

Swiss Institute of Bioinformatics

BIOLOGY-INFORMED MULTIOMICS DATA INTEGRATION AND VISUALIZATION

Introduction

Deepak Tanwar

June 16-17, 2025





Trainers/ organisers/ helpers

- » Deepak Tanwar: Trainer at SIB & Bioinformatics Specialist at UZH
- » Joana (Juna) Carlevaro Fita: Bioinformatics Trainer at SIB and UNIBE
- **Solution** Seest: Training Project Manager at SIB
- >> Patricia Palagi: Training Group Leader at SIB



Learning outcomes

- Import and integrate pre-processed ATAC-seq, RNA-seq, ChIP-seq, and Bisulfite-seq data using R and Bioconductor packages
- Generate and interpret overlap matrices to identify regions of cooccurrence and regulation
- >> Perform **functional analysis** of the results
- >>> Create informative plots to represent multi-omics data



Learning experiences

- » Lectures
- » Quizzes
- » Exercises



Quiz: 1-5



Communication

- Course website: <u>https://sib-swiss.github.io/biology-informed-multiomics-training/</u>
- >> 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.





Preference for using GUI vs command line

doi.org/10.1371/journal.pcbi.1003496

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.

Typical activities

Distribution of time between bench work and computational work

Preference using for GUI vs command line

 Drivers Understanding the relationship betwee sequence, structure function Application to targ discovery and valid 	en create a structure-to function pipeline for e and nolecular biologists Predict structures de from models of simila tation 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
discovery and valid	dation solved structures	adequate math

doi.org/10.1371/journal.pcbi.1003496

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 tin	neline		_	Software engineer with Great Barrier Metagenomics Consortium, UQ, Brisbane 35 40 45 50 55 60 65 Age									
	(BSc, Comp Science, U. Zagreb, Cro	uter batia		Software Great Ba Consorti	e engine arrier Me ium, UQ	er with etagenor , Brisbar	nics 1e						
	20	25	30		35		40	45		50	55		60	65
Ma info NS	ster's in Health ormatics, U. W, Australia		Softwar enginee Healths	erat oft										Age
	Typical act	ivities												
	Helpdesk s	upport and a user	ssisting training											
	Bu spec	uilding and cl	hecking platform											
	Developin	g new data a alg	analysis orithms											
	Readir unc	ng around su derstand use	ibject to r needs											
	Researching h decisions; sy	ardware pur stem admini	chasing stration											
	% of ty	pical working	g week 0)	1	2	3	4	5	6	7	8	9	10

Distribution of time between bench-work and computational work

Bench-work				Computa	tional work		Other (helpdesk)		
	0%			%	effort		80%		20%

Preference for using GUI vs command line

GUI		Command line
10%	% effort	90%
 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

Deepak Tanwar (Bioinformatics Specialist and Trainer)

Deepak is a Bioinformatics Specialist and Trainer at the SIB and UZH. He has a strong background in multi-omics research and has expertise in reproducible data analysis, benchmarking, and methods development.

Education tin	neline								
B. Tech. Bioinformatics (India)	M. Sc. Epigenomics (McGill, Canada	a) Doc Neur (ETH	ctorate roscience IZ, CH)						Age
20	25	30	35	40	45	50	55	60	65
Experimenta	l design								
Supervision a	& Mentorship)							
Research &	project mana	gement							
Reproducible	e research								
Teaching									
Multi-omics of	data analysis	& integ	ration						
Pipeline & Methods development									
Experience			Low Average			rage	ge High		
Distribution of	of time betwe	en benc	h work ar	nd comput	tational wo	ork			
Bench work					Comput	ational work			
0%						100%			

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

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