

Former Ph.D. Student in the Loschmidt Laboratories Published in Nature Neuroscience

– Interview with Jarda Bendl

Hardworking, quiet, and prudent. This is how we remember **Jarda Bendl** from his doctoral studies at Loschmidt Laboratories (LL). He moved for a postdoc to the Icahn School of Medicine at Mount Sinai in New York in 2017. Currently, he is Assistant Professor at the same school. One of his recent articles has been published in the top scientific journal Nature Neuroscience. On this occasion, we asked him for a short interview.



Jardo, could you tell us more about your childhood interests and dream job? What about your study at secondary school?

I was growing up in the pre-dot-com bubble era. Internet as a mass medium was still in diapers but newspapers were full of oracles that were predicting all sorts of implications of rapidly evolving tech in our everyday life. Like millions of teenagers back in the day, I wanted to be a part of that tech revolution so I started to code – and I found a liking for it. In light of

these facts, it is not surprising that I chose computer science specialization in high school and stuck with that during my pre-grad studies.

After completing your master's degree at Brno University of Technology (VUT), you came to LL for your doctoral study. Do you have any interesting memories at this time?

That was a lucky coincidence. After obtaining my Bachelor's degree, I felt I don't need more training in traditional computer science so I opted for the „bioinformatics and biocomputing“ Master program. While that choice was originally motivated by biology-inspired computing, I found myself being even more fascinated by Tom Martínek's bioinformatics lectures. Later, Tom introduced me to Loschmidt Labs and that's how my LL story started. When it comes to interesting memories, I must admit that the whole concept of biology research was completely new to me then. It took some time before I felt on board in terms of understanding of key concepts of the wet-lab work of my colleagues – and how to connect their experimental research to my computational work. Looking back, it paid off nicely since the ability to „cut to the chase“ and communicate in layman's terms is a fundamental skill for successful research collaborations and grant writing.

You left for a postdoc in the USA. Why just there? How was it to come to New York after your doctoral studies in LL? Did you experience something that you didn't expect? What obstacles did you face and where were you surprised pleasantly?

Back in 2016, I was lured by an opportunity to be one of the first analysts in a newly established research group that is committed to revealing regulatory mechanisms beyond specific neurodevelopmental and neurodegenerative diseases through an epigenomics lens. Since I joined, we processed and analyzed close to ten thousand brain samples through various functional omics assays capturing mostly gene expression and chromatin accessibility; that's very likely more than any other neurogenomics lab worldwide. This amount of data created endless opportunities for data-driven research and gave us a chance to make novel discoveries.

Living in a foreign country is always an adventure – in a good and bad way. New York can often be quite overwhelming. Thankfully, my first apartments were close to Central Park which is truly a green haven in the concrete jungle. Over the years and especially after the social unrest in 2020, I felt how much the city was deteriorating. Therefore, I decided to say goodbye to the city permanently and moved out to the suburbs where one can still feel the smell of the American dream: clean streets, well-maintained neighborhoods, and friendly smiling people. All of that is currently lacking in the Big Apple.

Could you compare how is the research done in LL and your current workplace? Are there any significant differences?

In the terms of project and team management, I do not see glaring differences. However, there is a striking difference in the number of funding opportunities: NIH grants are awarded for a longer period (usually 5 years) and can accommodate much larger budgets. Additionally, besides government funding, the US has a well-established culture of philanthropic foundations that take their share of responsibility in supporting basic science.

You are the first author of the research article published in Nature Neuroscience which is highly appreciated by the scientific community. Could you give the readers a simplified overview of what is the article about? How long were you working on it? What does this publication's success mean for you?



That manuscript represents the largest effort to profile chromatin accessibility in two brain regions and two cell types (neurons and non-neurons) of cases with Alzheimer's disease (AD). We initially used these data to expand the repertoire of identified cell type-specific regulatory regions and study their relationship to gene expression in the human brain. We then examined the shared and distinct molecular mechanisms associated with clinical dementia and neuropathological lesions. Subsequently, we identified regulatory genomic signatures associated with AD, including variability in discrete open chromatin

regions, transcription factor regulatory networks, and cis-regulatory domains. To validate our findings, we ran multiple validation experiments using CRISPRi on neuronal stem cells.

You spend many hours on computer work. How do you take your mind off things?

In my career stage and position, long hours are somehow excepted (but not enforced). Luckily, the post-covid world opened the possibilities for remote/hybrid work which allows me some flexibility in work organization so I can sometimes take off my bicycle to Westchester roads in the middle of the day.

What are your next goals?

The fast-paced growth of our team recently led to our transformation to a larger organization unit called the Center for Disease Neurogenomics. Within this center, I have an opportunity to lead the Multi-Omics integration unit that consists of four computational scientists. Some time ago, we re-shaped our focus on datasets generated by single-cell assays and we currently keep the largest single-cell datasets for three brain-related disorders. As much as it is super-exciting, it also brings a lot of issues on the computational side to properly deal with such a flood of data. But those are good problems to have.

In terms of future goals, I can imagine returning to the Central European space, yet I have to find an opportunity that would allow me to continue in the current research direction.

Jardo, thank you for the interview and we wish you much success in your future endeavors.