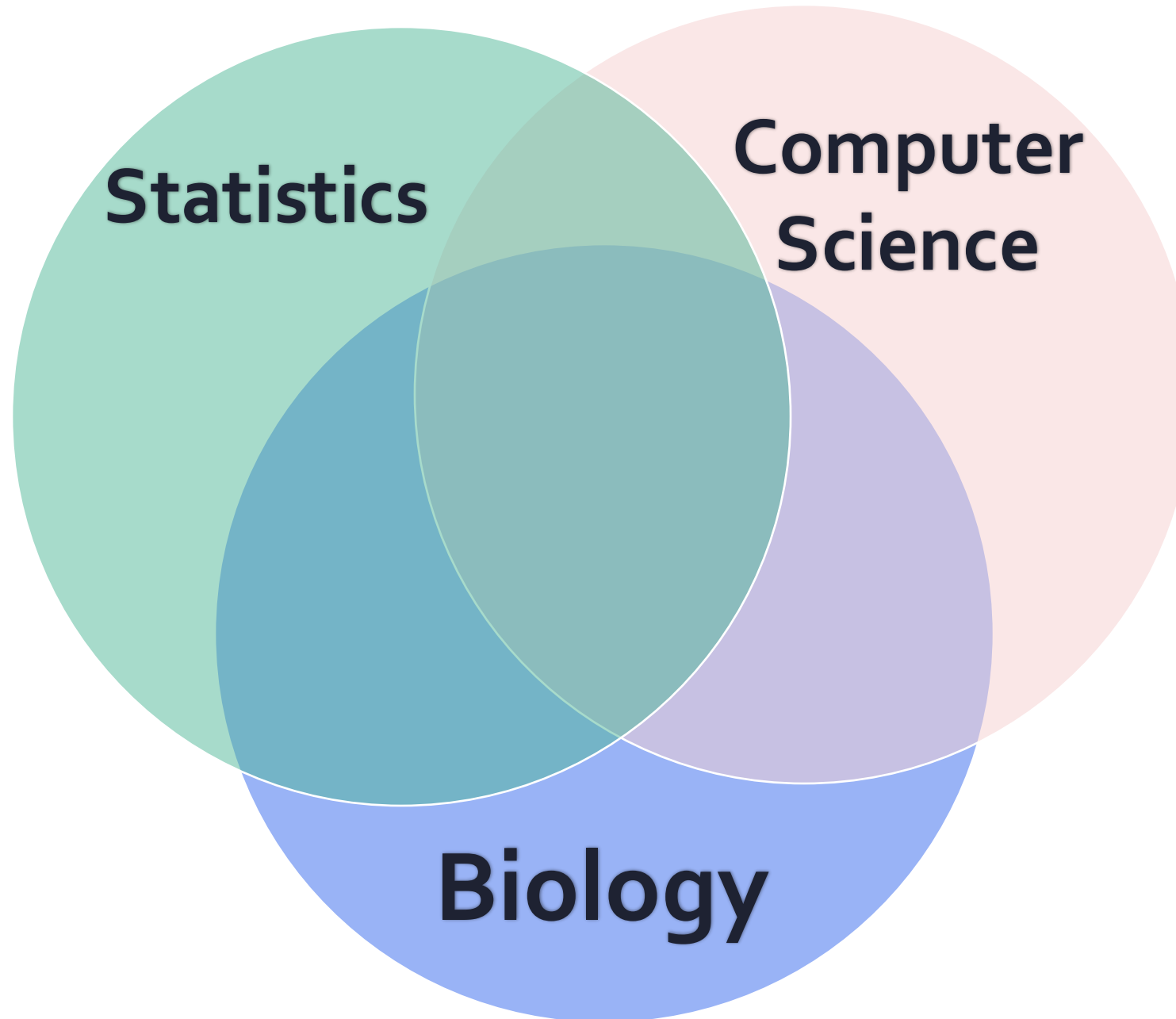
4 post-doc
5 PhD Student
Visiting Student from
Verona and Milan



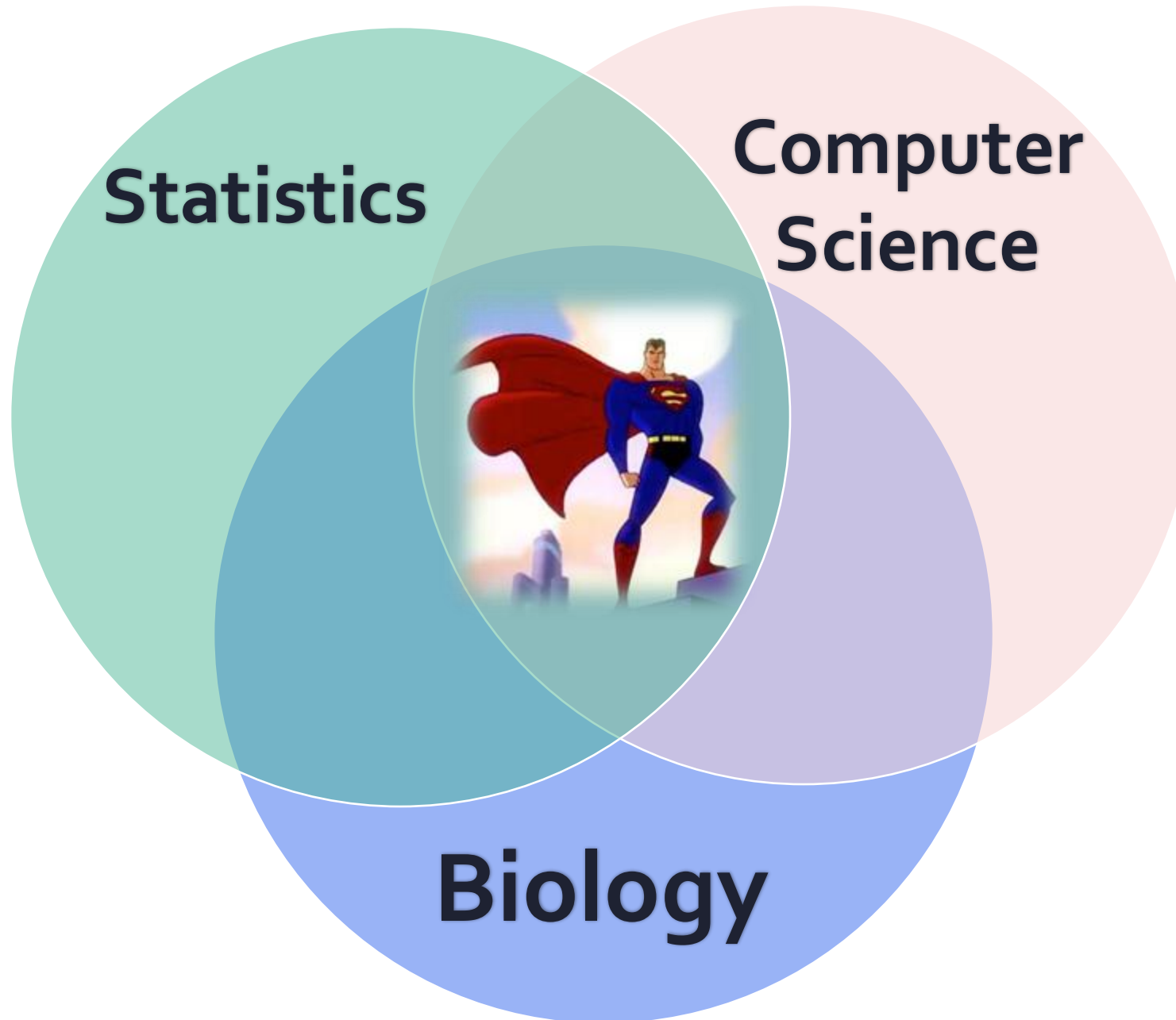
7 Groups
+
IELSG, EOC and IRB
(research projects)



What is a bioinformatician



What is a bioinformatician



Superwomen and Supermen



Daniele
Braga



Giada
Cassanmagnago



Lodovico
Terzi



Serena
Zambarbieri



Matin
Salehi



Jichang
Zhang



Davide
Castaldi



Martina
Troiani



Sara
Michel



Mahta
Mobarak



**Marco
Bolis
(co-head)**

Introduction round

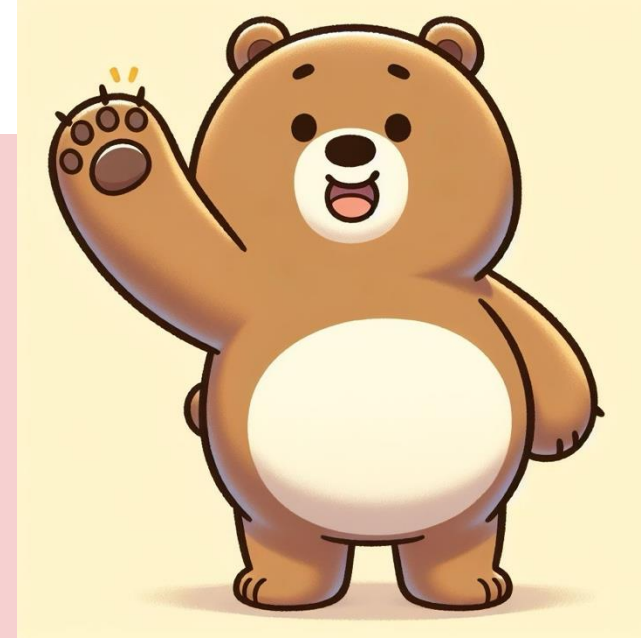
Your name

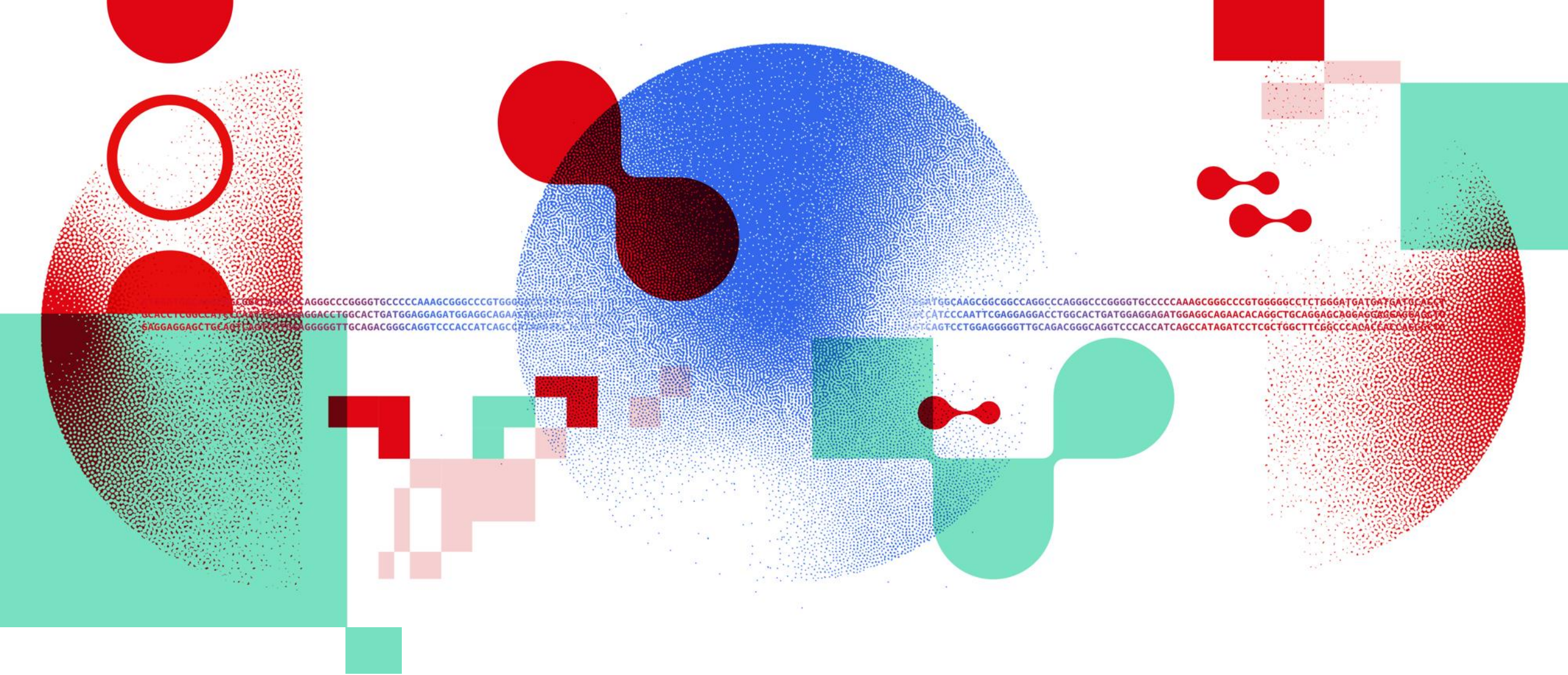
Bioinformatics user, scientist, or engineer

What do you do? (PhD/ postdoc)

Your topic of research.

Why are you joining the course?





Thank you

DATA SCIENTISTS FOR LIFE

sib.swiss