Machine Learning in Bioinformatics

Faculty
Computer
science

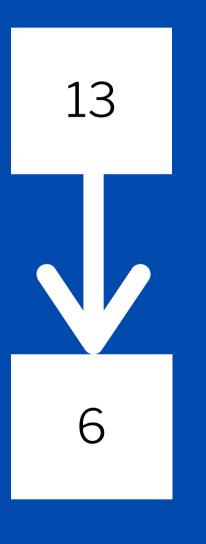






Participants



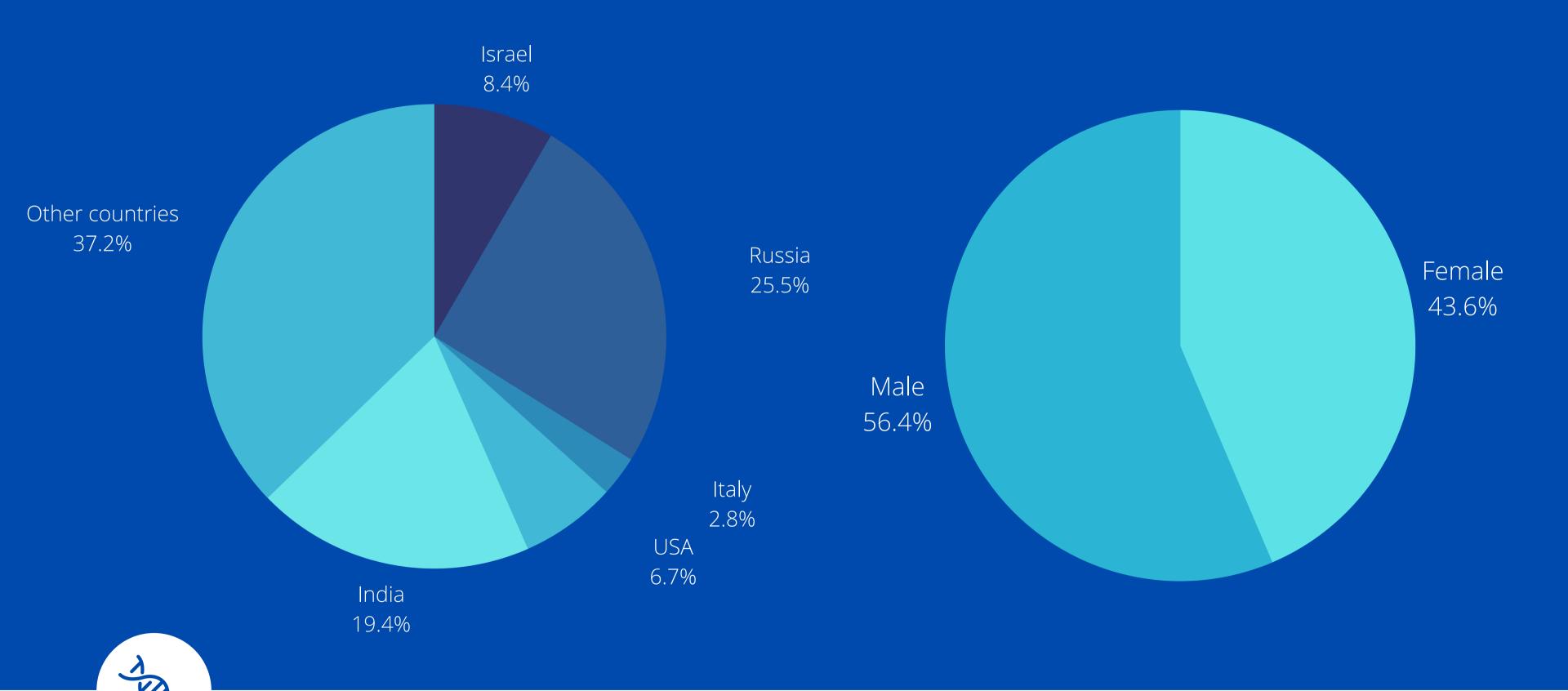


Main Speakers

Counties



PARTICIPANTS



MAIN SPEAKERS



Maria Poptsova, School Chair, HSE University



Asa Ben-Hur, Colorado State University



Daisuke Kihara, Purdue University



Evgeny Burnaev, Skoltech



Alexander Misharin, Northwestern University



Yaron Orenstein, Ben-Gurion University



Jose Miguel Hernandez Lobato, University of Cambridge



Ramana V Davuluri, Stony Brook University



Wesley De Neve, Ghent University



Matthias Heinig, Helmholtz Zentrum München



Shankai Yan, National Institutes of Healthng



Vsevolod Makeev,
Moscow Institute of
Physics and Technology



Sebastian Lapuschkin, Heinrich Hertz Institute

The school became a highlight of summer 2020. Lectures and seminars of the school covered various examples of applying ML to biological data and were delivered by the leading experts in the field. During the lectures basic concepts of ML were accompanied with more advanced techniques of data analysis, such as noise reduction, dealing with imbalanced datasets, overtraining. Warm and open atmosphere between participants and organisers of the school worth a special word.



Calvin Lee, Participant



Alice Aubert, Participant

I would have to say so far the Manifold Learning and the Interpretability of Neural Networks were the most interesting. I've already worked a bit with Deep Neural Networks in Genomics, so I appreciated learning about what exists beyond the standard 1D convolutional neural networks. It was also very helpful to have those refresher lectures, as they let me confirm that my knowledge of CNNs was solid and even reminded me of some technical details I had forgotten. All in all, I think your lecturers provide a good mix of topics and difficulty levels for all attendees.

I was very impressed by the bioinformatics & machine learning summer school run by HSE University. Professors from all around the world provided very interesting and in-depth educational content on these topics, what problems exist today and how they are trying to solve them. The Google Colabs were very engaging and allowed me to get my hands on some working machine learning code live during the seminars. I was able to talk to, and network with, many interesting people before, during and after the sessions.

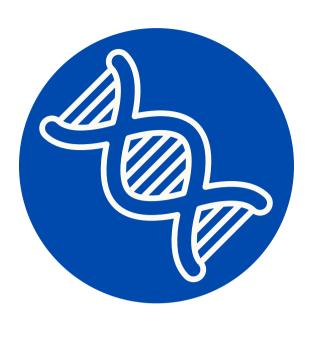


Christopher Searson, Participant



Claudia Greco, Participant

One of the aspects of this course that impressed me the most is how connected I feel both to the other students and the professors: we share resources by the Telegram group chat and lessons are not in the classic frontal format, but they feel more like an open discussion is given how many interesting questions keeps coming up. Overall, I believe this course is extremely valuable both due to the interesting topics it covers and for the network that the student can create, and I also think that what I'm learning will be useful during my further studies in bioinformatics.



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TELEGRAM CHANNEL

ML in Bioinformatics

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