The MOOD Platform
A novel contribution to epidemiological surveillance

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MOOD objectives

- Addressing challenges posed by **global, environmental, and climatic changes**

- **Assessment and monitoring** of infectious disease threats

- Monitoring **present and future** infectious diseases across Europe, including emerging diseases of unknown origins

- Improving **early detection** of infectious diseases and antimicrobial resistance (AMR)

- Implementing a **One Health** approach

➔ Development of an **Independent Epidemic Intelligence Platform**

➔ Establishment of **International Non-Profit Association** to run platform
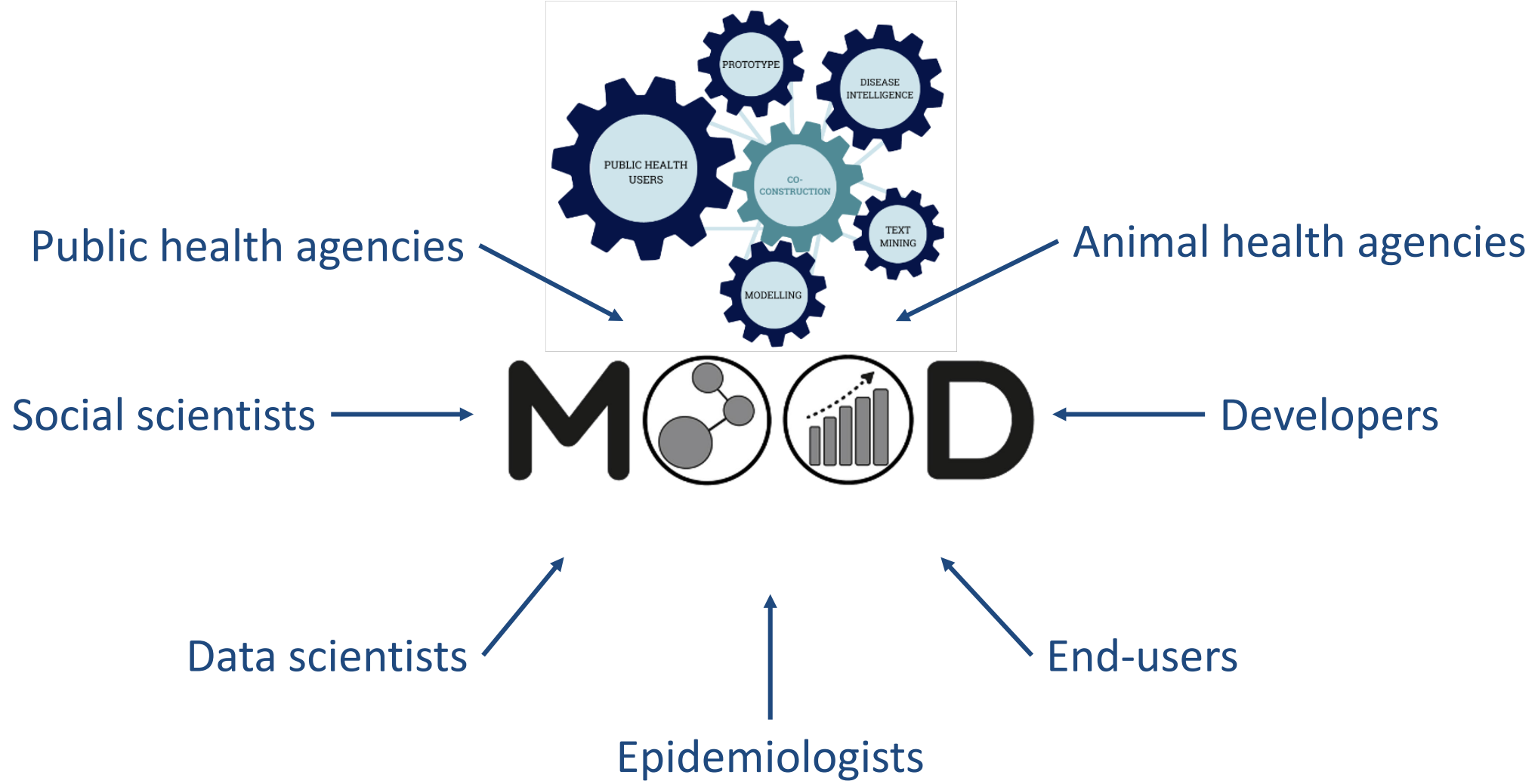
Sustainability!

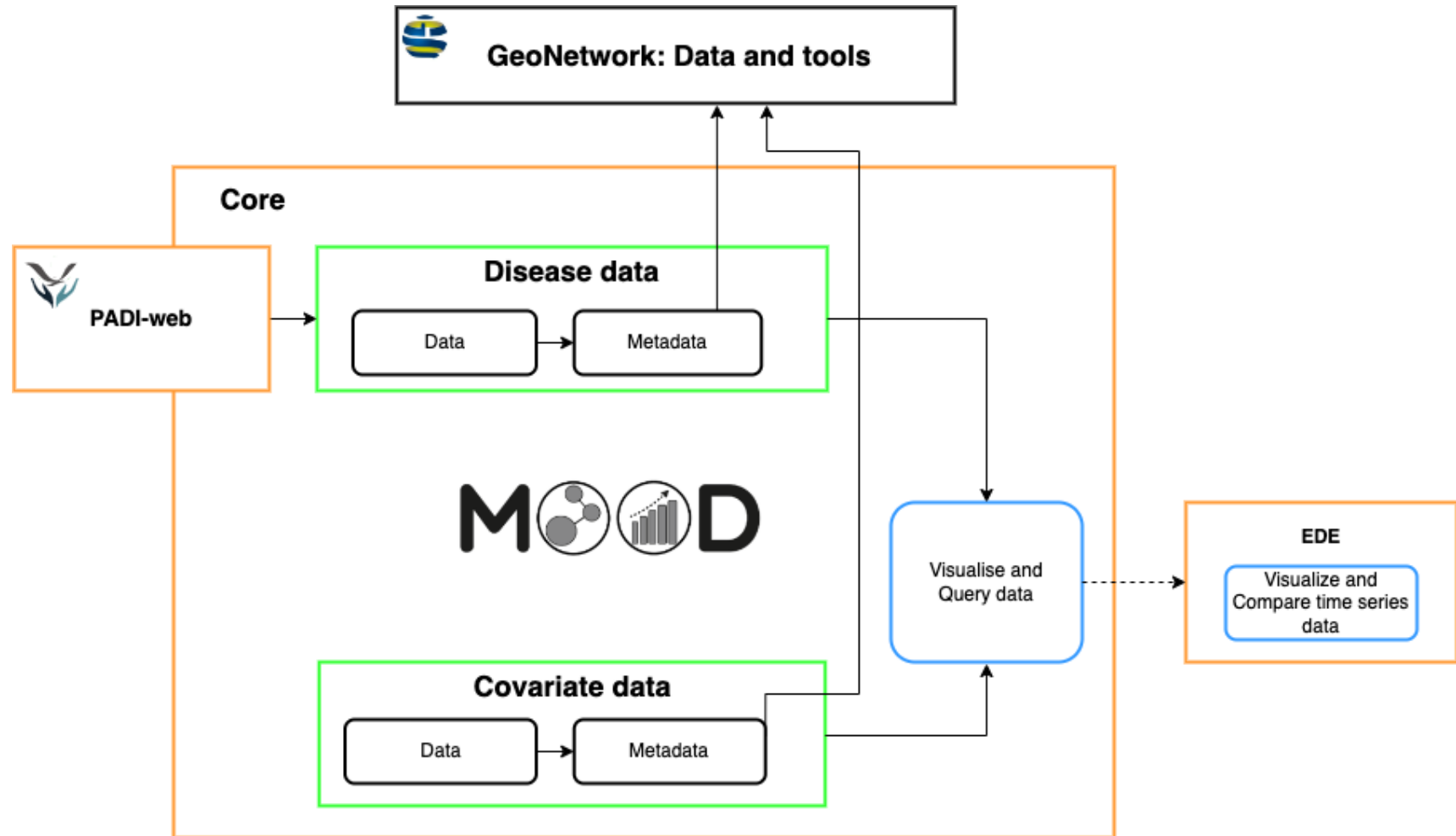# MOOD Disease Use Cases
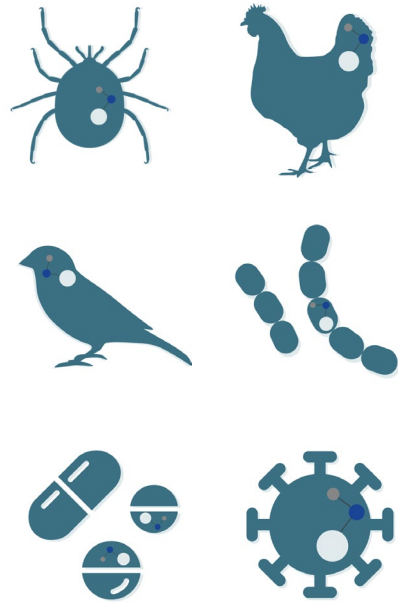
- Highly Pathogenic Avian Influenza (HPAI)
- Vector-borne diseases:
  - West Nile Fever (WNF)
  - Tick-borne encephalitis (TBE)
  - Dengue (DENV)
  - Chikungunya (CHIKV)
  - Crimean-Congo Hemorrhagic Fever (CCHF)
- Antimicrobial Resistance (AMR)
- Leptospirosis
- Covid-19

MOOD co-creation

Public health agencies

Animal health agencies

Social scientists

Developers

Data scientists

Epidemiologists

End-users

The MOOD Platform architecture

What can you do with the MOOD platform?

- Access a large set of environmental and other co-variate data:
  - Visualize and configure
  - Compare and query data layers
  - Create and query time series graphs
  - Query, extraction and download data (raster, polygons, CSV)
- Query vector and host suitability model outputs
- Query disease risk maps and prediction model outputs
- Access PADI-web, an integrated disease database based on event-based surveillance (EBS) data and other public disease data sources
- Import your own disease data sets
- Extract data to build your own models
- Access advanced tools: text-mining, normalization, risk-mapping, …

Co-variate datasets

- Administrative layers:
  - Europe, countries
  - NUTS 0-1-2-3
- Demography and socio-economics:
  - Human population
- Environmental data:
  - Altitude (DEM)
  - Daylight
  - Hydrography
  - Land cover / land use
  - Precipitation
  - Temperature (Land surface, Air, Day, Night)
  - Vegetation indices (NDVI, EVI)

Administrative data: countries and NUTS

Demographic data: Human population
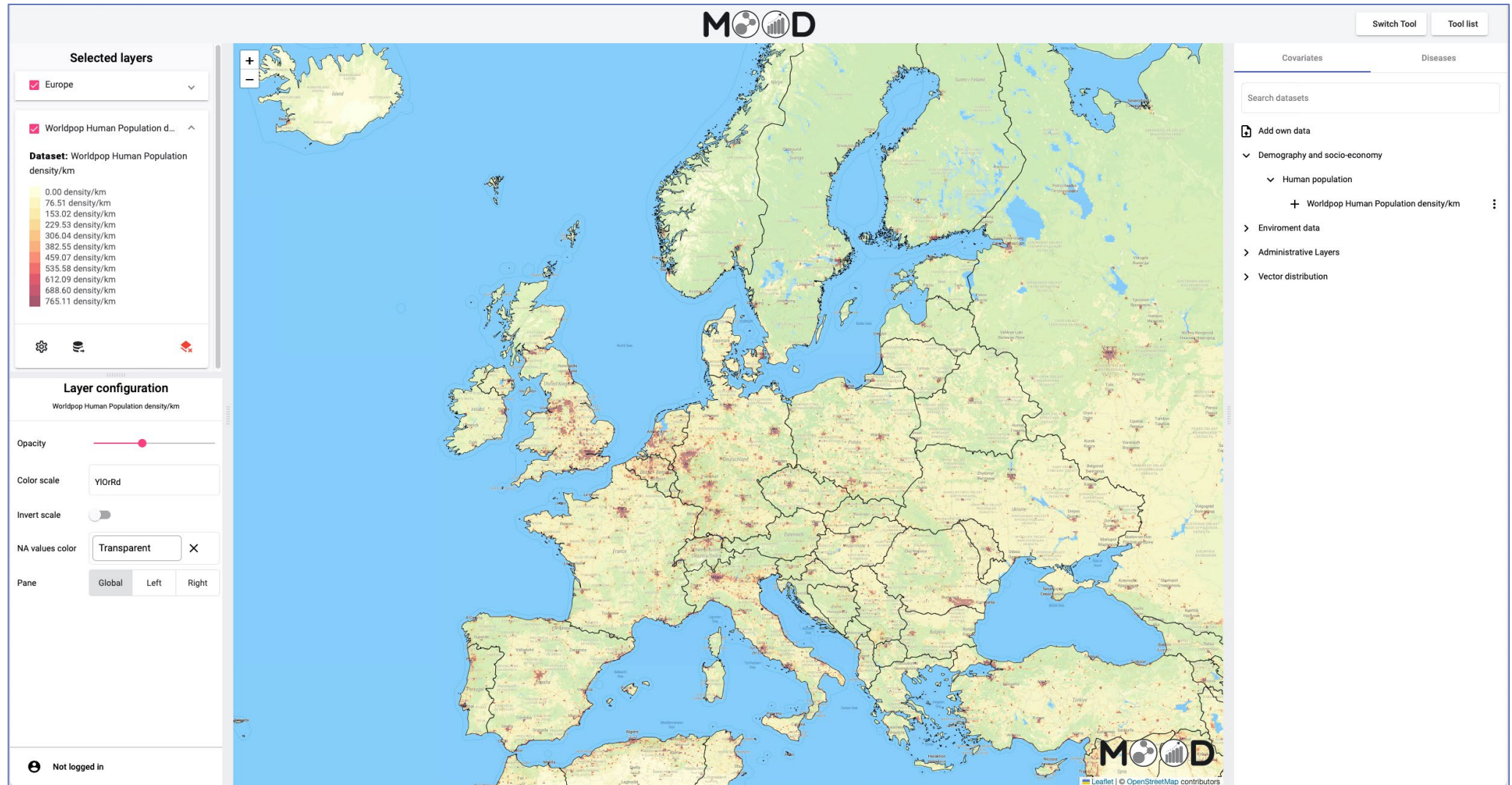
Vegetation: e.g. comparison NDVI-EVI
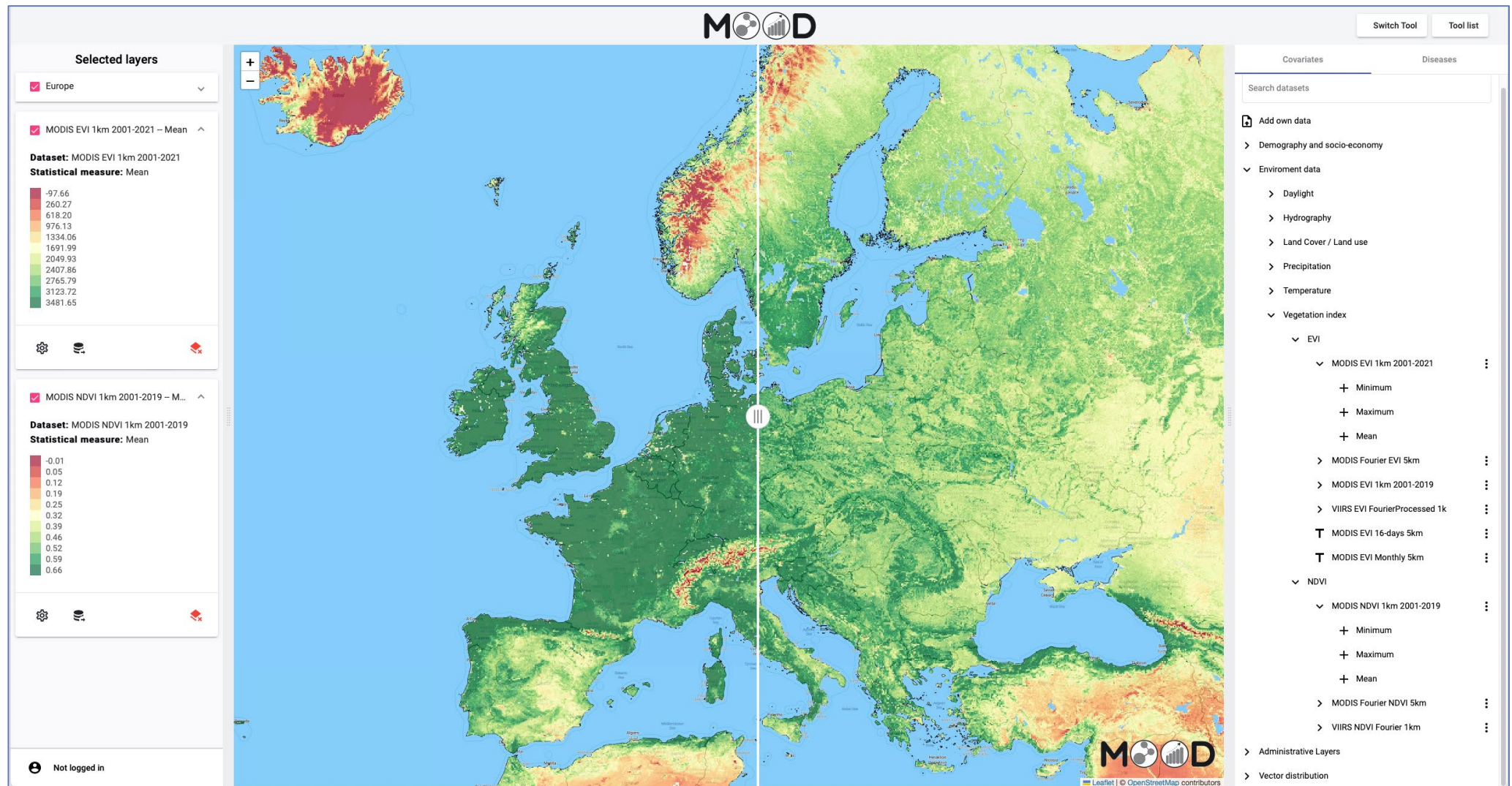
Temperature: e.g. time-series LST night

Vector & host suitability model outputs

- Vector suitability models:
  - Ticks: *Ixodes ricinus, I. persulcatus, Hyalomma marginatum, H. lusitanicum*
  - Mosquitoes: *Aedes albopictus, Ae. aegypti, Culex pipiens, Cx. torrentium, Cx. Perexiguus, Cx. Modestus*

- Host suitability models:
  - Rodents: *Apodemus flavicollis, Myodes glareolus*
  - Hares: *Lepus europeus, L. timidus*
  - Ruminants: *Cervus elephus, Capreolus capreolus, Dama dama*
  - Birds: 18 species linked to WNF and 10 species linked to HPAI

# Vector suitability: *Ixodes ricinus*
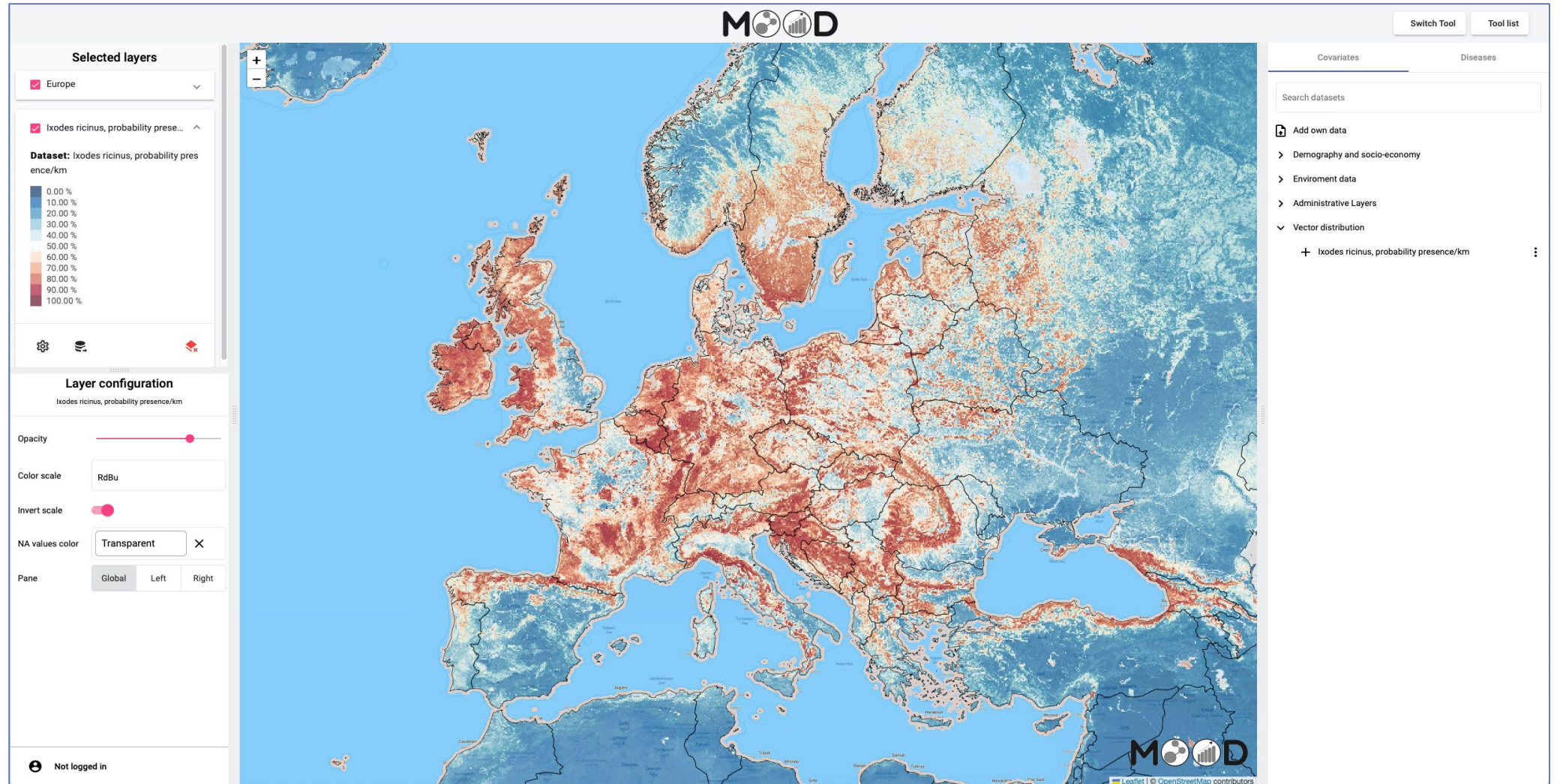
MOOD Disease Data

- Links to Open Access disease data sets:
  - Empres-I, PADI-web, (TESSy, WAHIS)
- MOOD disease model outputs:
  - Highly Pathogenic Avian Influenza (HPAI)
  - West Nile Fever (WNF)
  - Tick-borne encephalitis (TBE)
  - Dengue (DENV)
  - Chikungunya (CHIKV)
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  - Leptospirosis
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Diseases: HPAI suitability wild vs. domestic
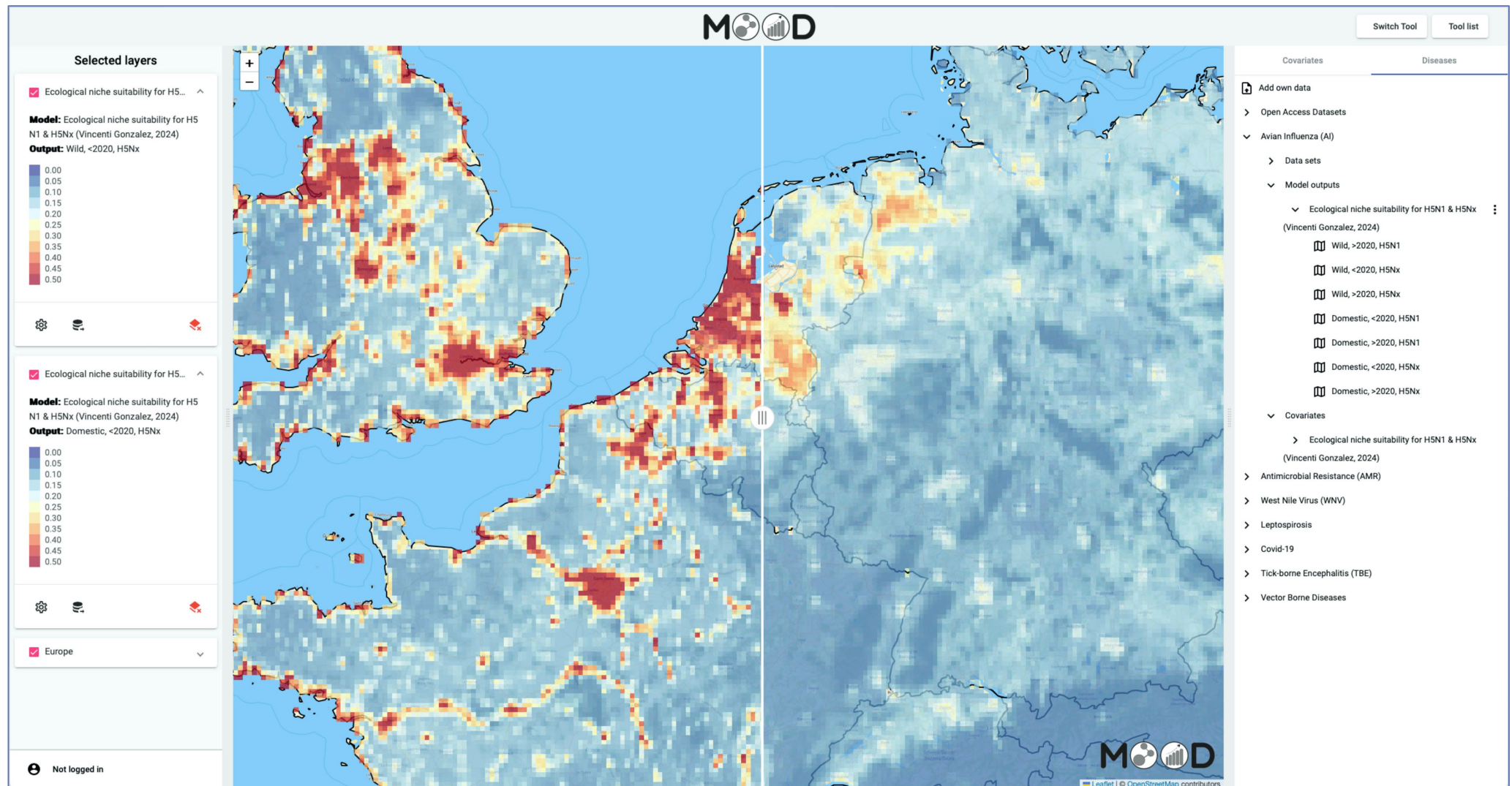
Work with disease data from other sources

- Data sources:
  - Own data
  - Indicator-based surveillance data (IBS): EMPRES-i (TESSy, WAHIS)
  - Event-based surveillance data (EBS): PADI-Web
- Download external data via side-menu MOOD platform
  - e.g. HPAI data from EMPRES-i
- Import disease outbreak data in MOOD platform
- Add available disease model if applicable
  - e.g. suitability for H5Nx in wild bird populations
- Add co-variate data as required for analysis
  - e.g. temperature, precipitation, vegetation index
- Extract co-variate data for each outbreak

Import and extract data

Import and extract data

MOOD GeoNetwork

Catalogue of additional resources developed by MOOD partners

PADI-web	Platform for Automated extraction of Disease Information from the web
Covid-19 tweets	Spatial Opinion Mining of COVID-19 Tweets through H-TFIDF and other features
Classification of news articles	Avian Influenza relevant articles and irrelevant articles classification
GeospaCy	Relative spatial information extraction and its geographical referencing
arbocartoR	Modeling the risk of emergence of aedes-borne diseases - Shiny interface
epiCurve	Model the force of infection in the case of seasonal vector-borne pathogens
Gazetteer Access Tool	MOOD data normalisation tool
EpiDCA	Links epidemiological data from EBS systems with environmental risk factors to classify and detect outbreak events in textual data
Different source disease data linking	Framework to compare official and unofficial disease data
GeoNLPlify	Generate new labelled data for text classification related to crises using Language Models.
SNEToolkit	Spatial named entity disambiguation toolkit
MOOD Press Tweets Collector	Python script designed to gather tweets
Extension of actinia for COG import	Cloud based geoprocessing platform
EpiNorm	MOOD structured data normalisation tool
EpidBioBERT	BioSurveillance Document Classifier
EpidBioELECTRA	Enhanced and Explainable BioSurveillance Document classifier

Save the date!

MOOD FINAL WORKSHOP

Wed October 23rd – Thu October 24th 2024
Institute of Tropical Medicine (Antwerp) + On-line

Final testing and launch of the platform

https://mood-h2020.eu/about-mood/

Thank you for your questions!