BioQuant, Heidelberg University

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Data scientist tackling biomedical challenges

Education

Heidelberg University Heidelberg, Germany

CONTINUATION OF PHD IN COMPUTATIONAL BIOMEDICINE

2019-now

· From gene expression to pathway and transcription factor activities to acquire functional and mechanistic insight into chronic liver diseases

RWTH Aachen Aachen, Germany

PhD in Computational Biomedicine

2017-19

· From gene expression to pathway and transcription factor activities to acquire functional and mechanistic insight into chronic liver diseases

Bielefeld University Bielefeld, Germany

MASTER OF SCIENCE - GENOME BASED SYSTEMS BIOLOGY

2014-17

• Thesis: Coupling of Metabolism and Gene Regulation to identify Gene Targets in Living Cells

Bielefeld University Bielefeld, Germany

BACHELOR OF SCIENCE - MOLECULAR BIOTECHNOLOGY

2011-14

· Thesis: Effect of overexpression of xanA on the growth and xanthan production of Xanthomonas campestris pv. Campestris in the laboratory and in the model

Working Experience _____

Roche pRED PS BEDA Basel Switzerland

ROCHE INTERNSHIPS FOR SCIENTIFIC EXCHANGE

2021 (6 month)

• Multi-omics guided construction of cell-type specific gene regulatory networks

Insilico Biotechnology AG

Stuttgart, Germany

MASTER STUDENT

2016-2017 (9 month)

• Coupling of Metabolism and Gene Regulation to identify Gene Targets in Living Cells

Alacris Theranostics GmbH

Berlin, Germany

2015 (3 month)

INTERNSHIP 2016 (3 month)

· Application of a mechanistic model and an artificial neural network for simulation and parameter optimization of the drug response model in the context of personalized medicine

Reseach Center Jülich Jülich, Germany

• Studying Escherichia coli metabolism with focus on the uncertainties of the biomass equation

Teaching Experience

Bielefeld University Bielefeld, Germany

STUDENT ASSISTANT JOB - MATHEMATICS FOR BIOLOGISTS

Bielefeld University

Bielefeld, Germany

STUDENT ASSISTANT JOB - STATISTICS/INFORMATICS FOR BIOLOGISTS

2013-15

Skills

MARCH 2021

INTERNSHIP

Programming

R (EXPERT), PYTHON (PROFICIENT), BASH (PROFICIENT), MATLAB (NOVICE)

Packages

TIDYVERSE, SHINY, RMARKDOWN, BOOKDOWN, PKGDOWN, TESTTHAT, PANDAS, NUMPY

Tools

GIT, CI (TRAVIS OR GHA), LATEX

Software development

dorothea Available since Bioc 3.11

BIOCONDUCTOR PACKAGE

• Tool to infer transcripion factor activities from gene expression data (Lead developer)

progeny Available since Bioc 3.6

BIOCONDUCTOR PACKAGE

SBMC

• Tool to infer pathway activities from gene expression data (Contributor)

Conferences Attended

EuroBioc Online conference

TALK: ESTIMATION OF TRANSCRIPTION FACTOR AND PATHWAY ACTIVITIES FROM BULK AND SINGLE-CELL TRANSCRIPTOMICS DATA WITH DOROTHEA AND PROGENY

2020

ISMB/ECCB Basel, Switzerland

POSTER: ROBUSTNESS AND APPLICABILITY OF FUNCTIONAL GENOMIC TOOLS ON SCRNA-SEQ DATA

2019

RECOMB/ISCB

New York City, USA

Bremen, Germany

 $Poster:\ Unveiling\ of\ conserved\ transcriptomics\ perturbation\ responses\ in\ mice\ and\ human$

2018

TALK: UNVEILING OF CONSERVED TRANSCRIPTOMICS PERTURBATION RESPONSES IN MICE AND HUMAN

2018

Selected Publications

- 1. Mohs, A., Otto, T., Schneider, K. M., Peltzer, M., Boekschoten, M., Christian H. Holland, Hudert, C. A., Kalveram, L., Wiegand, S., Saez-Rodriguez, J., Longerich, T., Hengstler, J. G., & Trautwein, C. (2021). Hepatocyte-specific NRF2 activation controls fibrogenesis and carcinogenesis in steatohepatitis. *Journal of Hepatology*, 74(3), 638–648. https://doi.org/10.1016/j.jhep.2020.09.037
- 2. Christian H. Holland, Tanevski, J., Perales-Patón, J., Gleixner, J., Kumar, M. P., Mereu, E., Joughin, B. A., Stegle, O., Lauffenburger, D. A., Heyn, H., Szalai, B., & Saez-Rodriguez, J. (2020). Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. *Genome Biology*, 21(1). https://doi.org/10.1186/s13059-020-1949-z
- 3. Christian H. Holland, Szalai, B., & Saez-Rodriguez, J. (2020). Transfer of regulatory knowledge from human to mouse for functional genomics analysis. *Biochimica Et Biophysica Acta (BBA) Gene Regulatory Mechanisms*, 1863(6), 194431. https://doi.org/10.1016/j.bbagrm.2019.194431
- 4. Flores, R. O. R., Lanzer, J. D., Christian H. Holland, Leuschner, F., Most, P., Schultz, J.-H., Levinson, R. T., & Saez-Rodriguez, J. (2020). A consensus transcriptional landscape of human end-stage heart failure. *medRxiv*. https://doi.org/10.1101/2020.05.23.20110858
- 5. Ghallab, A., Myllys, M., Christian H. Holland, Zaza, A., Murad, W., Hassan, R., Ahmed, Y. A., Abbas, T., Abdelrahim, E. A., Schneider, K. M., Matz-Soja, M., Reinders, J., Gebhardt, R., Berres, M.-L., Hatting, M., Drasdo, D., Saez-Rodriguez, J., Trautwein, C., & Hengstler, J. G. (2019). Influence of liver fibrosis on lobular zonation. *Cells*, 8(12), 1556. https://doi.org/10.3390/cells8121556
- 6. Szalai, B., Subramanian, V., Christian H. Holland, Alföldi, R., Puskás, L. G., & Saez-Rodriguez, J. (2019). Signatures of cell death and proliferation in perturbation transcriptomics datafrom confounding factor to effective prediction. *Nucleic Acids Research*, 47(19), 10010–10026. https://doi.org/10.1093/nar/gkz805
- 7. Garcia-Alonso, L., Christian H. Holland, Ibrahim, M. M., Turei, D., & Saez-Rodriguez, J. (2019). Benchmark and integration of resources for the estimation of human transcription factor activities. *Genome Research*, 29(8), 1363–1375. https://doi.org/10.1101/gr.240663.118