# Modular pathogens analysis with safe, seamless, and user-friendly epidemiology methods

EMBLEM
TECHNOLOGY TRANSFER

## Challenge

- Whole genome sequencing has the potential to be used within timescales short enough to inform interventions against infectious diseases.
- Advancements in sequencing technology and genomic surveillance have exponentially increased pathogens' genome availability.
- Current methods are struggling to handle the speed and scale at which sequence data is now being generated.
- Despite the volume of genome data available, gene prediction and annotation are currently conducted in isolation on individual genomes, which is computationally inefficient and frequently inconsistent across genomes.
- There is a need for innovative, ethical, and sharable approaches to harness the power of sequencing to control pathogen threats and to broaden and deepen our understanding of disease transmission mechanisms.

## Technology *(TRL7 and above)*

Our team of experts specializes in providing cutting-edge and modular tools and methodologies to tackle critical challenges in pathogen transmission, evolution, and epidemiology analysis. Leveraging the power of data analysis, statistical genetics, and high-performance computing, we offer fast and flexible algorithms that enable swift real-time data analysis for effective pathogen surveillance. Next to our core activities, we engage in microbiome sequencing, exploiting our ability to handle extensive genomic data. Moreover, our methods empower ambitious analyses of large datasets, unlocking even greater potential for discoveries. Through mathematical modelling and statistical genetics, we develop and refine professional models that capture the dynamics of pathogen competition and transmission within- and between-host. Through other models, we uncover evolutionary signatures in genomic data and establish their functional relevance, even at the population level. We accurately identify and quantify critical variants and predict critical pathogen traits such as pathogenicity, host affinity or replication. Our automated tools allow the monitoring of concerning lineages as they emerge, predict antimicrobial resistance status, determine resistance phenotypes, and follow the effects of vaccination on local populations. We demonstrate great accuracy in performing antigen and/or vaccine target discovery. Our privacy-focused algorithms are modular and seamlessly deployable in web browsers or on-site, ensuring data confidentiality. By applying these user-friendly methods to diverse genomic data, we rapidly generate valuable biological insights for genomic epidemiology analysis and projection, predicting phenotypes from genotypes.

**Internal EMBLEM Reference**

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**Key Inventors**

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## Applications

- **Healthcare:** pathogen surveillance, antigen discovery, vaccine target discovery, prediction of vaccines and antimicrobial resistance, assessing vaccine efficacy on local populations, disease diagnosis and monitoring, diagnostics for AMR …

- **Pharmacology:** drug development, targeted medicine, AMR prediction, …

- **Research:** pathogen evolution study, pathogens identification and characterization, transmission dynamics, …

- **Education:** training for the computational inexperienced in the field of epidemiology, …

- **AgriTech:** development of non-antibiotic methods, genetic analysis and trait prediction, enhancement of agricultural practices, …

## Keywords

\# Microbial genomics
\#Epidemiology
\#Genomic Epidemiology
\#Infection Biology
\#Phenotyping
\#Computational biology

\#Machine Learning
\#Method Development
\#Interoperability
\#Bioinformatics
\#Modelling

## Software

- ggCaller
- SKA2
- PopPUNK and PopPIPE
- pp-sketchlib

## Modelling

- odin, dust and mcstate

## Benefits

- Unparalleled speed
- On-site execution
- Pathogen-agnostic approach
- Expert curation
- Energy-efficient designs

## Intellectual Property

☒ Know-how based

☒ Copyright

## Commercial Opportunity

We provide a professional pipeline for genomic epidemiology analysis and are looking for support and collaboration to scale up our offer.

## Seeking:

☒ Development partner

☒ Commercial partner

☒ Academic partner

## Further Reading

[1] https://doi.org/10.1101/2023.01.24.524926
[2] https://doi.org/10.1098/rstb.2021.0237
[3] https://doi.org/10.7554/eLife.69244

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