Curriculum Vitae

Jonas Simon Fleck

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I like to work towards predictive biology.

Education & Experience

PhD in Systems Biology
01/2019 - now

ETH Zürich, D-BSSE, Basel, Switzerland

For my PhD research in the group of Barbara Treutlein, I am currently investigating fate decision logic in brain organoids.

For this, I am using a wide range of statistical and machine learning methods, primarily on single-cell (multi-)omics data. I also developed a number of tools myself, such as VoxHunt for organoid phenotyping and Pando for regulatory network inference.

I am primarily a computational biologist, but I also have experience designing and conducting bench experiments.

MSc in Molecular Biotechnology
04/2016 - 09/2018

Heidelberg University, Heidelberg, Germany
Final grade: 1.0 (best grade: 1.0), focus: Bioinformatics

During my master studies, I obtained hands-on experience in broad biomedical research topics by working on various computational and experimental projects.

Among others, I worked on structural biology (Karolinska Institute), bioinformatic analysis of mutational signatures in cancer (DKFZ) and optogenetics (BioQuant).

In my thesis in the group of Georg Zeller at EMBL, I focused on developing computational methods for functional analysis of the gut microbiome and it's role in colorectal cancer. During this time, I developed GECCO, a tool for predicting novel biosynthetic gene clusters in microbial genomes.

BSc in Biosciences
10/2012 - 01/2016

Heidelberg University, Heidelberg, Germany
Final grade: 1.2 (best grade: 1.0)

I did my bachelor thesis in the group of Irmgard Sinning, where I worked on the structural and functional characterization of the SRP Alu domain in *Plasmodium falciparum*.

I also spent some time in Scotland for an exchange semester and in Australia for a summer research project.

Abitur
2011

Johannes-Kepler-Gymnasium, Reutlingen, Germany

Languages

German	*native*
English	●●●
Spanish	●

Programming

Python, R, Unix Shell	●●●
JavaScript, CSS	●●
C, Perl	●

Frameworks

tensorflow, sklearn, numpy, pandas, git, ggplot2, tidyverse	●●●
pytorch, JAX, mlR	●●

Other Skills

Single-cell genomics	●●●
Machine/deep learning	●●●
Affinity/Illustrator	●●●
Molecular biology	●●
Brain organoid culture	●●
Protein biochemistry	●●
Confocal microscopy	●●
Handling mice	●

(Open Source) Projects

Pando, VoxHunt, Latent Lego, GECCO, Slic

Hobbies & Interests

Food, drinks and all things culinary

Bouldering, climbing, scuba diving and some other outdoorsy stuff

Designing logos for the tools I develop

●●● = *proficient*
●● = *experienced*
● = *basics*

Awards & Fellowships

Boehringer Ingelheim Fonds PhD fellowship	*2020 - now*
Erasmus+ scholarship for a research project at the Karolinska Institute in Stockholm, Sweden	*03/2017 - 08/2017*
DAAD-RISE scholarship for a summer research project in Sydney, Australia	*06/2014 - 08/2014*

Conference Talks & Posters

Inferring and perturbing cell fate regulomes in human brain organoids. *Poster*, GRC conference	*02.05.2022*
Inferring regulomes from multi-modal single-cell measurements with Pando, *Talk*, ISMB/ECCB conference	*28.07.2021*
VoxHunt: Resolving brain organoid heterogeneity by projecting single-cell transcriptomes to spatial brain maps, *Poster*, SCOG meeting	*07.03.2019*

Other Things

Teaching assistant in the Single-Cell Technologies lecture	*2020 - 2022*
Co-organizer of the 2021 ETH/UZH systems biology PhD retreat	*2020 - 2021*
Civil service in New Zealand, working with mentally challenged adolescents	*2011 - 2012*
Elected member of the local youth council, Reutlingen	*2009 - 2011*

Publications & Preprints

Fleck, J.S.*, Jansen, S.M.J.*, Wollny, D., Zenk, F., Seimiya, M., Santel, M., He, Z., Gray Camp, J.G., and Treutlein, B. (2022). Inferring and perturbing cell fate regulomes in human brain organoids. Accepted in *Nature*

Lust, K.*, Maynard, A.*, Gomes, T.*, **Fleck, J.S.**, Camp, J.G., Tanaka, E.M., and Treutlein, B. (2022). Single-cell analyses of axolotl forebrain organization, neurogenesis, and regeneration. Accepted in *Science*

Wahle, P.*, Brancati, G.*, Harmel, C.*, He, Z.*, Gut, G., Santos, A., Yu, Q., Noser, P., **Fleck, J.S.**, [...], Treutlein, B. and Camp, J.G. (2022). Multimodal spatiotemporal phenotyping of human organoid development. *bioRxiv*

Fleck, J.S.*, Sanchís-Calleja, F.*, He, Z., Santel, M., Boyle, M.J., Camp, J.G., and Treutlein, B. (2021). Resolving organoid brain region identities by mapping single-cell genomic data to reference atlases. *Cell Stem Cell*

Carroll, L.M.*, Larralde, M.*, **Fleck, J.S.***, Ponnudurai, R., Milanese, A., Cappio, E., and Zeller, G. (2021). Accurate de novo identification of biosynthetic gene clusters with GECCO. *bioRxiv*

Kanton, S.*, Boyle, M.J.*, He, Z.*, Santel, M., Weigert, A., Sanchis-Calleja, F., Guijarro, P., Sidow, L., **Fleck, J.S.**, [...], Treutlein, B. and Camp, J.G. (2019). Organoid single-cell genomic atlas uncovers human-specific features of brain development. *Nature*

Wirbel, J.*, Pyl, P.T.*, Kartal, E., Zych, K., Kashani, A., Milanese, A., **Fleck, J.S.**, [...], Zeller, G. (2019). Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. *Nature Medicine*