



## Sebastian Müller

### **Integrated genome-wide data analysis by ensemble learning methods to understand infection processes**

Transcription analysis can be a valuable approach to better understand regulatory processes and complex gene-protein interaction-networks. To explore such a transcriptome, data from two state of the art methods, namely microarray-analysis and next-generation-sequencing techniques, will be analysed and compared by means of supervised and unsupervised ensemble learning methods.

In particular, such an analysis will be performed to understand infection processes and virulence of *Aspergillus fumigatus* by gene expression analysis of infected murine macrophages.

#### **Publications**

Fischer J, Müller SY, Netzker T, Jäger N, Gacek-Matthews A, Scherlach K, Stroe MC, García-Altres M, Pezzini F, Schoeler H, Reichelt M, Gershenzon J, Krespach MK, Shelest E, Schroeckh V, Valiante V, Heinzl T, Hertweck C, Strauss J, Brakhage AA (2018) Chromatin mapping identifies BasR, a key regulator of bacteria-triggered production of fungal secondary metabolites. *Elife* 7, [Details PubMed](#)

Kastner S, Müller S, Natesan L, König GM, Guthke R, Nett M (2012) 4-Hydroxyphenylglycine biosynthesis in *Herpetosiphon aurantiacus*: a case of gene duplication and catalytic divergence. *Arch Microbiol* 194(6), 557-566. [Details PubMed](#)

Tierney L, Linde J, Müller S, Brunke S, Molina JC, Hube B, Schöck U, Guthke R, Kuchler K (2012) An Interspecies Regulatory Network Inferred from Simultaneous RNA-seq of *Candida albicans* Invading Innate Immune Cells. *Front Microbiol* 3, 85. [Details PubMed](#)

Müller S, Fleck CB, Wilson D, Hummert C, Hube B, Brock M (2011) Gene acquisition, duplication and metabolic specification: the evolution of fungal methylisocitrate lyases. *Environ Microbiol* 13(6), 1534-1548. [Details PubMed](#)

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**Start of PhD**

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**Doctoral Disputation**

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