

R for bioinformatics

Intro, syllabus and other pertinent ponderings

Who I am

- My name is Dmitri. Dr. Dmitri Kazmin if you want to get formal.
- I speak both English and Russian
- I have a PhD in biochem
- I started as a wet-lab biologist and gradually transitioned to bioinformatics
- I have been a professional bioinformatician for ~15 years
- I do quite a bit of coding, but I don't consider myself a programmer
- I am a biologist, who uses the tools of bioinformatics to seek answers to biological questions

Class structure

- Each class period will contain a (brief) presentation and lots of hands-on practice
- Source data, PDFs and codes for each class will be posted on Github (<https://github.com/DmitriKazmin/R.class>)
- Participants are encouraged to submit their homework by uploading to Github instead of using email
- The course will use actual data from a novel immunological clinical study
- We will explore and analyze the real-world data and will come up with biological hypotheses about the mechanisms of immunity to influenza vaccine

Course syllabus

Week	Topics
1	Hello world, R basics
2	Exploring built-in datasets; basic statistical analysis and plotting practice
3	Gene expression dataset: finding differentially regulated genes, and graphically representing the effects of vaccination on the blood transcriptome
4	Gene set enrichment analysis: making biological sense of the gene expression patterns
5	Antibody data: analyzing and representing the effects of vaccine on accumulation of antibodies against the flu virus
6	Cellular data: analyzing and plotting the changes in cellular populations in the blood of vaccine recipients
7	Ouchie! Vaccine reactogenicity: redness, swelling, fever. Which genes control the appearance of adverse effects to vaccine
8	Putting it all together: Finding the important correlates of vaccine efficacy