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RESEARCH AREA

The recent emergence of the field of systems biology brought a new era in the research of evolution. The novel methods and largescale datasets enable the systematic exploration of the elements of biological systems and the interactions between them. Our group is particularly interested in studying the evolution of metabolism. By measuring the intracellular metabolite levels, that is, the metabolome in different yeasts we can assess how fast metabolism evolves and what are the driving forces behind its evolution. We are also studying the evolution of the metabolic network, that is, how can organisms gain novel enzymes and biochemical pathways to better adapt to the environmental conditions. We utilize this knowledge for strain design by discovering genetic modifications that can boost the microbial production of chemicals with industrial importance.

TECHNIQUES AVAILABLE IN THE LAB

Metabolic network modelling, phylogenetic and comparative genomics methods, bioinformatic analysis of metabolomic and transcriptomic data, statistics and machine learning. Programming in R, Python, Perl and Matlab languages.

SELECTED PUBLICATIONS

Zampieri, M., **Szappanos, B.**, Buchieri, M.V., Trauner, A., Piazza, I., Picotti, P., Gagneux, S., Borrell, S., Gicquel, B., Lelievre, J., Papp, B., Sauer, U. (2018) High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. **Sci Transl Med 10:** eaal3973.

Szappanos, B., Fritzemeier, J., Csörgő, B., Lázár, V., Lu, X., Fekete, G., Bálint, B., Herczeg, R., Nagy, I., Notebaart, R.A., et al. (2016) Adaptive evolution of complex innovations through stepwise metabolic niche expansion. **Nat Commun 7:** 11607.

Notebaart, R.A., **Szappanos, B.**, Kintses, B., Pál, F., Györkei, A., Bogos, B., Lázár, V., Spohn, R., Csörgő, B., Wagner, A., Ruppin, E., Pál, C., Papp, B. (2014) Network-level architecture and the evolutionary potential of underground metabolism. **Proc Natl Acad Sci U S A 111:** 11762-11767.

Szappanos, B., Kovács, K., Szamecz, B., Honti, F., Costanzo, F., Baryshnikova, A., Gelius-Dietrich, G., Lercher, M.J., Jelasity, M., Myers, C.L., Andrews, B.J., Boone, C., Oliver, S.G., Pál, C., Papp, B. (2011) An integrated approach to characterize genetic interaction networks in yeast metabolism. **Nat Genet 43:** 656-62.