



## UFZ-Seminar „Water and Environment“



5. March 2018, 1 p.m.

Seminar Room 1, Brückstr. 3a, Magdeburg

### Florian Leese

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will give a talk on:

### **New options - new challenges. Application of novel genomic tools to study responses of freshwater biodiversity under stress**

Freshwater ecosystems are impacted by multiple stressors and the loss of biological diversity has been shown to be substantially greater than in marine and terrestrial ecosystems. In particular organic pollution, land-use change and effects of climate change impact on these heterogeneous habitats. At the same time, freshwater ecosystems provide important services to humans and therefore the effective management is of pivotal importance. Precise data on biological diversity changes are key for such management decisions. Until to now only a limited number of biological quality elements, in particular macroinvertebrates, phytobenthic taxa and fish species are studied to quantify stressor impacts. Given the difficulty to identify all many macroinvertebrate and phytobenthic taxa stressor responses have been deduced from based on coarse taxonomic level following the taxonomic sufficiency concept (species inside a family/genus should stand for similar ecological preferences). Several recent studies show that this concept does not always hold true. With the rise of novel genomic analysis techniques such as High-Throughput Sequencing (HTS), new options to quickly and reliably identify hundreds of even closely related species from complex environmental samples have been proposed. In the first part of my talk I will present a number of case studies that clearly highlight the power of such novel Genomic techniques to improve our understanding of stressor - biodiversity relationships and thus biomonitoring. I will also show where current limitations of e.g. metabarcoding approaches are and how these can be overcome. In the second part of my talk I will show how novel population genomic tools can be used to assess responses of freshwater taxa (not only model species) at population level. With these approaches the impacts of anthropogenic stressors such as pollution or physical barriers (weirs, dams) on the level of genetic diversity are demonstrated. I will end with a vision of how these novel genetic and bioinformatic tools, in concert with established ecological and taxonomic assessments, will significantly improve environmental management and counteract the loss of biodiversity - from the level of genes to ecosystems.