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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. Zhu C., Miller M., Lusskin N., **Mahlich Y.**, Wang Y., Zeng Z., Bromberg Y., (2019) Fingerprinting cities: differentiating subway microbiome functionality. *Biology Direct, invited & in review*

2. **Mahlich Y.**, Steinegger M., Bromberg Y., Rost B., (2018) HFSP: High speed homology-driven function annotation of proteins. *Bioinformatics*, vol. 34, no. 13, pp. p. i304 – i312

3. 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.

4. **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

5. 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.

6. 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.

7. 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.

TALKS

ISMB, Proceedings Talk @ Function SIG, Chicago, United States July 2018
HFSP: High speed homology-driven function annotation of proteins

Rutgers University, Fermentation Seminar, New Brunswick, United States February 2018
HFSP: High speed homology-driven function annotation of proteins

ISMB/ECCB 2017, Function SIG, Prague, Czech Republic July 2017
fusionDB: assessing microbial diversity and environmental preference via functional similarity networks

POSTERS

RU Symposium 2019, New Brunswick, NJ, USA January 2019
Zhu, C., **Mahlich, Y.**, and Bromberg, Y. FusionDB: Assessing Microbial Diversity and Environmental Preferences Via Functional Similarity Networks

IAS General Assembly 2017, Reitenhaslach, Germany May 2017
Mahlich, Y., Zhu, C., Miller, M., Brombrg, 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 form medical publications