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EDUCATION

Ph.D. student, Bioinformatics and Computational Biology **Dec. 2014 – present**

Institution: Technical University Munich, Department for Bioinformatics and
Computational Biology

Preliminary title: Predicting functional capabilities of microbial metagenomes, using similarity
graph approaches

Advisor: Prof. Yana Bromberg

M.Sc., Bioinformatics **Nov. 2014**

Institution: Technical University Munich, Department for Bioinformatics and
Computational Biology

Thesis title: Evidence for evolutionary distance visible in effect scores of amino acid
substitutions between species

Advisor: Prof. Burkhard Rost

B.Sc., Bioinformatics **May 2012**

Institution: Technical University Munich, Department for Bioinformatics and
Computational Biology

Thesis title: Sole usage of amino acid propensities results in robust performance for
predicting structural change in protein fragments

Advisor: Prof. Burkhard Rost

PUBLICATIONS

1. **Mahlich Y.**, Steinegger M., Bromberg Y., (2018) HFSP: High speed homology-driven function annotation of proteins. *in review*
 2. Zhu C., **Mahlich Y.**, Miller, M., Bromberg, Y., (2018) fusionDB: assessing microbial diversity and environmental preferences via functional similarity networks. *Nucleic Acids Res* **46**(D1): D535-D541.
 3. **Mahlich, Y.**, Reeb, J., Hecht, M., Schelling, M., De Beer, T.A.P., Bromberg, Y., Rost, B. (2017) Common sequence variants affect molecular function more than rare variants? *Scientific Reports*, 2017. 7: 1608
 4. Reeb, J., Hecht, M., **Mahlich, Y.**, Bromberg, Y., and Rost, B. (2016) Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. *PLoS Comput Biol*, 2016. 12(8): p. e1005047.
 5. Radivojac, P., Clark, W.T., Ronnen Oron, T., Schnoes, A.M., Wittkop, T., Sokolov, A., Graim, K., Funk, C., Verspoor, K., Ben-Hur, A., Pandey, G., Yunes, J.M., Talwalkar, A.S., Repo, S., Souza, M.L., Piovesan, D., Casadio, R., Wang, Z., Cheng, J., Fang, H., Gough, J., Koskinen, P., Törönen, P., Nokso-Koivisto, J., Holm, L., Cozzetto, D., Buchan, D.W.A., Bryson, K., Jones, D.T., Limaye, B., Inamdar, H., Datta, A., Manjari, S.K., Joshi, R., Chitale, M., Kihara, D., Lisewski, A.M., Erdin, S., Venner, E., Lichtarge, O., Rentzsch, R., Yang, H., Romero, A.E., Bhat, P., Paccanaro, A., Hamp, T., Kassner, R., Seemayer, S., Vicedo, E., Schaefer, C., Achten, D., Auer, F., Böhm, A., Braun, T., Hecht, M., Heron, M., Hönigschmid, P., Hopf, T., Kaufmann, S., Kiening, M., Krompass, D., Landerer, C., **Mahlich, Y.**, Roos, M., Björne, J., Salakoski, T., Wong, A., Shatkay, H., Gatzmann, F., Sommer, I., Wass, M.N., Sternberg, M.J.E., Škunca, N., Supek, F., Bošnjak, M., Panov, P., Džeroski, S., Šmuc, T., Kourmpetis, Y.A.I., van Dijk, A.D.J., ter Braak, C.J.F., Zhou, Y., Gong, Q., Dong, X., Tian, W., Falda, M., Fontana, P., Lavezzo, E., Di Camillo, B., Toppo, S., Lan, L., Djuric, N., Guo, Y., Vucetic, S., Bairoch, A., Linial, M., Babbitt, P.C., Brenner, S.E., Orengo, C., Rost, B., Mooney, S.D. and Friedberg, I. (2013) A large-scale evaluation of computational protein function prediction. *Nature methods*, 2013. 10(3): p. 221-227.
 6. Hamp, T., Kassner, R., Seemayer, S., Vicedo, E., Schaefer, C., Achten, D., Auer, F., Boehm, A., Braun, T., Hecht, M., Heron, M., Hönigschmid, P., Hopf, T.A., Kaufmann, S., Kiening, M., Krompass, D., Landerer, C., **Mahlich, Y.**, Roos, M., and Rost, B. (2013) Homology-based inference sets the bar high for protein function prediction. *BMC Bioinformatics*, 2013. 14(3): p. S7.
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TALKS

ISMB/ECCB 2017, Function SIG, Prague, Czech Republic

July 2017

fusionDB: assessing microbial diversity and environmental preference via functional similarity networks

POSTERS

IAS General Assembly 2017, Reitenhaslach, Germany

May 2017

Mahlich, Y., Zhu, C., Miller, M., Bromberg, Y. Bacterial proteomes and microbial communities: environmental preferences and functional profiles

RU Symposium 2017, New Brunswick, NJ, USA

January 2017

Zhu, C., Mahlich, Y., and Bromberg, Y. FusionDB: Assessing Microbial Diversity and Environmental Preferences Via Functional Similarity Networks

RESEARCH EXPERIENCE

Research Visit

Mar. 2017 – present

Rutgers University, New Brunswick, NJ, USA – Department of Biochemistry and Microbiology
Continuation of Ph.D. project with advisor Prof. Yana Bromberg

Research Visit

Jan. 2015 – Oct. 2016

Rutgers University, New Brunswick, NJ, USA – Department of Biochemistry and Microbiology
Kick-off of Ph.D. project with advisor Prof. Yana Bromberg

Student Assistant

2011 – 2014

Technical University Munich, Munich, Germany – Rostlab, Department for Bioinformatics and Computational Biology

Effect analysis of functional impact induced by single nucleotide variation in human populations and between species

Student Assistant

2012

Helmholtz Zentrum München, Munich, Germany

Organizing text mining results extracted from medical publications