

Dr. Jürgen Dönitz

Curriculum Vitae

Career progression

Since end 2019	Group leader "Knowledge Management" at the Inst. for Medical Bioinformatics
Since 03/2019	Postdoc at Dept. of Evolutionary Developmental Genetics, Coordinator of the DFG project " iBeetle-Base: Building an Interconnected, Interactive and Extendable Repository for Phenotypic Data"
Since 09/2016	Postdoc at the Inst. for Bioinformatics
02/2013 – 08/2016	Software developer at the State and University Library Göttingen
03/2012 – 12/2018	Bioinformatician at the Dept. of Developmental Biology
05/2003 – 01/2013	Bioinformatician at the Inst. of Bioinformatics

Education

02/2016	PhD thesis completed „Development and application of ontologies for biological applications “
01/1995 – 07/2001	Study of biology at the University of Cologne
10/2000 – 03/2004	Study of computer science at the distance learning university Hagen

Research fokus

I am interested in the knowledge management in the biology and the biomedical field. This ranges from network analysis over the semantic web to infrastructure conception and software design. My background is in the biology. From where I proceeded to the field of bioinformatics. After three years as software developer at the State and Library of Göttingen; I made my PhD and am working now in the Institute of Medical Bioinformatics of the University Medical center and the Dept. of Evolutionary Development Genetics of the University Göttingen.

Current projects

MTB-Reporting

In this project we aim to develop a tool that suggest therapies for tumor patients based on their biomarkers. For more details please see the [project page](#).

iBeetle-Base

iBeetle-Base is a joined project together with the **Dept. of Evolutionary Developmental Genetics**. Initially this database provides access to the phenotypic annotations gathered by a whole genome RNAi screen in the red flour

beetle *Tribolium castaneum*. Currently iBeetle-Base is funded by the DFG in the project titled "iBeetle-Base: Building an Interconnected, Interactive and Extendable Repository for Phenotypic Data". [More ...](#)

TFClass

Transcription factors are a key player in gene regulation. Beside of binding sequence, the evolution and relations of transcription factors are important to understand and predict the function of transcription factors. In the [transcription factor classification project](#) we build up the classification of transcription factors TFClass based on their DNA binding domain.

MyPathSem

In the MyPathSem project we aim, in a collaboration with other institutes of the UMG, to extract the patient specific parts of the molecular networks. For more information please check the [project site](#).

EndoNet

The intercellular signalling is crucial for every multicellular organism. The manual annotated information resource [EndoNet](#) collects information about the participants of this network, i.e. messenger, receptors, cells or tissues, and combines them with stimuli and phenotypes to network.

Publications

Selected publications:

- Dönitz J, Gerischer L, Hahnke S, Pfeiffer S, Bucher G. Expanded and updated data and a query pipeline for iBeetle-Base. *Nucleic Acids Res.* 2018;46:D831–5.
- Wingender E, Schoeps T, Haubrock M, Krull M, Dönitz J. TFClass: expanding the classification of human transcription factors to their mammalian orthologs. *Nucleic Acids Res.* 2018;46:D343–7.
- Nemajerova A, Kramer D, Siller SS, Herr C, Shomroni O, Pena T, et al. TAp73 is a central transcriptional regulator of airway multiciliogenesis. *Genes Dev.* 2016;30:1300–12.
- Ulrich J, Dao VA, Majumdar U, Schmitt-Engel C, Schwirz J, Schultheis D, et al. Large scale RNAi screen in *Tribolium* reveals novel target genes for pest control and the proteasome as prime target. *BMC Genomics.* 2015;16. doi:10.1186/s12864-015-1880-y.
- Schmitt-Engel C, Schultheis D, Schwirz J, Ströhlein N, Troelenberg N, Majumdar U, et al. The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. *Nat Commun.* 2015;6:7822.
- Dönitz J, Schmitt-Engel C, Grossmann D, Gerischer L, Tech M, Schoppmeier M, et al. iBeetle-Base: a database for RNAi phenotypes in the red flour beetle *Tribolium castaneum*. *Nucleic Acids Res.* 2015;43:D720–5.

Professional activities

...more soon...

Contact information

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