

# Genomic-based health-screening of reintroduced *Emys orbicularis*

Eichert C.<sup>1</sup>, Meka J.<sup>2,3</sup>, Baranski D.<sup>4</sup>, Schell T.<sup>4</sup>, Romahn J.<sup>4</sup>, Georges J.-Y.<sup>3</sup>, Quintard B.<sup>5</sup>, Theissinger K.<sup>2</sup>

<sup>1</sup>Department of Biogeography, University of Trier, Trier, Germany; <sup>2</sup>Justus Liebig University Giessen, Institute for Insect Biotechnology, Giessen, Germany; <sup>3</sup>Université de Strasbourg, CNRS, IPHC, UMR7178, Strasbourg, France; <sup>4</sup>Senckenberg Gesellschaft für Naturforschung, Georg-Voigt-Straße 14-16, Frankfurt/Main, Germany; <sup>5</sup>Parc Zoologique et Botanique de Mulhouse, Mulhouse, France



## Introduction

**Emys-R:** participatory action-oriented research for defining the most effective methods of wetland restoration in favor of *Emys o.* reintroduction and associated biodiversity throughout Europe ([one health](#))

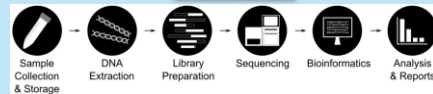
**Microbiome research:** integrative understanding of patterns of microbial diversity and early signs of impending microbial disruption -> valuable tool for promoting individual health for most operational conservation strategies



## Methodology



- screening gut microbial community along broad biogeographic gradient (FR, LV, ES)
- scanning microbiome and infective pathogen load via turtles' fecal, cloacal & combined oral cloacal swabs
- metagenomic approach based on Next Generation Sequencing (NGS)



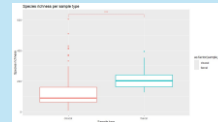
## Prospect

- biomarker identification + functional annotation -> dysbiosis index -> health status
- screening of pathogens (*Rana*-, *Adeno*-, *Herpesvirus*, *Mycoplasma*) of larger sample size + at the breeding centres
- combine microbiome data with information on turtles' diet (J. Meka)
- combine microbiome with SMI and reproductive output (J.-Y. Georges)

## Hypotheses

- Microbiome <-> immune system & host physiology interactions: change in taxonomic community structure in health impaired turtles
- => a calculated body condition index will positively correlate with a more heterogenous (presumably healthier) turtle gut microbiome

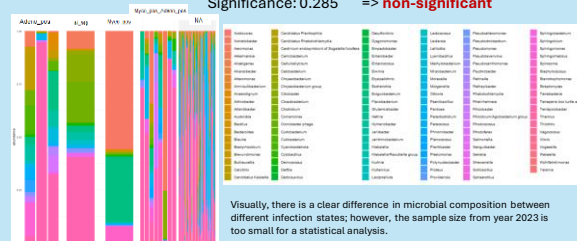
## Preliminary results



<- Bacterial species richness significantly higher in faecal samples compared to cloacal swab samples.

Mantel statistic based on Pearson's product-moment correlation between bacterial species richness and body condition index (SMI):

Mantel statistic  $r: 0.02821$   
Significance: 0.285 => **non-significant**



Visually, there is a clear difference in microbial composition between different infection states; however, the sample size from year 2023 is too small for a statistical analysis.