Christian H. **Holland**

PHD STUDENT

BioQuant, Heidelberg University

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Data scientist tackling biomedical challenges

Education

Heidelberg University
CONTINUATION OF PHD IN COMPUTATIONAL BIOMEDICINE
Heidelberg, Germany
2019-now
- From gene expression to pathway and transcription factor activities to acquire functional and mechanistic insight into chronic liver diseases

RWTH Aachen
PHD IN COMPUTATIONAL BIOMEDICINE
Aachen, Germany
2017-19
- From gene expression to pathway and transcription factor activities to acquire functional and mechanistic insight into chronic liver diseases

Bielefeld University
MASTER OF SCIENCE - GENOME BASED SYSTEMS BIOLOGY
Bielefeld, Germany
2014-17
- Thesis: Coupling of Metabolism and Gene Regulation to identify Gene Targets in Living Cells

Bielefeld University
BACHELOR OF SCIENCE - MOLECULAR BIOTECHNOLOGY
Bielefeld, Germany
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
ROCHE INTERNSHIPS FOR SCIENTIFIC EXCHANGE
Basel Switzerland
2021 (6 month)
- Multi-omics guided construction of cell-type specific gene regulatory network

Insilico Biotechnology AG
MASTER STUDENT
Stuttgart, Germany
2016-2017 (9 month)
- Coupling of Metabolism and Gene Regulation to identify Gene Targets in Living Cells

Alacris Theranostics GmbH
INTERNSHIP
Berlin, Germany
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
INTERNSHIP
Jülich, Germany
2015 (3 month)
- Studying Escherichia coli metabolism with focus on the uncertainties of the biomass equation

Teaching Experience

Bielefeld University
STUDENT ASSISTANT JOB - MATHEMATICS FOR BIOLOGISTS
Bielefeld, Germany
2013-15

Bielefeld University
STUDENT ASSISTANT JOB - STATISTICS/INFORMATICS FOR BIOLOGISTS
Bielefeld, Germany
2013-15

Skills

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

Packages

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

Tools

GIT, TRAVIS CI, LATEX

Developed software

dorothea *Available since Bioc 3.11*

BIOCONDUCTOR PACKAGE *2021-03-22*

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

progeny *Available since Bioc 3.6*

BIOCONDUCTOR PACKAGE *2021-03-22*

- Tool to infer pathway activities from gene expression data (contributor).

Conferences Attended

BioC *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*

POSTER: UNVEILING OF CONSERVED TRANSCRIPTOMICS PERTURBATION RESPONSES IN MICE AND HUMAN *2018*

SBMC *Bremen, Germany*

TALK: UNVEILING OF CONSERVED TRANSCRIPTOMICS PERTURBATION RESPONSES IN MICE AND HUMAN *2018*

Selected Publications

1. 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`

2. 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`

3. 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`

4. 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`

5. 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`

6. 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`

7. 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`