Microbiome reveals history of human interactions in the museum - a pilot project

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The pilot project guiding question: can the microbiome inform about the environment in which the object was created, collected or stored?

Aims:

- develop best practice methods for sampling and analyzing the   microbiome of heritage objects

- focus on non-invasive sampling methods, microbial profiling (DNA-sequencing, cultivation) and data analysis

- explore new scientific approach to investigate authenticity & provenance

- Initial research outcomes and planned follow-up steps are presented -

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The Microbiome of Cultural Heritage Objects

Location: Pergamon Museum, Berlin

Pergamonmuseum

Zeus Sosipolis Temple

Ishtar Gate   Gate Lion Sam'al   Procession Street

The Microbiome of Cultural Heritage Objects

Location: Museum für Naturkunde, Berlin

Collection of molluscs and fossils

Chiton   Triton Horn   Tendaguru

WetLab + Bioinformatic Workflow
Microbial community analysis: 16S rRNA gene profiling

Extraction kits / Procedures

1. QIAamp DNA Micro Kit   **2.** DNeasy PowerBiofilm Kit
(enzymatic lysis)   (enzymatic + mechanic)

Direct + Pre Elution   Direct + Pre Elution
a – b   a – b   a – b   a - b
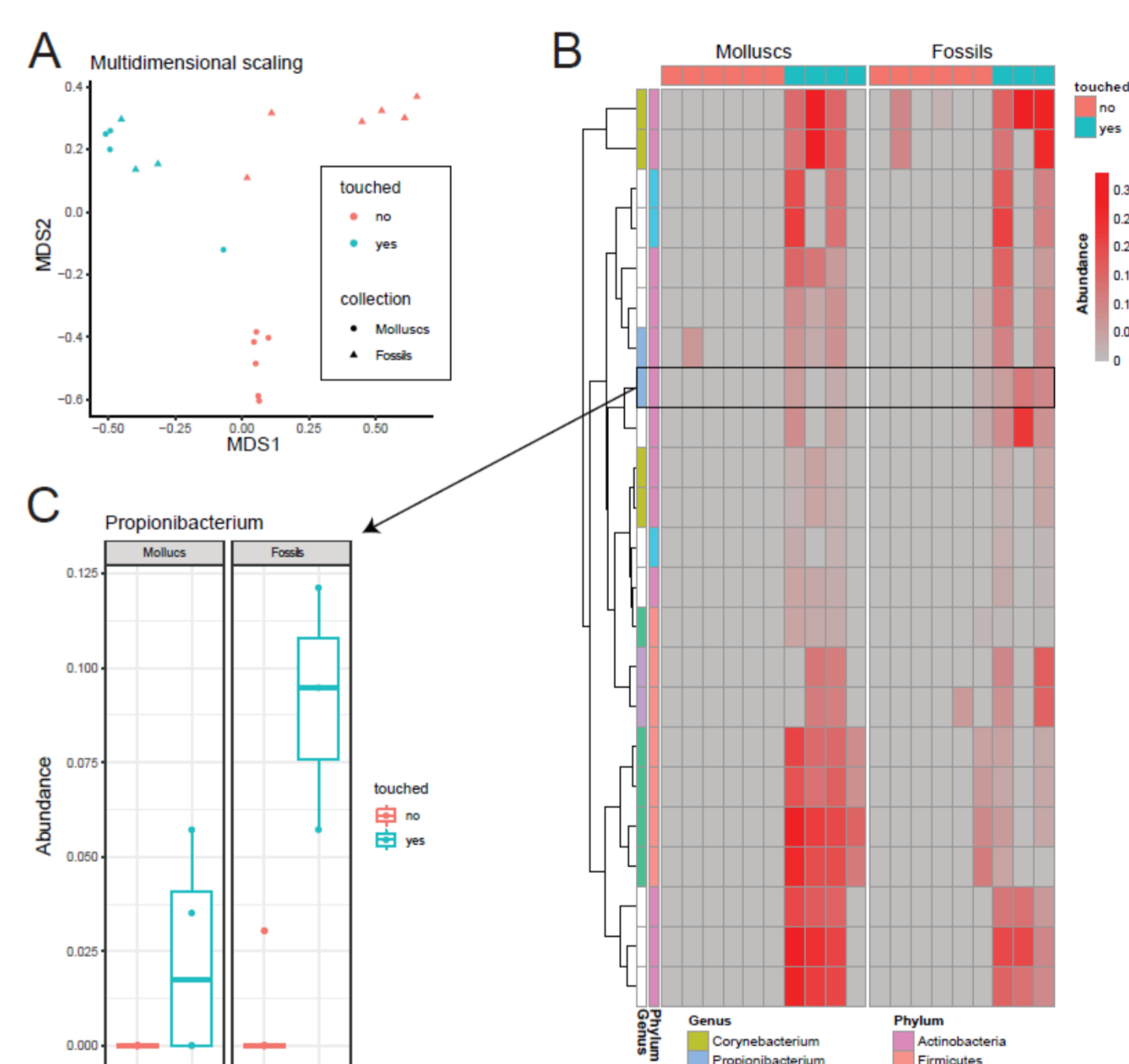
Outputs

1. DNA extraction efficiency
   a. DNA yield (PicoGreen)
   b. DNA yield, quality and sizing (FemtoPulse System)
2. Amplification tests 16rRNA gene regions
   16S PCR: V3 and V3+V4
3. Machine learning, data curation, denoising, analysis
4. . Bacterial Community Profile / Catalogue 16S rRNA gene amplicons

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Discovery of a „touch" signature
Fossils & molluscs, Museum für Naturkunde

Samples obtained from molluscs and fossils were subjected to unsupervised dimension reduction using multidimensional scaling (MDS). Frequently touched (blue) objects formed a distinct cluster separated from untouched (red) objects indicating differential microbiome profiles (A). (B) Heatmap displays the abundance of microbial features (rows) specifically detected on touched objects (columns). The genera of these features have previously been associated with the microbiome of human skin[1], demonstrating that the microbiome of these heritage objects contains a human fingerprint derived from touch. For example, Propionibacterium was specifically detected in touched versus untouched objects (C).
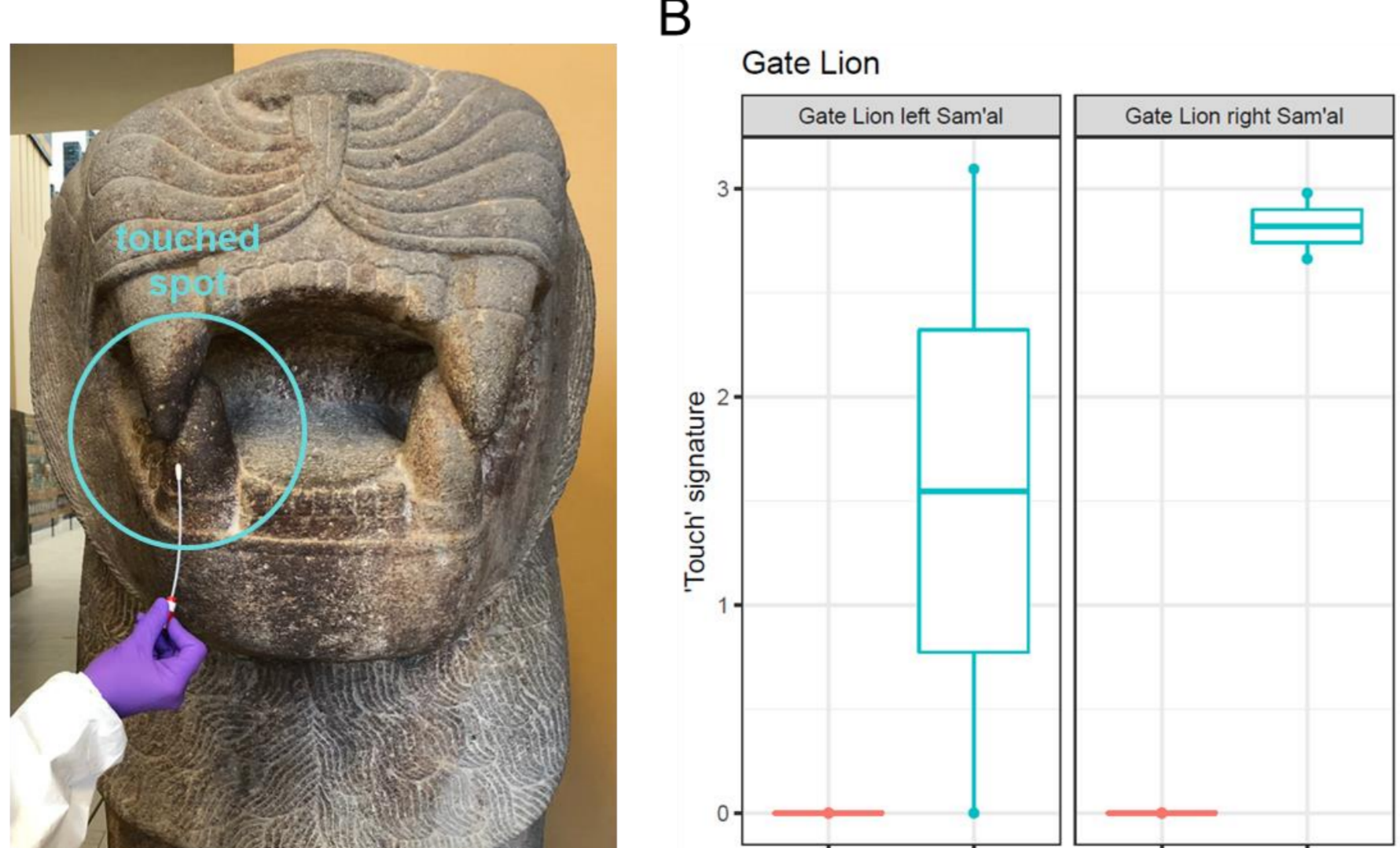
1. Byrd et al. *Nat Rev Microbiol.* 2018.

Validation of the „touch" signature
Gate lion Sam`al, Pergamon Museum

Having identified a "touch" microbiome signature we set out to validate this signature in objects from the Pergamon Museum. A tooth of each Sam'al gate lion is frequently touched by visitors (A). Compared to samples taken from a mostly untouched area of the lions, the teeth contained increased levels of the "touch" signature in both lions (B), indicating that the microbiome reflects the history of human interactions.

Summary and Next Steps

- Cultural heritage objects from the Pergamon museum and Museum für Naturkunde in Berlin were profiled using 16S rRNA amplicon sequencing
- Optimization of library preparation protocols enabled extraction of biological signal from very low input DNA
- Analysis of microbial expression patterns revealed "touch" signature associated human skin microbiome, which was robustly validated across different objects and institutions
- Taken together our results demonstrate that the microbiome reveals the history of human-interactions in the museum

- We plan to generate additional samples to increase statistical power and use whole shotgun metagenomics sequencing on selected samples for improved sensitivity of microbial profiles

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DSMZ   MUSEUM FÜR NATURKUNDE BERLIN   Baylor College of Medicine   Rathgen-Forschungslabor Staatliche Museen zu Berlin   RICHARD LOUNSBERY FOUNDATION