COmpare

COllaborative Management Platform for detection and Analyses of (Re-) emerging and foodborne outbreaks in Europe

New horizons in EID detection: the era of next generation sequencing and bioinformatics

A global platform for the sequence-based rapid identification of pathogens

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research and innovation programme under grant agreement No 643

Infectious diseases in the current era

- Dynamics of common infectious diseases are changing
  - Demographic change, population density, anti vaccine, AMR, etc.
- New diseases emerge frequently
  - Deforestation, population growth, health system inequalities, travel, trade, climate change
- Effects are difficult to predict due to complexity of problems
  - Rapid flexible response
- Public health and clinical response depend on global capacity for disease surveillance
  - Rapid sharing, comparison and analysis of data from multiple sources and using multiple methodologies

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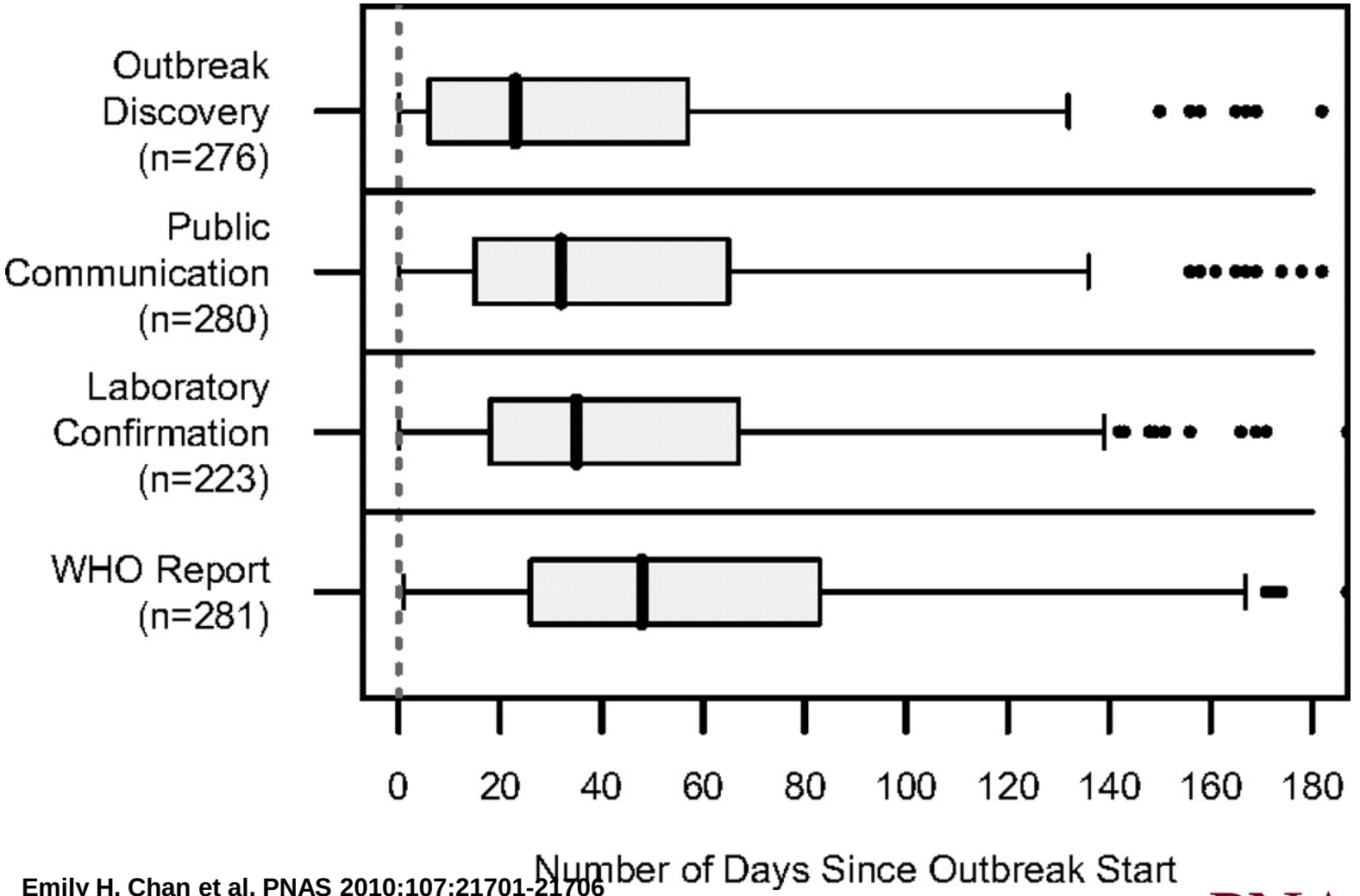
Current performance

late detection, human disease first



Emily H. Chan et al. PNAS 2010;107:21701-21706

Priority research questions EID after disease emergence

Clinic/public health

- How to diagnose/rule out?
- How t
- When
- Mode
- Source
- Role o
- Risk fa
- Potent interventions/prevention

Basic

- Comparison with other
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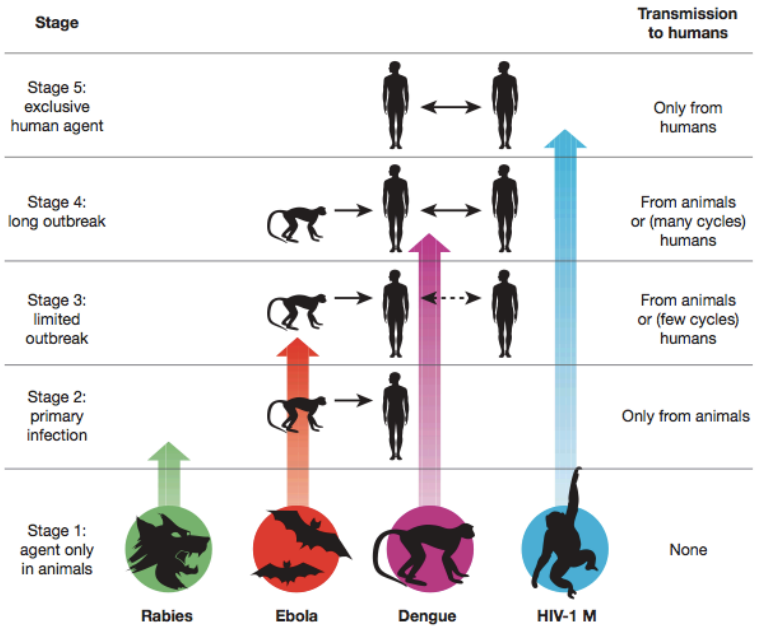
  virals
- Potential vaccines

Main aspects

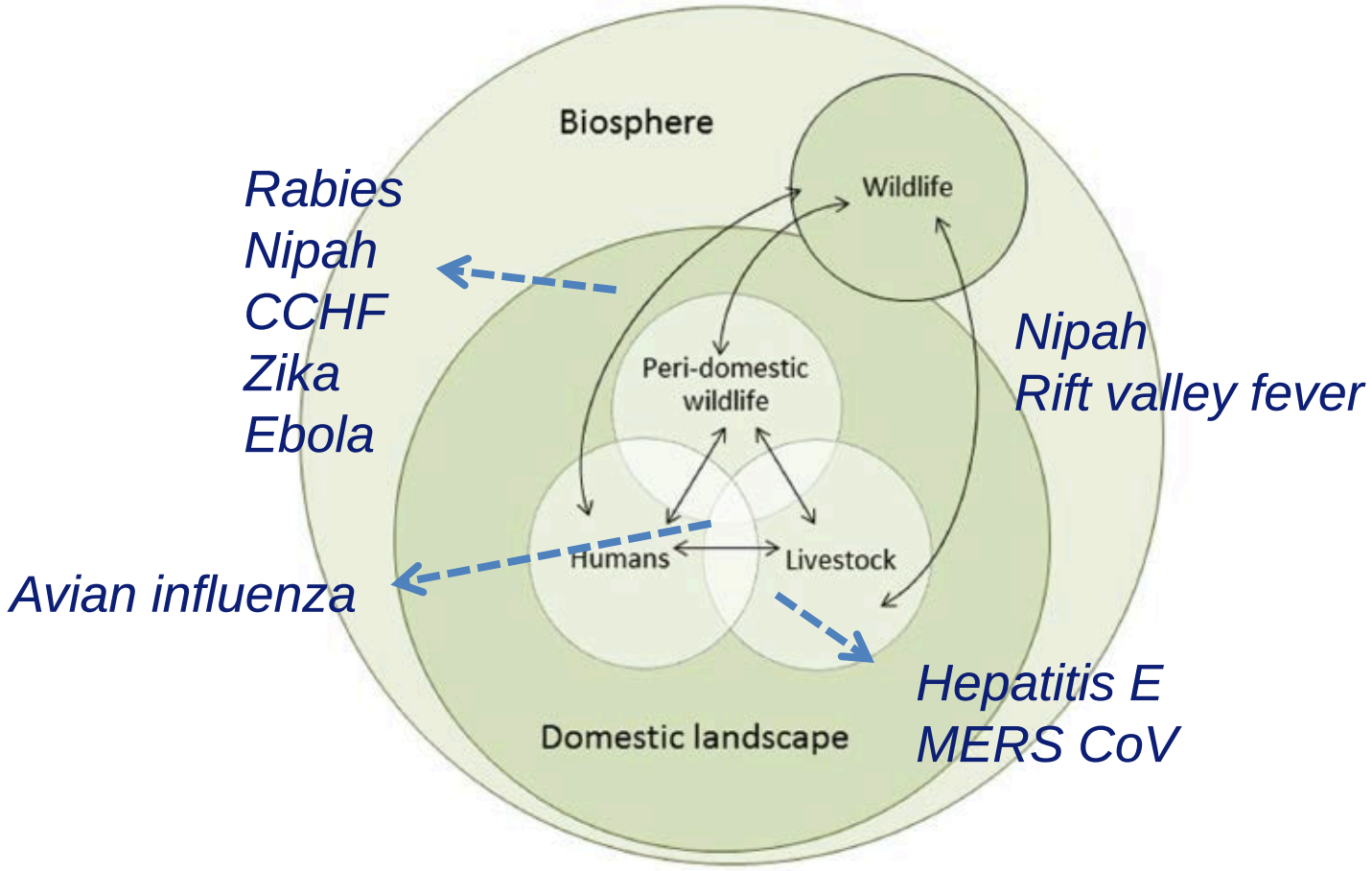
- Increased likelihood of new (zoonotic) pathogens
- Increased opportunity for global spread



Challenges

- Competing priorities
- Inequality in health care systems
- Clinician knowledge of EID
- Privacy laws
- Poor prediction

EID require multidisciplinary research



COMPARE: developing an enabling system and tools for collaborative preparedness and outbreak research

- Collaboration between “users” of NGS and bio-informaticians
- Develop validated workflows for top 5 questions in disease preparedness research and outbreak research
- sector-, domain- and pathogen-independent (ONE HEALTH)
- Flexible, scalable and open-source based
- Data and information-sharing platforms
- building from sustainable infrastructure

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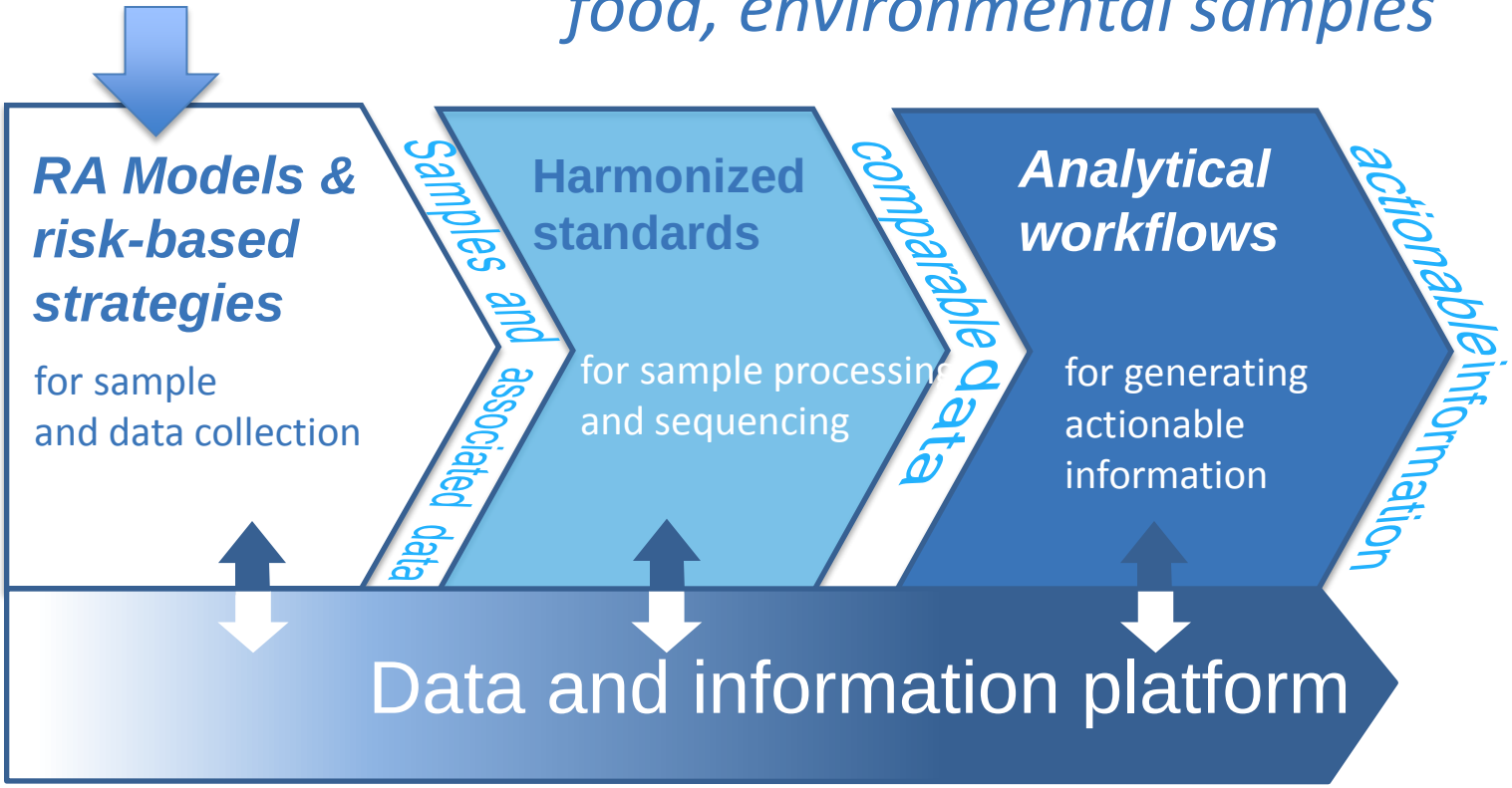
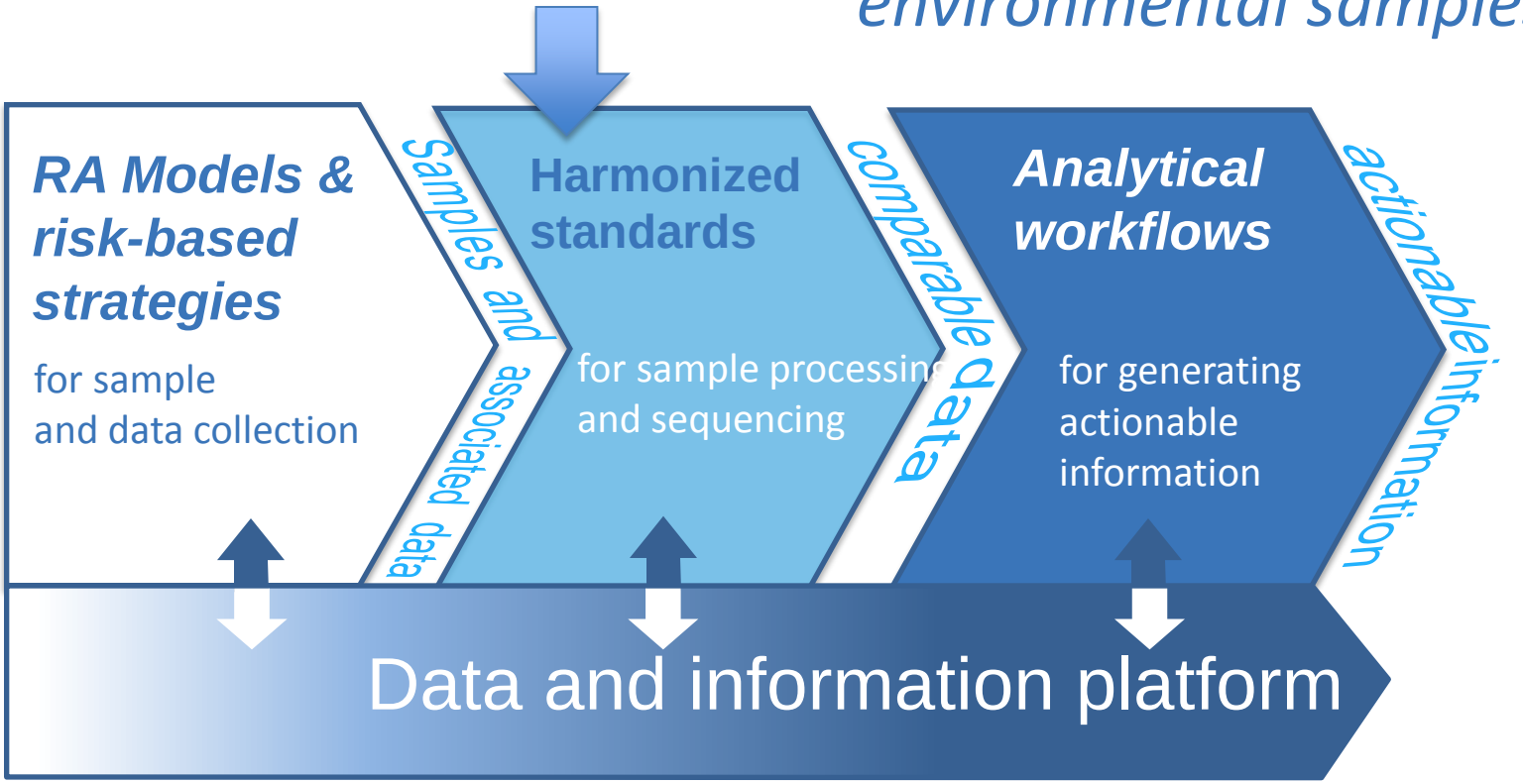
What to sample?
Where?
When?
How?

Humans, livestock, wildlife, food, environmental samples



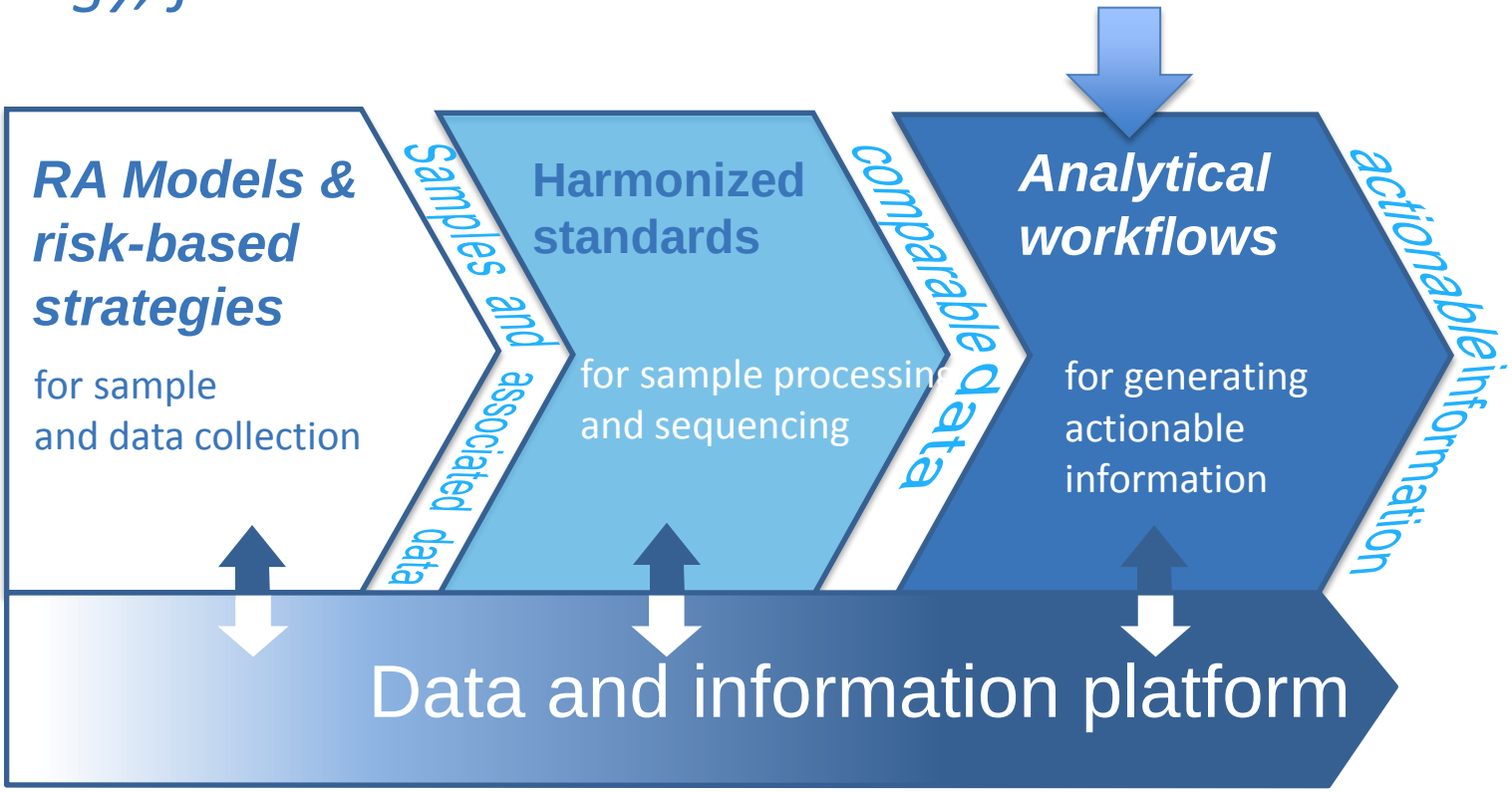
How to sequence?
Pathogen targeted
Metagenomic, Deep sequencing
Viruses, bacteria, parasites
QUALITY ASSURANCE

Clinical, tissue, food, environmental samples

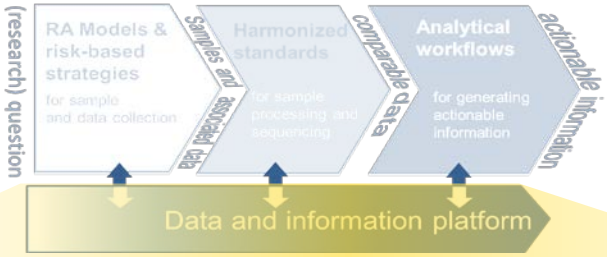


Clinical, public health, research
Human, veterinary
Ecology, food

How to analyze?
What does the analysis mean?
How do I use it ?



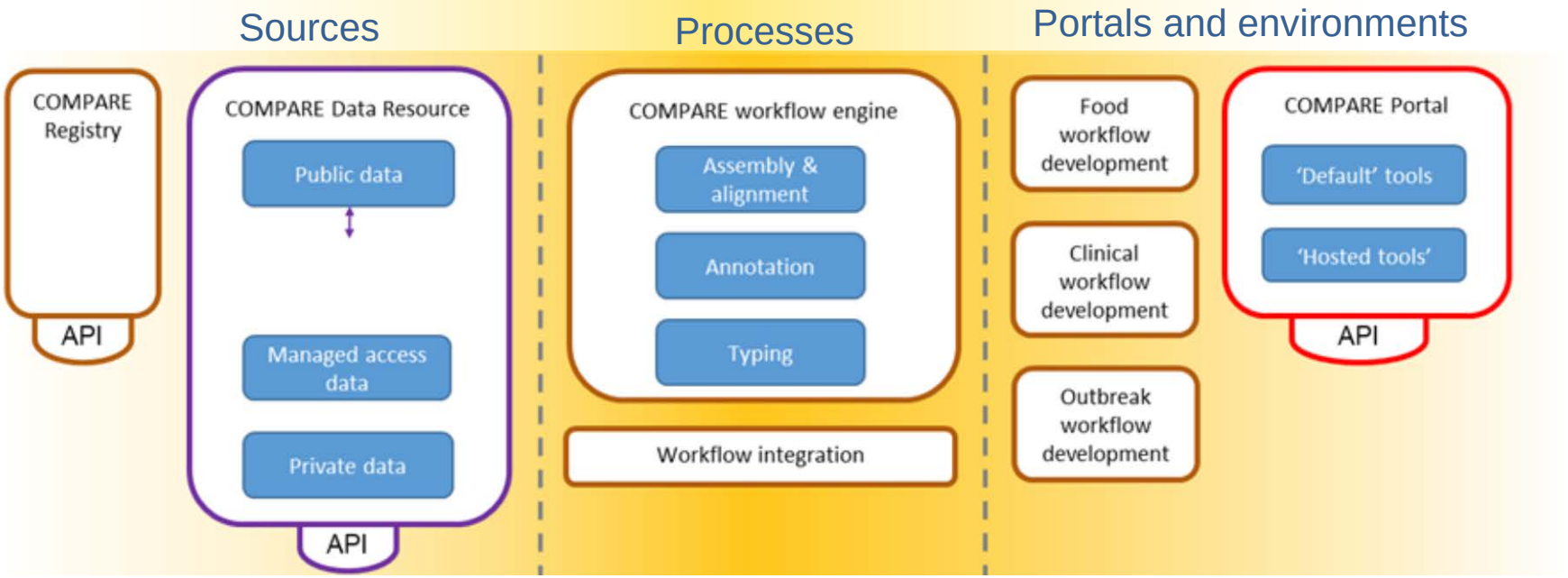
WP9 Information sharing platform



Guy Cochrane
WP leader

Ole Lund
WP co-leader

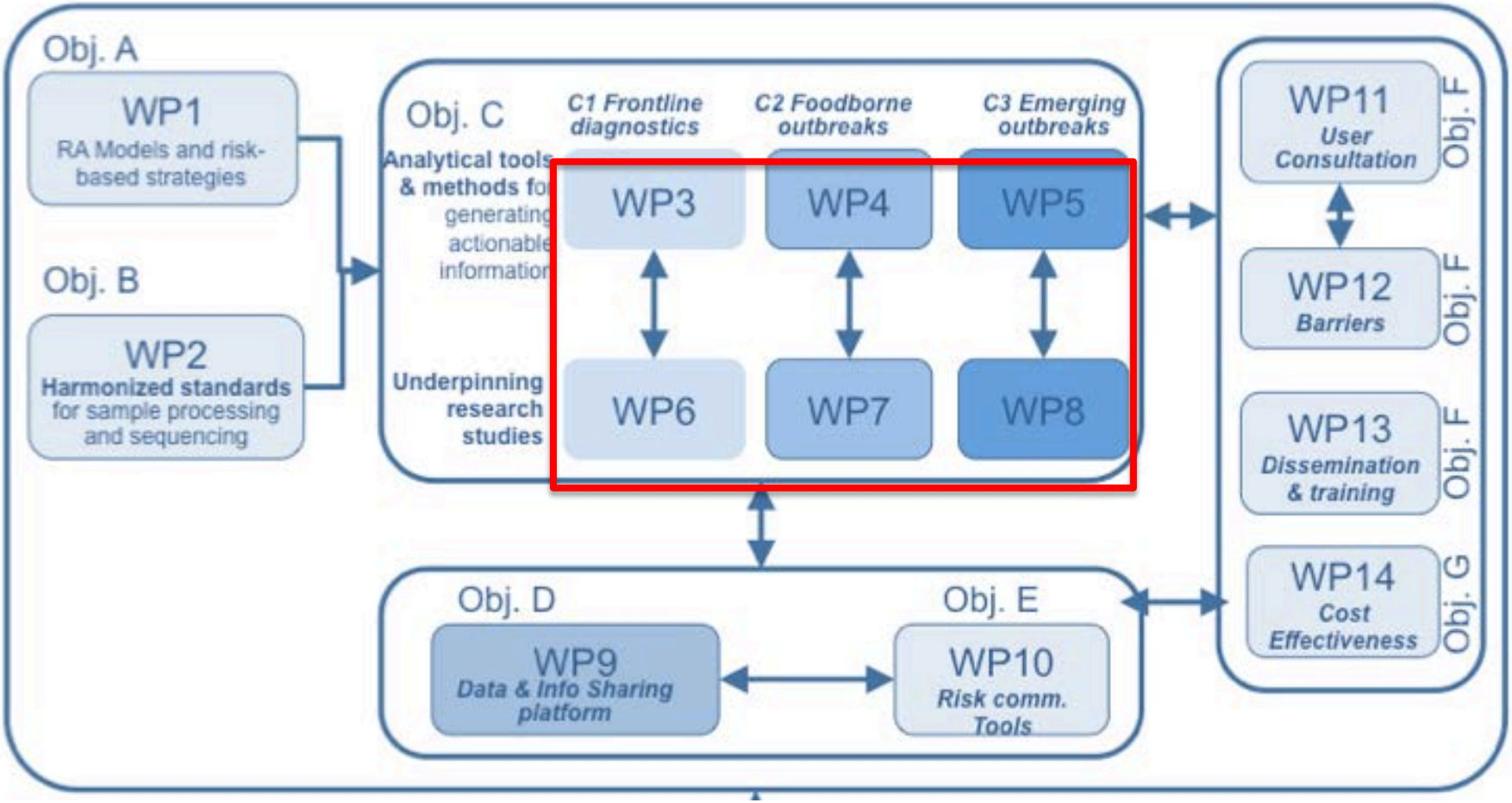
Istvan Csabai
WP co-leader



Building on the EU ESFRI Elixir, EMBL and DTU infrastructures

...20
...research and innovation programme under grant agreement No ...

Develop a “catch all” metagenomics approach for surveillance of pathogens transmitted via fecal-oral and environmental, and respiratory routes with user friendly data analysis



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Shotgun metagenomics

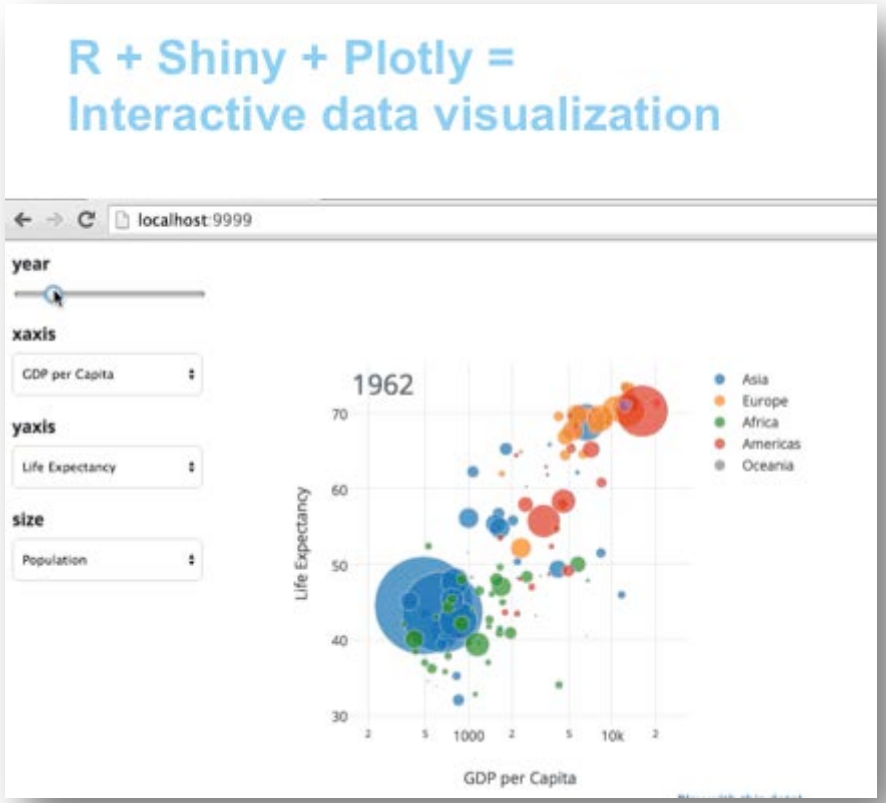
"Sampling of all genetic material in all organisms present in a given complex sample"

- Sample preparation by filtering and centrifugation
- Nuclease treatment
- DNA+RNA extraction
- Random nucleic acid amplification
- Sequencing library preparation
- High throughput sequencing (Roche 454/Illumina)

Metagenomics Analysis Workflow

- *Remove low quality reads* — *Newbler QC*
- *Generate contigs* — *Iterative assembly with Newbler assembler + CAP3*
- *Map sequencing reads to contigs* — *Newbler read mapper*
- *Filter low quality + off-target contigs* — *Dustmasker + HostBLAST*
- *Taxonomically identify genomes* — *BLASTN + BLASTX*

R + Shiny + Plotly = Interactive data visualization



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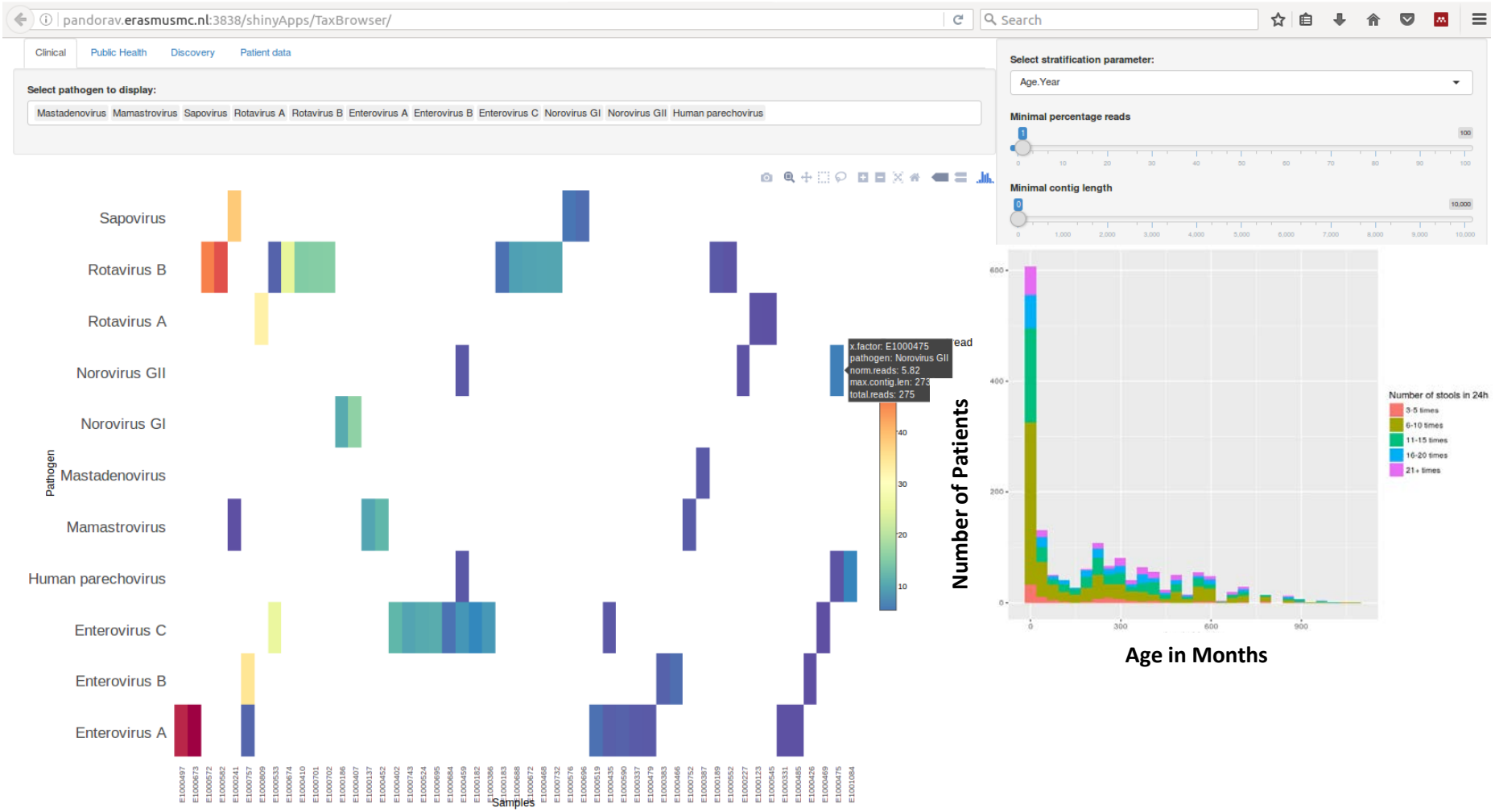
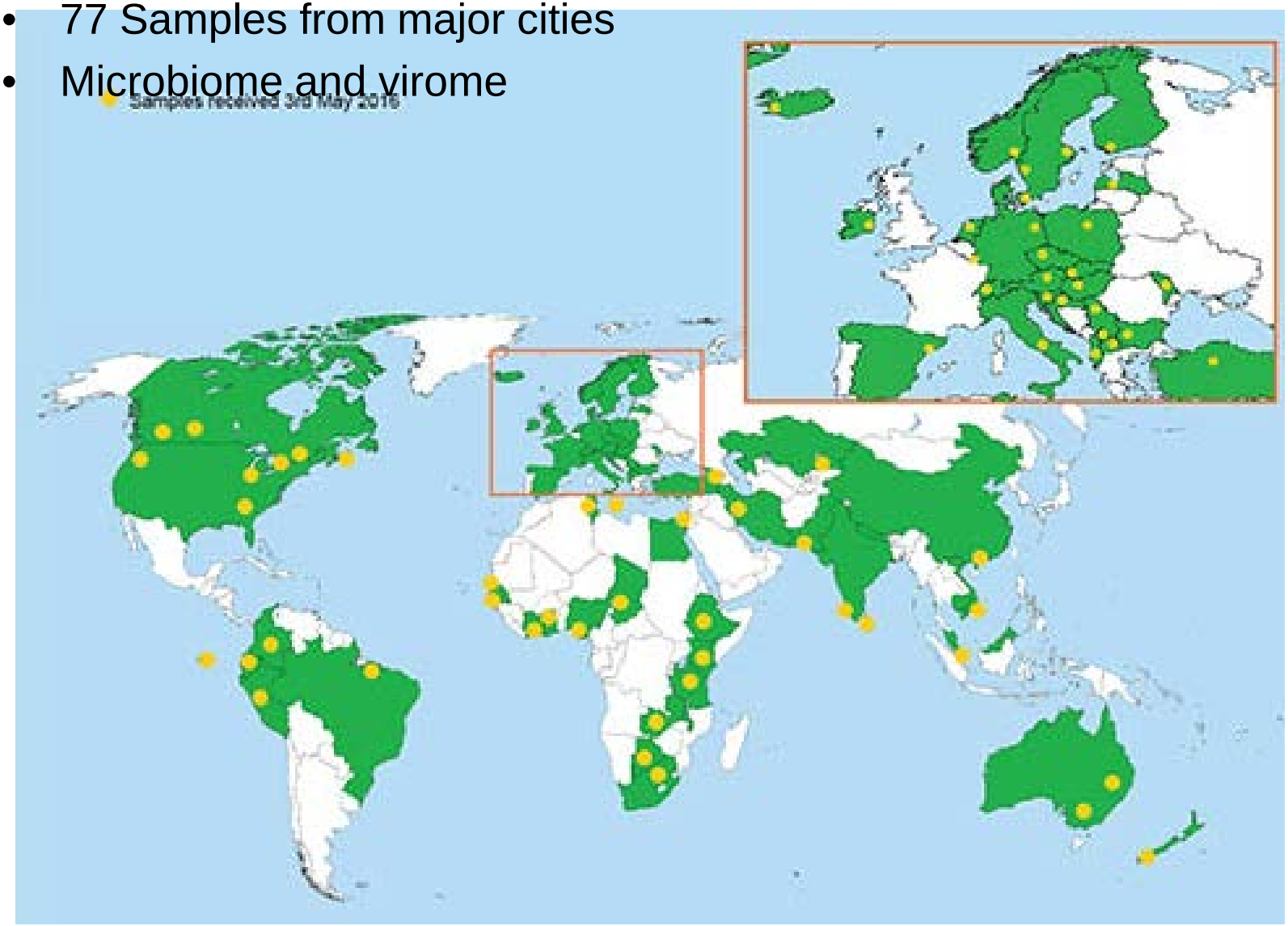
Analysis of samples from diarrheal disease surveillance (Bangladesh), virome



Global urban sewage project

- 77 Samples from major cities
- Microbiome and virome



Results sofar (>3 years to go)

1. Uniform protocols and workflows for NGS detection of a range of viruses, bacteria and parasites in different sample types

2. Pilot studies to develop customized analytical workflows for -
the top 6 food borne diseases

- tracking of avian influenza outbreak in wildlife
- support of outbreaks (Ebola, H5N8 AIV, norovirus, AMR-colistine, Zika)
- -metagenomic analysis of a global urban sewage snapshot as experimental surveillance tool

3. First version of data sharing hubs for collaboration between data providers and data users

4. Initial analysis of impact of Nagoya protocol

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Mateneh Ebola Treatment Centre
Makeni Sierra Leone

1 of 6 DfID-funded treatment centres

Part of network of diagnostic labs set up by EML, DML, PHE, many other groups

Ian Goodfellow
Univ of Cambridge
Sequencing
Tent

Diagnostic
Lab

This project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 643476.

Sequencing Tent

Ian Goodfellow

My Phan

Clinical diagnostic sample → Convert to cDNA amplification adapter ligation → Library preparation → Sequencing run → Genome assembly preliminary analysis

6 hours | 10 hours | 4 hours | 3 hours

24 hours

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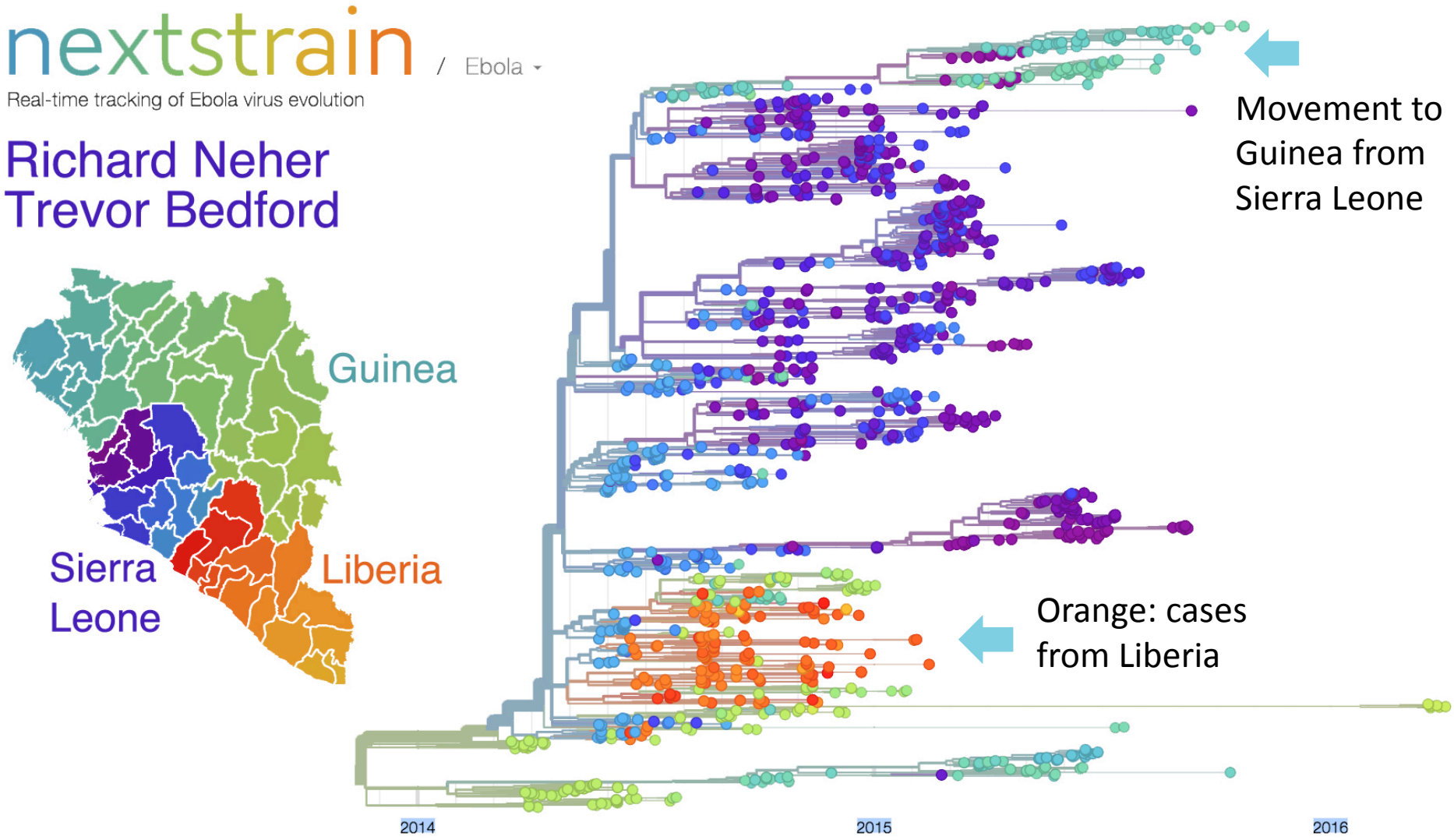
Rapid NGS of all Ebola cases to track source of new infections



Research needs

1. Affordable and robust technology
2. The translation of genetic information into properties that are important for risk assessment (virulence, transmissibility, susceptibility to population immunity).

3. Technological solutions for innovative surveillance (e.g. similar to air pollution technology)

Other

2. Sustainability of COMPARE

3. Embedding of NGS technology in health systems strengthening programs, which can be across programs (polio, TB, HIV, malaria ao)

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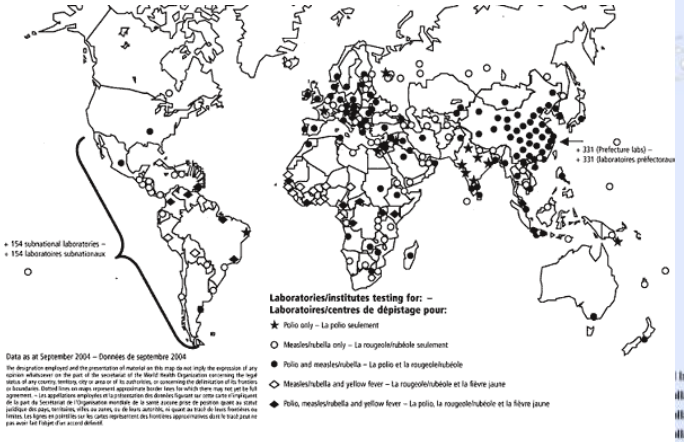
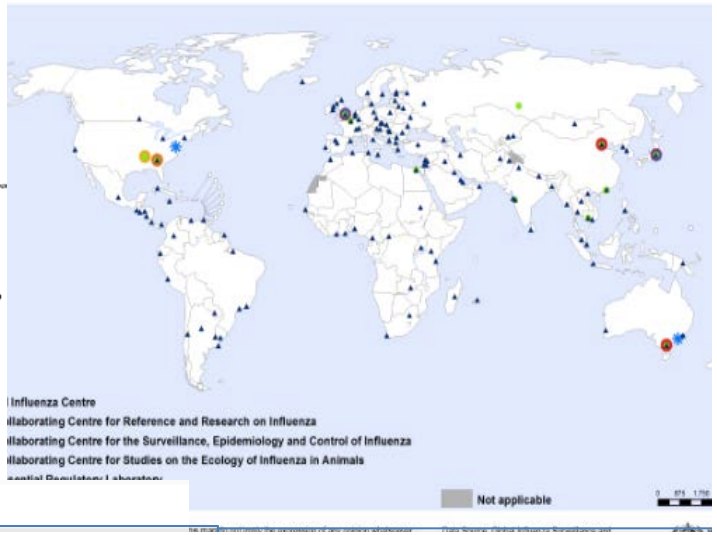
We could do things on the fly if capitalizing on existing networks





OIO, FAO, WHO networks

Polio, Measles, Flu, TB, HIV, VHF, malaria, Dengue, Salmonella, AMR, Zika

…….

PERSPECTIVES

Laboratory support during and after the Ebola virus endgame: towards a sustained laboratory infrastructure

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