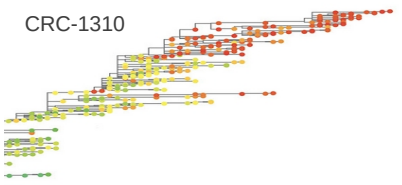
Prediction of sequence divergence from the quality of mapping

University of Cologne

INSTITUTE FOR BIOLOGICAL PHYSICS

CRC-1310



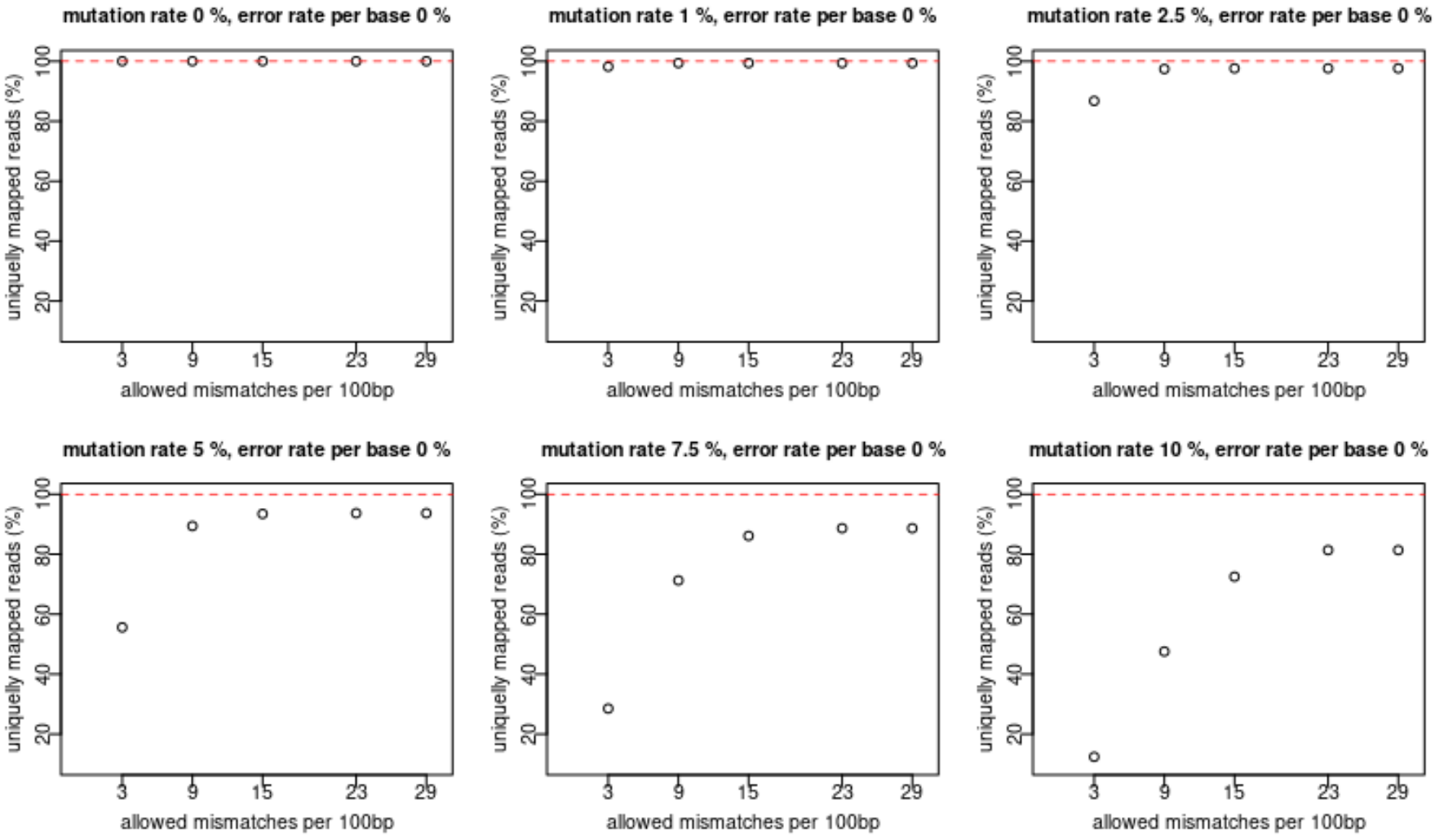
With a profound focus on:

- microorganisms (bacteria, viruses)
- FFPE samples

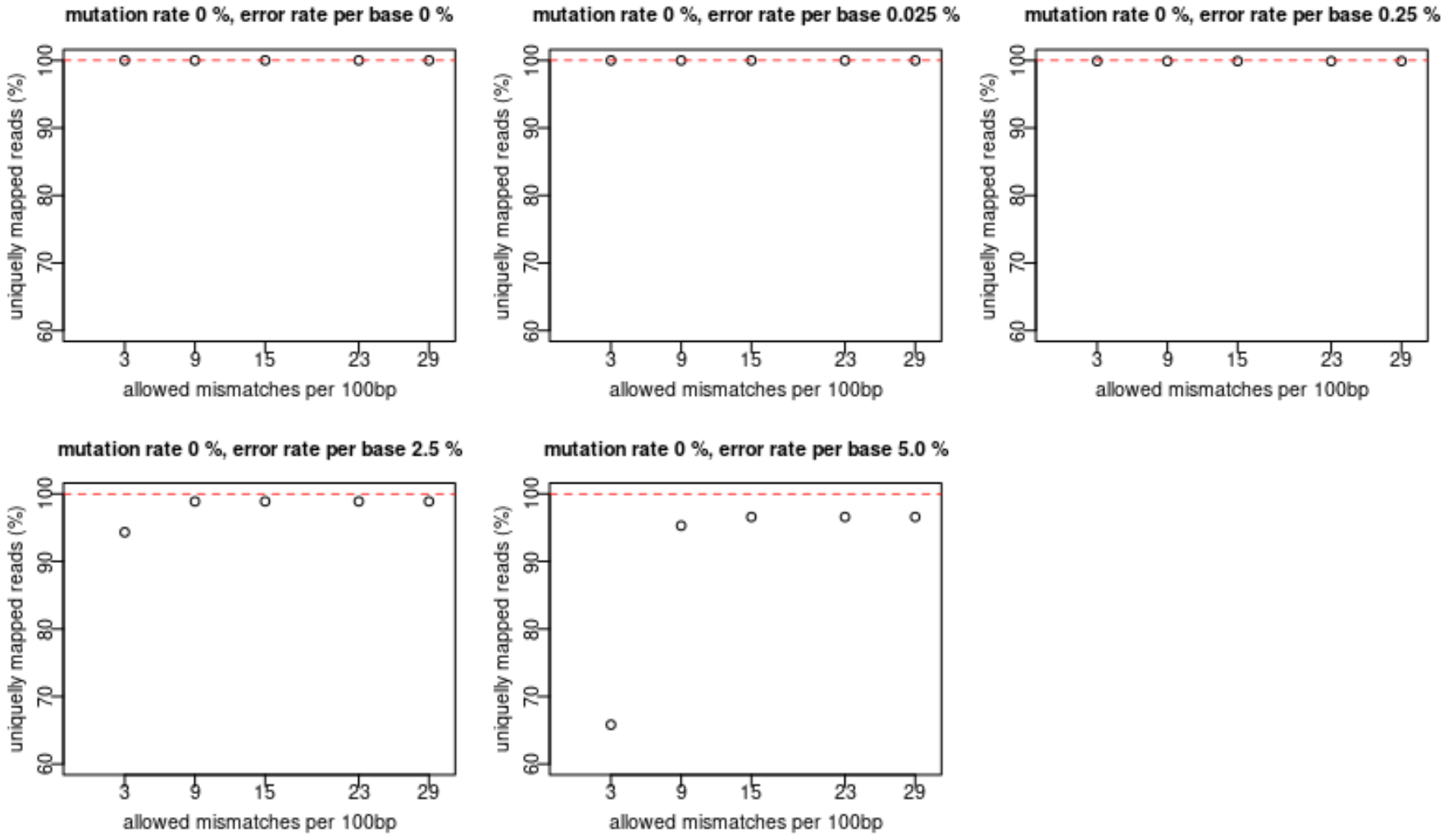
How much does genomic divergence influence genome-wide mappability?

Simulation.

The mutation rate has a great impact on the mappability.



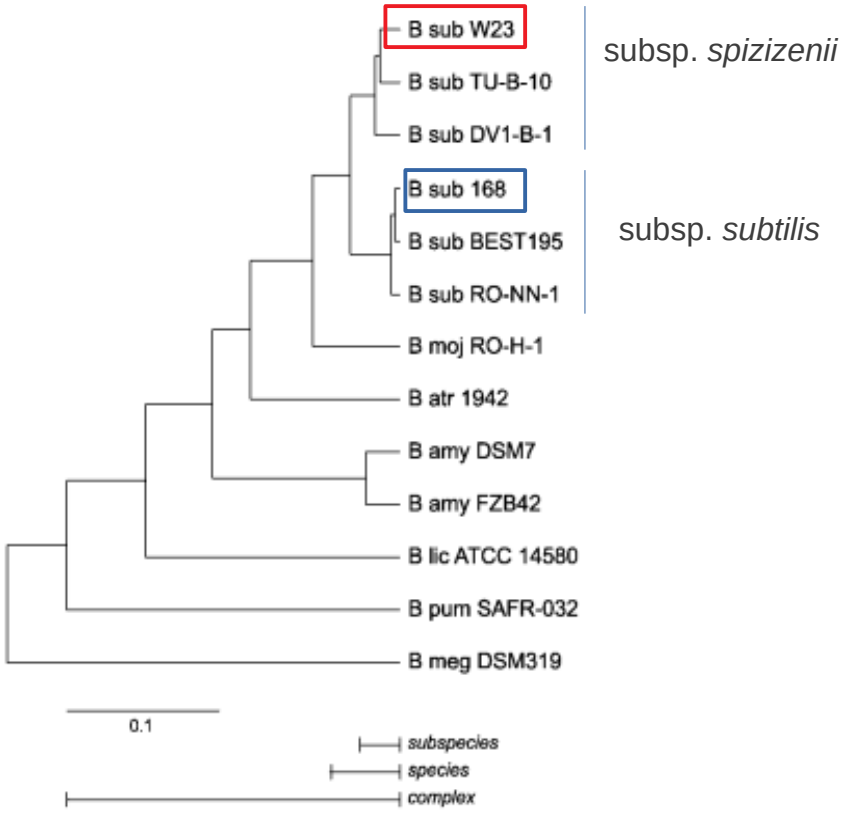
Sequencing errors have no impact.



Getting wet-lab.

Cross-lineage gene transfer shapes the systems biology and the evolution of hybrids.

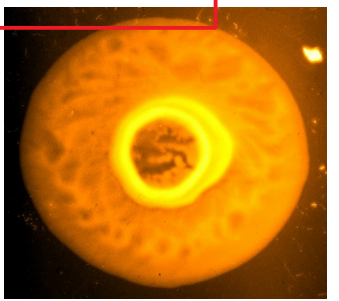
Powet et al, PNAS, 2021



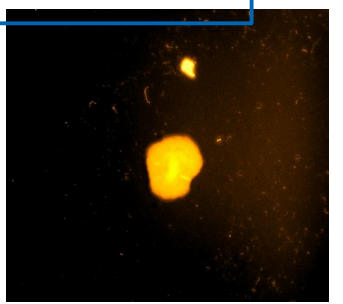
Zeigler, *Microbiology*, 2011

- 6.8% average sequence divergence:

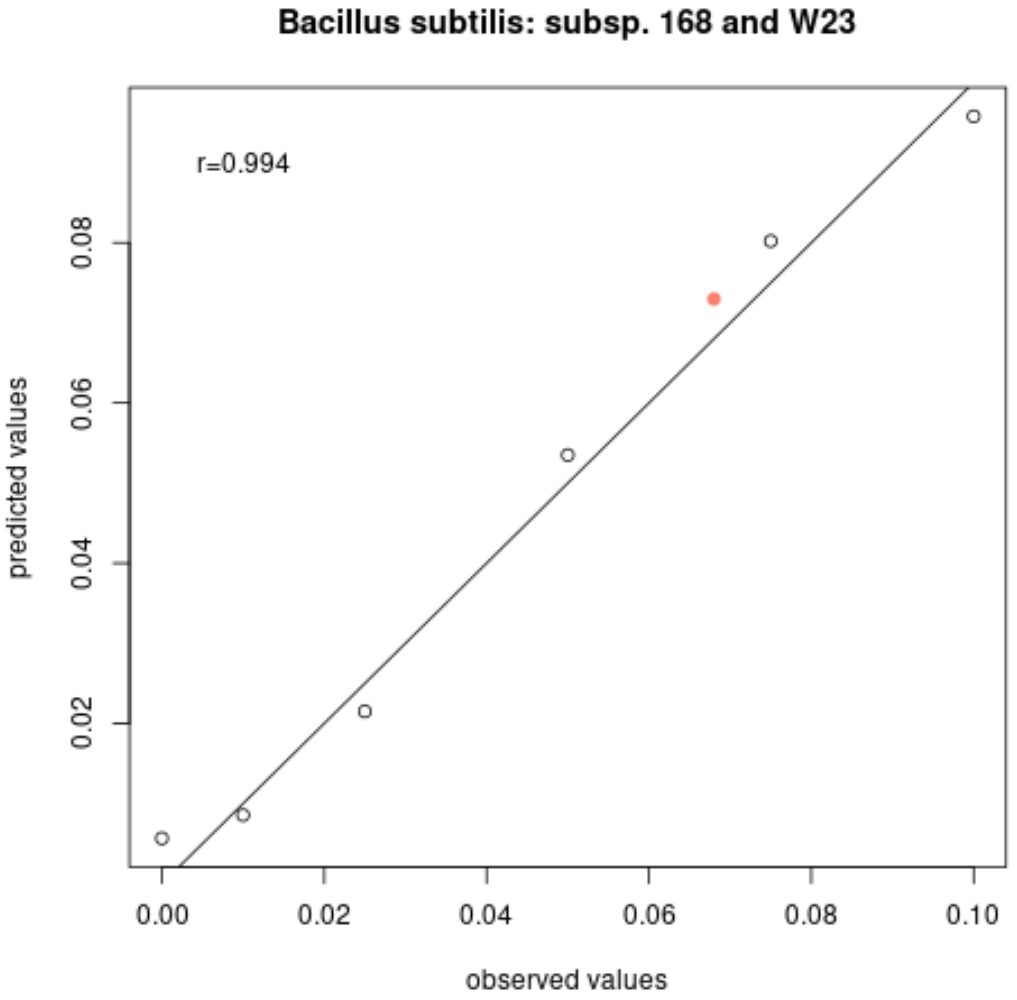
Donor: Bacillus subtilis W23



Recipient: Bacillus subtilis 168



Reliable prediction of the sequence diverence at a (sub-)species level.



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