

Omics Integration and Systems Biology course

Nikolay Oskolkov, Lund University, NBIS SciLifeLab, Sweden

VT2023
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Omics Integration and Systems Biology

DOI: [10.5281/zenodo.4084627](https://doi.org/10.5281/zenodo.4084627)

[Github repository](#)

8 - 10 February 2023

Online

[Connection details](#)

[Invited lectures](#)

[Schedule](#)

[Start here](#)

[FAQs](#)

The aim of this workshop is to provide an integrated view of data-driven hypothesis generation through machine learning, graph and network analysis as well as constraint-based modelling integration methods. A general description of different approaches for working with multiple layers of biological information, i.e. Omics data (e.g. transcriptomics and genomics) will be presented with some of the lectures discussing their advantages and pitfalls. The techniques will be discussed in terms of their rationale and applicability.

Covered topics

- Data pre-processing and cleaning prior to integration;
- Application of key machine learning methods for multi-omics analysis including deep learning;
- Multi-omics factor analysis, dimension reduction and clustering;
- Biological network inference, community and topology analysis and visualization;
- Condition-specific and personalized modeling through Genome-scale Metabolic models for integration of transcriptomic, proteomic, metabolomic and fluxomic data;
- Identification of key biological functions and pathways;
- Identification of potential biomarkers and targetable genes through modeling and biological network analysis;
- Application of network approaches in meta-analyses;
- Similarity network fusion and matrix factorization techniques;
- Integrated data visualization techniques



Nikolay Oskolkov



Rui Benfeitas



Ashfaq Ali



Sergiu Netotea

Technical Assistance Team:



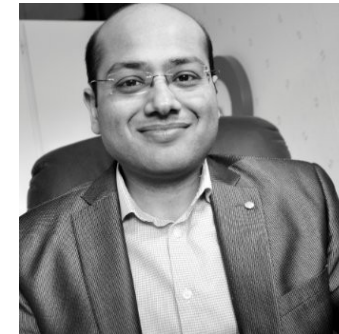
Paul Pyl



Nima Rafati



Rasool Saghaleyni



Praseon Agarwal



Payam Emami

10th of February, 13:45 – 14:40 CET

Single cell Omics integration

Dr. Paulo Czarnewski

Bioinformatician, NBIS SciLifeLab
Sweden



Paulo Czarnewski NBIS expert

RNA-seq, scRNAseq, transcriptomics, Proximity Extension Assay (PEA), microbiome profiling, Flow cytometry (FACS)



paulo.czarnewski@scilifelab.se



<https://orcid.org/0000-0001-8150-4021>

Wednesday the 8th of February

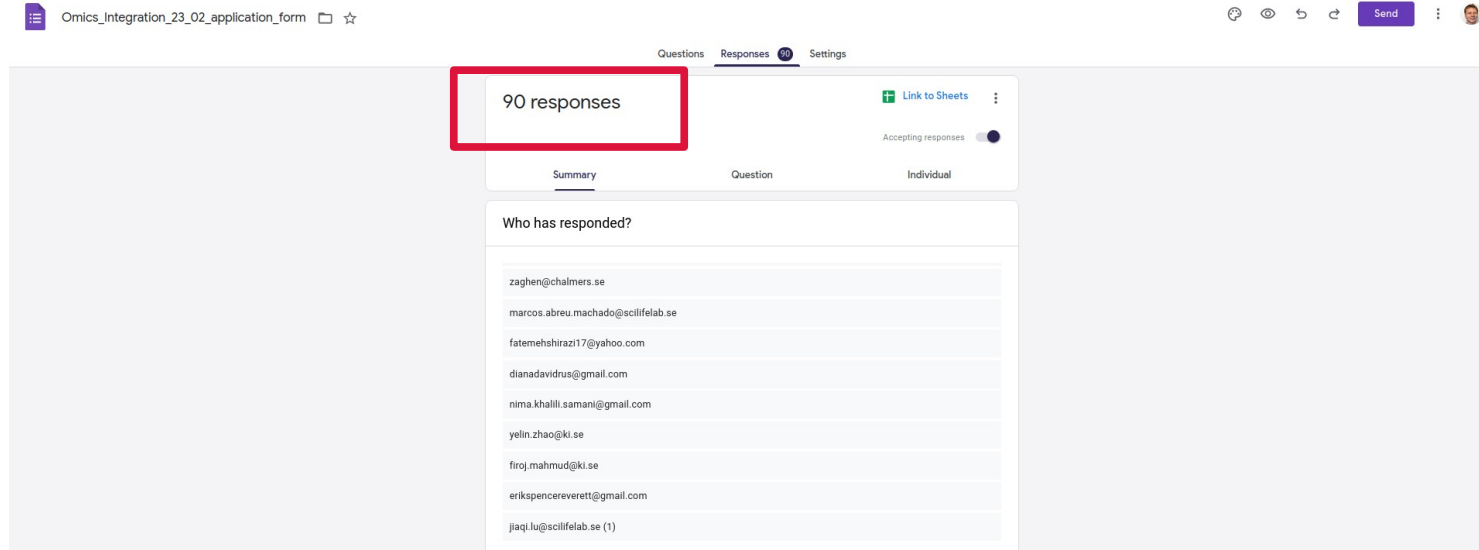
09.00 - 09.20 - Intro and contextualization (Nikolay Oskolkov)
 09.20 - 10.00 - Machine learning view of Omics integration, part 1 (Nikolay Oskolkov)
 10.00 - 10.10 - Break
 10.10 - 11.00 - Machine learning view of Omics integration, part 2 (Nikolay Oskolkov)
 11.00 - 11.10 - Break
 11.10 - 12.00 - Feature selection and supervised Omics integration (Nikolay Oskolkov)
 12.00 - 13.00 - Lunch
 13.00 - 14.00 - Unsupervised Omics integration (Nikolay Oskolkov)
 14.00 - 14.10 - Break
 14.10 - 15.00 - **Hands-on:** Supervised and unsupervised Omics integration (Nikolay Oskolkov)

Thursday the 9th of February

09.00 - 10.00 - Graphs and networks for Omics integration (Rui Benfeitas)
 10.00 - 10.10 - Break
 10.10 - 10.50 - **Hands-on:** Graphs and networks for Omics integration (Rui Benfeitas)
 10.50 - 11.00 - Break
 11.00 - 12.00 - Dimension reduction and UMAP for Omics integration (Nikolay Oskolkov)
 12.00 - 13.00 - Lunch
 13.00 - 13.50 - Deep Learning for Omics integration (Nikolay Oskolkov)
 13.50 - 14.00 - Break
 14.00 - 15.00 - **Hands-on:** UMAP and Deep Learning for Omics integration (Nikolay Oskolkov)

Friday the 10th of February

09.00 - 10.00 - Gene set analysis, reporter features and network meta-analysis (Ashfaq Ali)
 10.00 - 10.10 - Break
 10.10 - 10.50 - **Hands-on:** GSA, reporter features and network meta-analysis (Ashfaq Ali)
 10.50 - 11.00 - Break
 11.00 - 12.00 - Non-negative matrix factorization and similarity network fusion (Sergiu Netotea)
 12.00 - 13.00 - Lunch
 13.00 - 13.40 - **Hands-on:** Non-negative matrix factorization and SNF (Sergiu Netotea)
 13.40 - 13.45 - Break
 13.45 - 14.40 - **Invited lecture:** Single cell Omics integration (Paulo Czarnewski)
 14.40 - 14.45 - Break
 14.45 - 15.00 - Final words and course end



- 1) We accepted everyone, but modified the 3-days (very short!) online course accordingly
- 2) Focus on lectures, notebooks available, labs – going through notebooks (skip copy-paste)
- 3) This is an advanced course: we do not teach coding, but rather explain concepts
- 4) We deliver ideas and codes, you can concentrate on labs most relevant for your research
- 5) Course runs from 9 am to 3 pm (to account for zoom tiredness and family commitments)



Please remain muted
during lectures



Camera on
throughout, if possible



Raise your hand
to ask questions



Chat
Please refrain from using the chat
Use [HackMD](#)



Important links
are on [canvas](#)

HackMD

Full-text search on all paid plans

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21

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# Omics Integration and Systems Biology

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## Resources

Course website: https://uppsala.instructure.com/courses/75208
HackMD: https://hackmd.io/AjoVRvYCTgitnKRhgXznJQ
Connection via Zoom: https://lu-se.zoom.us/j/66468616131?pwd=ZUIrNUhQOUxDUmVLRW1ycLR0ZXJ5Zz09

## Course Organizers

**Nikolay Oskolkov** - Course co-leader, NBIS bioinformatician, Lund University Sweden. I have my background in genomics and medical genetics. Interested in evolution and ancient DNA research. Working on different data types.

**Rui Benfeitas** - Course leader, NBIS bioinformatician, Stockholm University. Work in integrative omics projects, mostly employing transcriptomic, metabolomic, proteomic, epigenomic data. Favorite programming language is Python.

**Ashfaq Ali** - Course co-leader, NBIS bioinformatician, Lund University Sweden. Work with omics data using statistical and systems biology approaches to analyze and integrate omics data for biomarker/target discovery.

## Questions?

- I am having some issues in creating the containers by downloading the images. I copied and pasted the code in Windows Powershell, replacing the password and the path. However, I get an error saying the the terms -e, -v and ruibenfeitas are not recognised as cmdlet, functions, programs or scripts. Could you please help me? Thank you very much.

- *Nikolay Oskolkov*: please do not follow the container way so far. I know it is written on the course web-page, in the pre-course material section, but this remained from the previous version of the course, and will be modified or removed soon. We decided not to follow the container way this time. The labs will not be run within containers and conda environments, but will simply be presented as html-files to the participants. The participants later can install the software and run the labs on their own. The focus this time will be on lectures and explaining concepts. Nevertheless, all the codes and notebooks will be provided for the participants to run them on their own. I will send pre-course instructions 1-2 days before the course start.
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Line 21, Columns 439 - 21 Lines Spaces: 4 Breaks SUBLINE Length: 2086

CHANGED A FEW SECONDS AGO

Omics Integration and Systems Biology

- Omics Integration and Systems Biology
 - Resources
 - Course Organizers
 - Questions?

Resources

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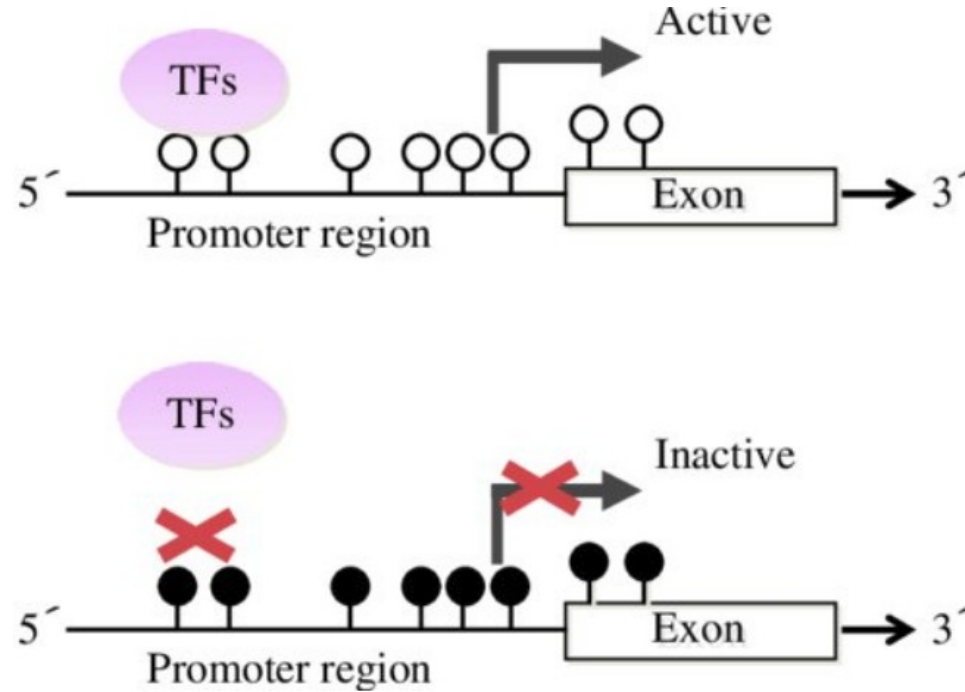
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- 1) No break-out rooms, we discuss all together in the main room, please be active!
- 2) There are no stupid questions: not obvious to you - not obvious to 80% of audience
- 3) How much you can (or know) is less important, motivation is what matters the most
- 4) You can unmute yourself and ask (preferred!) or write your question in Hack MD



From single gene to genome-wide (high-throughput) description

There are many ways
to do the same thing



There is only one truth!