

Applications des grilles aux sciences du vivant

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Credit: A. Da Costa, P. De Vlieger, J. Salzemann



- **Grid technology provides services to do science differently, opens new avenues for**
 - Large scale on demand computing
 - Secure data sharing
 - dynamic data analysis
- **Goals of my talk**
 - Share some of our ideas for using grid services in life sciences and healthcare
 - Share my enthusiasm for what is ahead of us

All grid applications described in this talk use gLite as grid middleware

Table of content

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- **Introduction**
- **Grid added value for large scale computing**
 - Example: grid-enabled in silico drug discovery
- **Grid added value for distributed data management**
 - Example: cancer surveillance network
- **Grid added value for dynamic data analysis**
 - Example: avian flu surveillance
- **Conclusion**

Grid services have made huge progresses

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- **Distributed computing has been available for 5 years for scientific production**
 - ☺ : access to very large number of CPUs (>20.000 for biomed Virtual Organization)
 - ☺ : web service APIs lead to improved interoperability (EGEE, OSG, Digital Ribbon, ...)
 - ☹: job efficiency and resource stability are still a problem
 - ☹: MPI is still available on a limited number of clusters (<10% of CPUs on EGEE biomed VO)
- **Distributed data management has recently become available (AMGA, iRODS)**
 - ☺: secured access
 - ☺: easy installation
 - ☺: good performances
 - ☹: critical mass of developers for software maintenance and evolution

What can I do with these services I could not do before ?

- **Possibility to scale up by one or two orders of magnitude the volume of computations**
 - On demand access to > 20.000 CPU cores instead of cluster
 - Freedom to think big
- **Use cases**
 - Protein structure computations (e-NMR)
 - From docking 1000 drug-like molecules to testing all the compounds currently available on market
 - From updating monthly to updating daily a molecular biology database
 - From studying the impact of single DNA mutations (SNPs) to multiple correlated mutations (Haplotypes) on diseases

Genome Wide Haplotype analyses of human complex diseases with the EGEE grid

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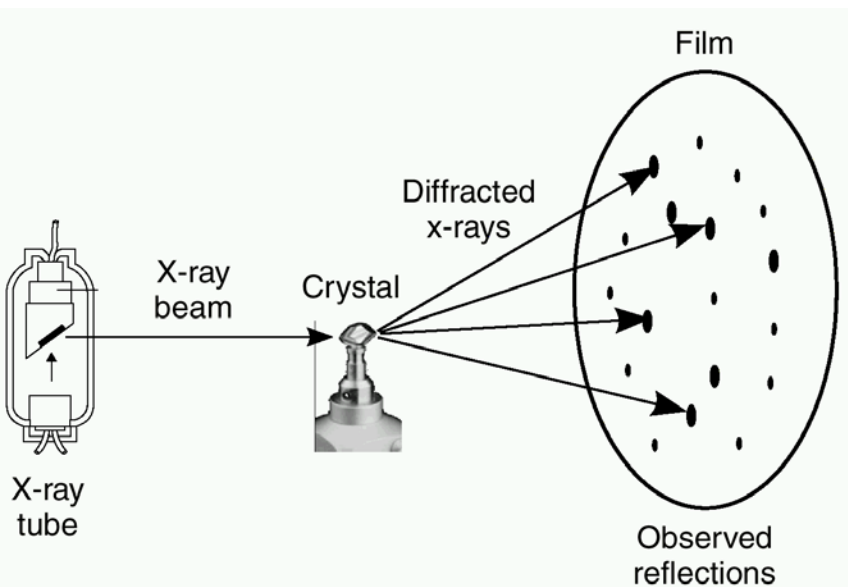
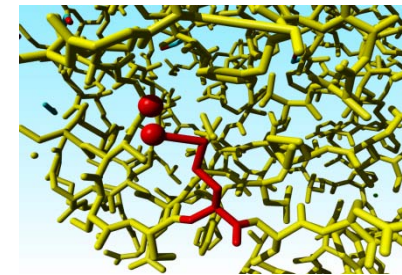
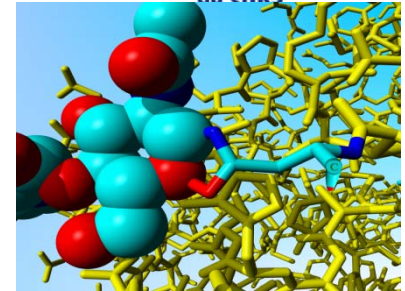
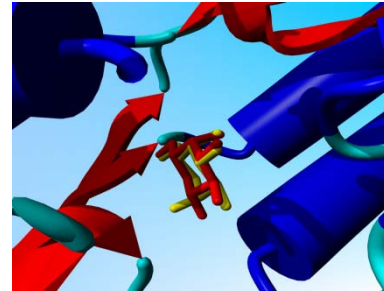
- **Goal: study the impact of DNA mutations on human coronary diseases**
- **Very CPU demanding analysis to study the impact of correlated (double, triple) DNA mutations**
- **Deployment on EGEE Grid**
 - 1926 CAD (Coronary Artery Diseases) patients & 2938 healthy controls
 - 378,000 SNPs (Single Nucleon Polymorphisms = local DNA mutations)
 - 8.1 millions of combinations tested in less than 45 days (instead of more than 10 years on a single Pentium 4)
- **Results published in *Nature Genetics* March 2009 (D. Tregouet et al)**
 - Major role of mutations on chromosome 6 was confirmed

Application: recalculating protein 3D structures in PDB

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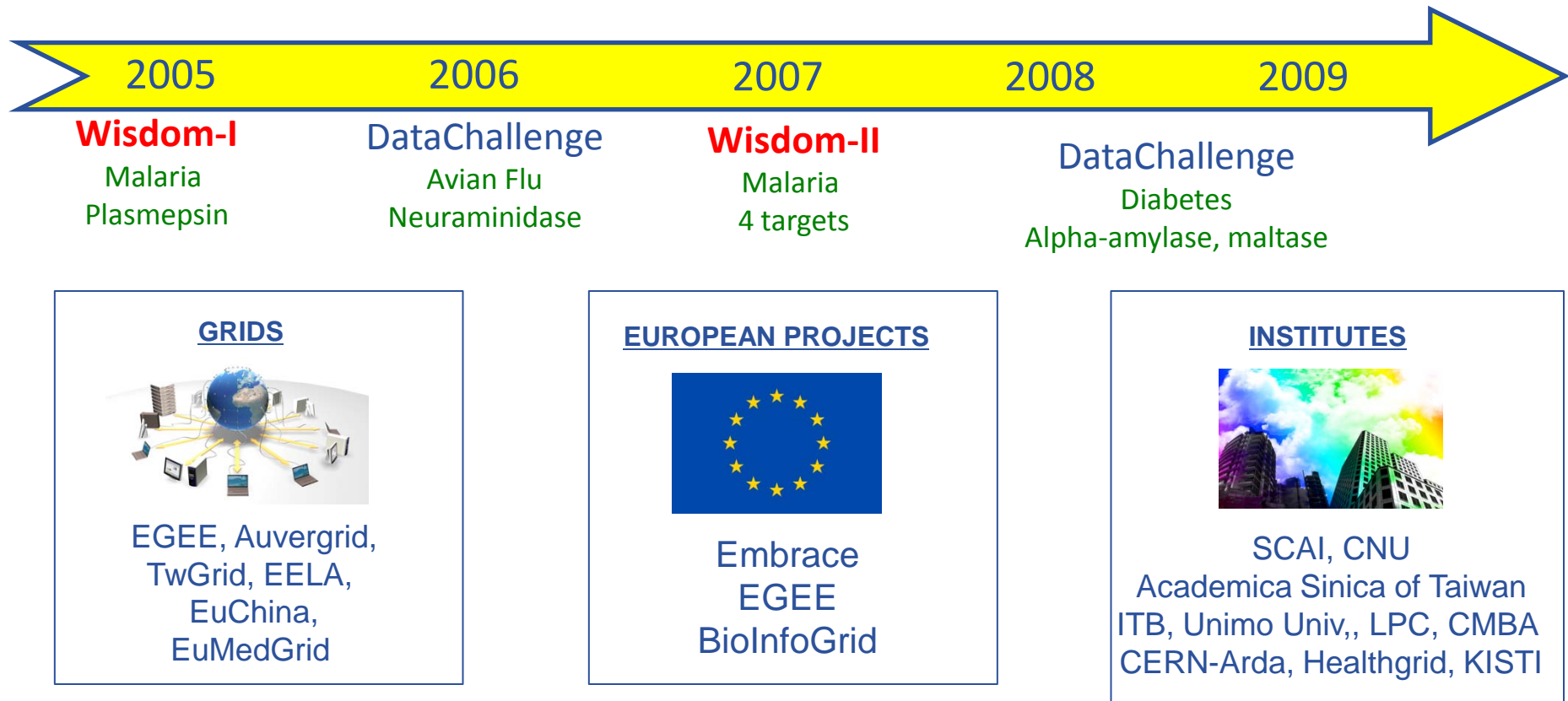
- The PDB data base gathers publicly available 3D protein structures
 - Full of bugs
- Goal: redo the structures by recalculating the diffraction patterns



PDB-files	42.752
X-ray structures	36.124
Successfully recalculated	~36.000
Improved R-free	12.500/17000
CPU time estimate	21.7 CPU years
Real time estimate	1 month on Embrace VO on EGEE

R.P Joosten et al, Journal of Applied Crystallography, (2009) 42, 1-9

WISDOM (World-wide In Silico Docking On Malaria) is an initiative aiming to demonstrate the relevance and the impact of the grid approach to address drug discovery for neglected and emerging diseases.



WISDOM partners

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LPC Clermont-Ferrand:
Biomedical grid

CEA, Acamba project:
Biological targets,
Chemogenomics

HealthGrid:
Biomedical grid,
Dissemination

Univ. Los Andes:
Biological targets,
Malaria biology

Univ. Pretoria:
Bioinformatics,
Malaria biology

SCAI Fraunhofer:
Knowledge extraction,
Chemoinformatics

Univ. Modena:
Biological targets,
Molecular Dynamics

ITB CNR:
Bioinformatics,
Molecular modelling

KISTI
Grid technology

Chonnam Nat. Univ.
In vitro tests

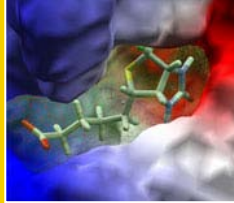
Academica Sinica:
Grid user interface

Grid-enabled *in silico* drug discovery

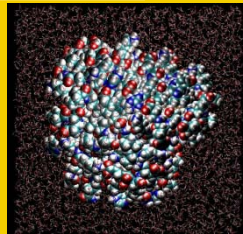
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FLEXX/
AUTODOCK



AMBER



1 Million drug-like chemical compounds

Molecular docking

10.000 drug-like compounds

Molecular dynamics

1000 drug-like compounds

Complex
visualization

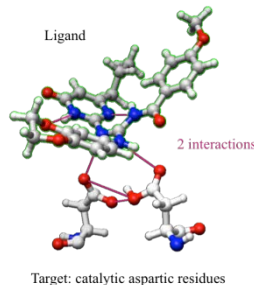
100 drug-like compounds

in vitro tests

in vivo tests

20%
success
rate for in
vitro
tests

CHIMERA



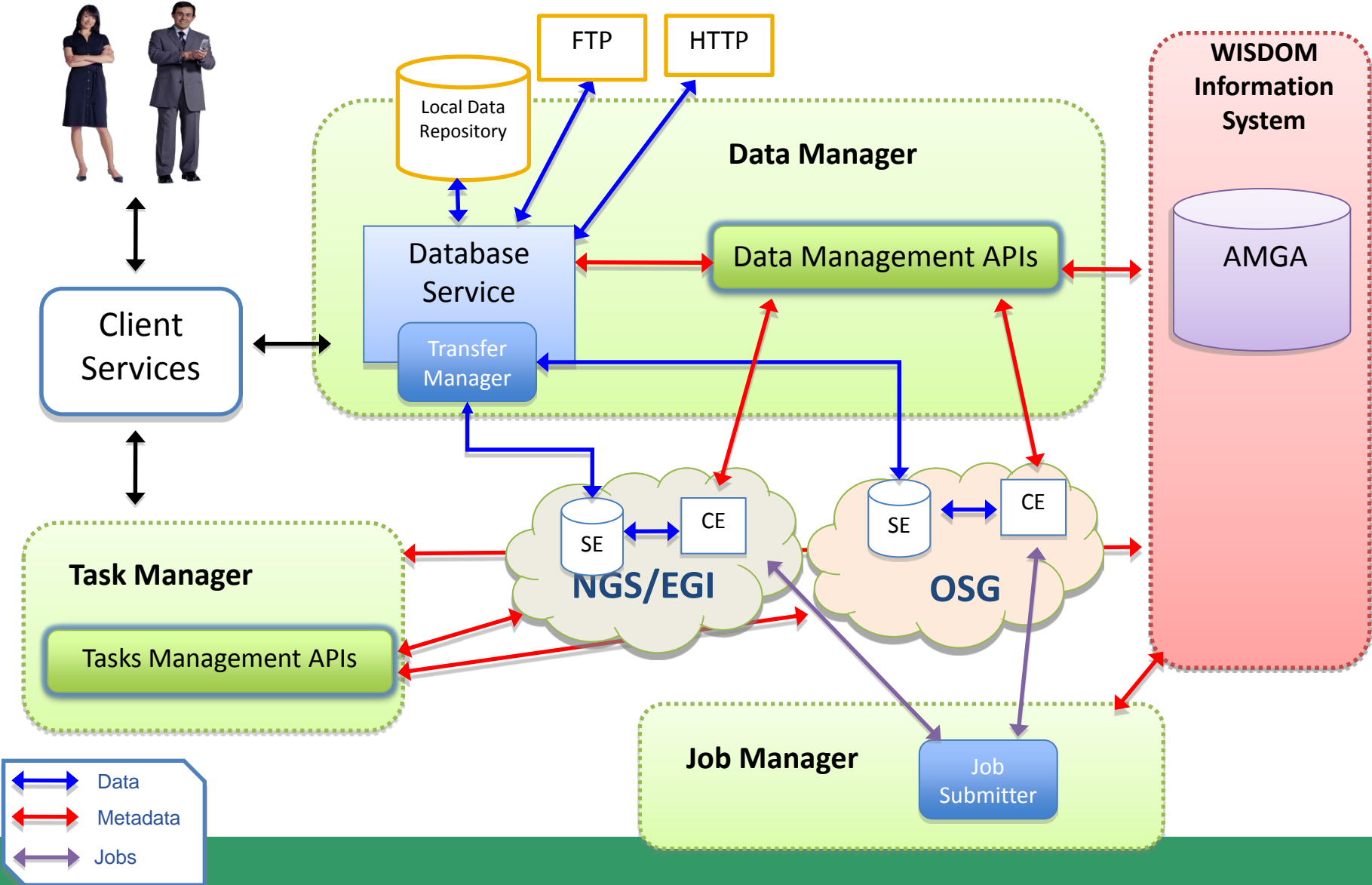
WET LABORATORY



Cost for *in silico*
experiment:
100 CPU Years
Cost for in vitro
tests:
1-10\$ per
compound

WISDOM production environment

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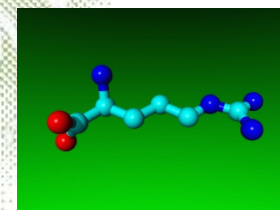
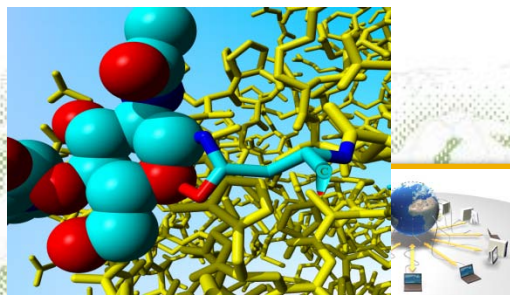


Discovering new drugs in Vietnam

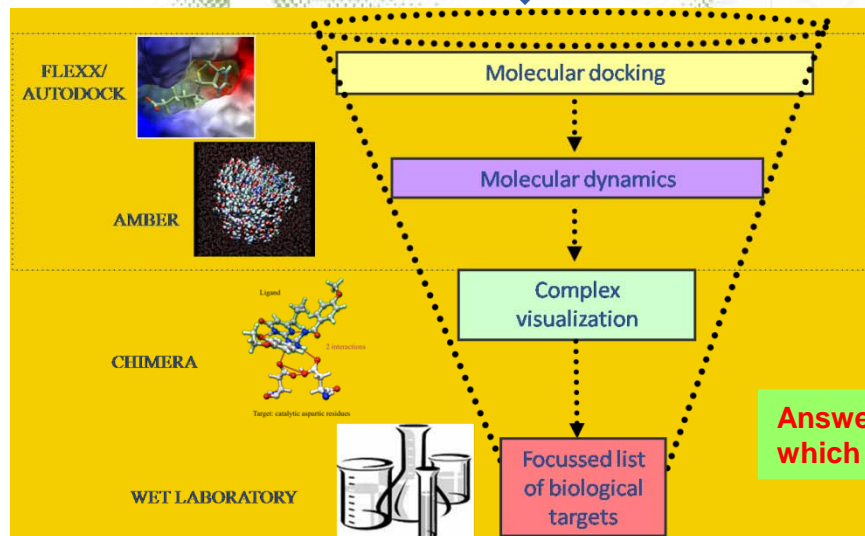
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PDB database
> 50.000 3D structures
including biological targets
for cancer, malaria, AIDS...



Question: are these products
potentially
active against cancer, malaria,
AIDS ?



Hanoi
INPC

Local DataBase of
Natural chemical
products extracted
from local
biodiversity

Answer: focussed list of biological targets on
which the compound is most active *in silico*

Share my data while keeping them !

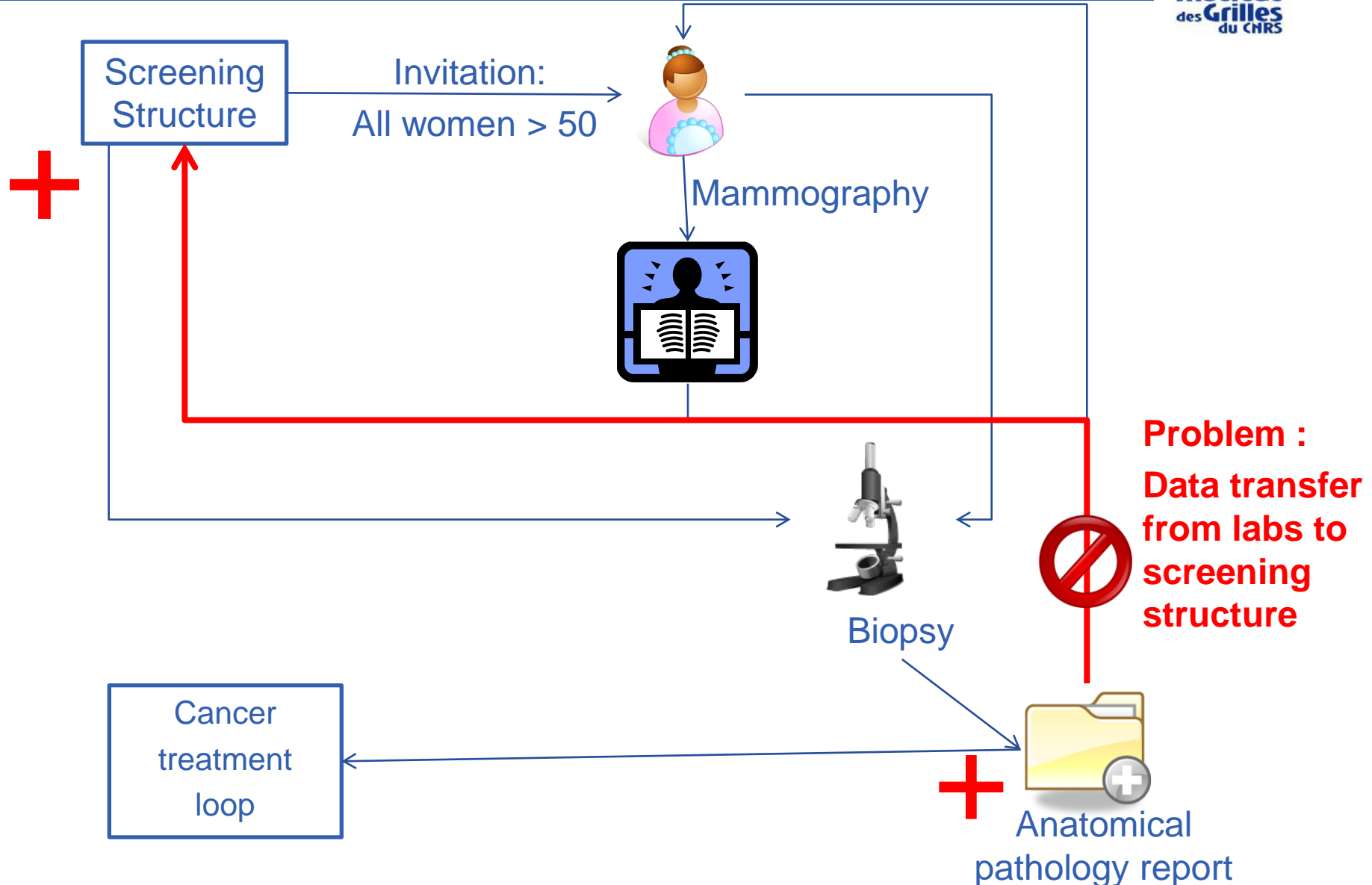
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- **Share securely data without having to put them in a central repository**
 - Data are left where they are produced
 - Authorized users have a customized view of a subset of the data
 - Data owners keep a full control of their data
- **Use cases**
 - Federation of mammography databases (MammoGrid) to improve cancer detection
 - Federation of brain medical image databases (BIRN, NeuroLog, NeuGrid) for neurosciences

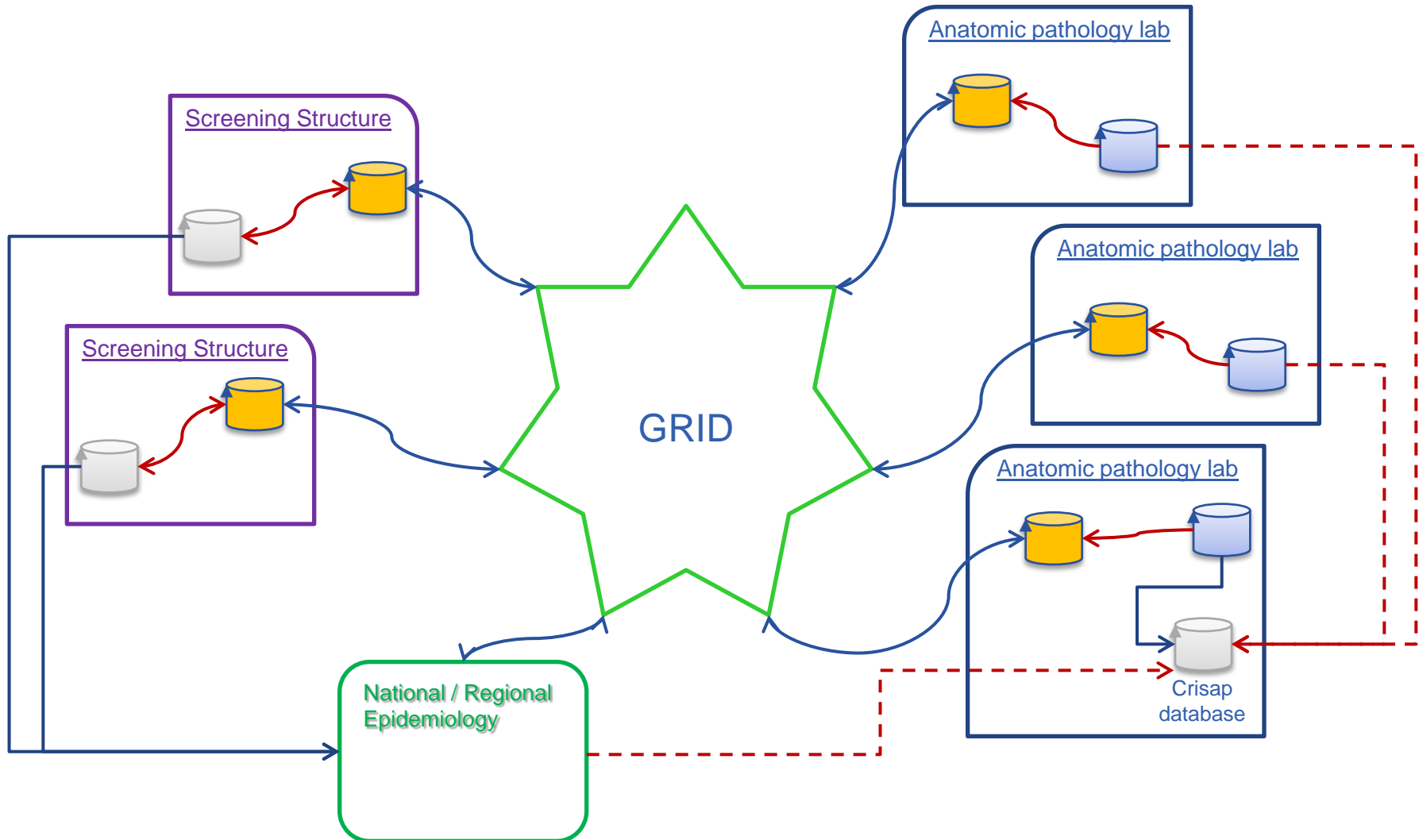
Breast cancer screening

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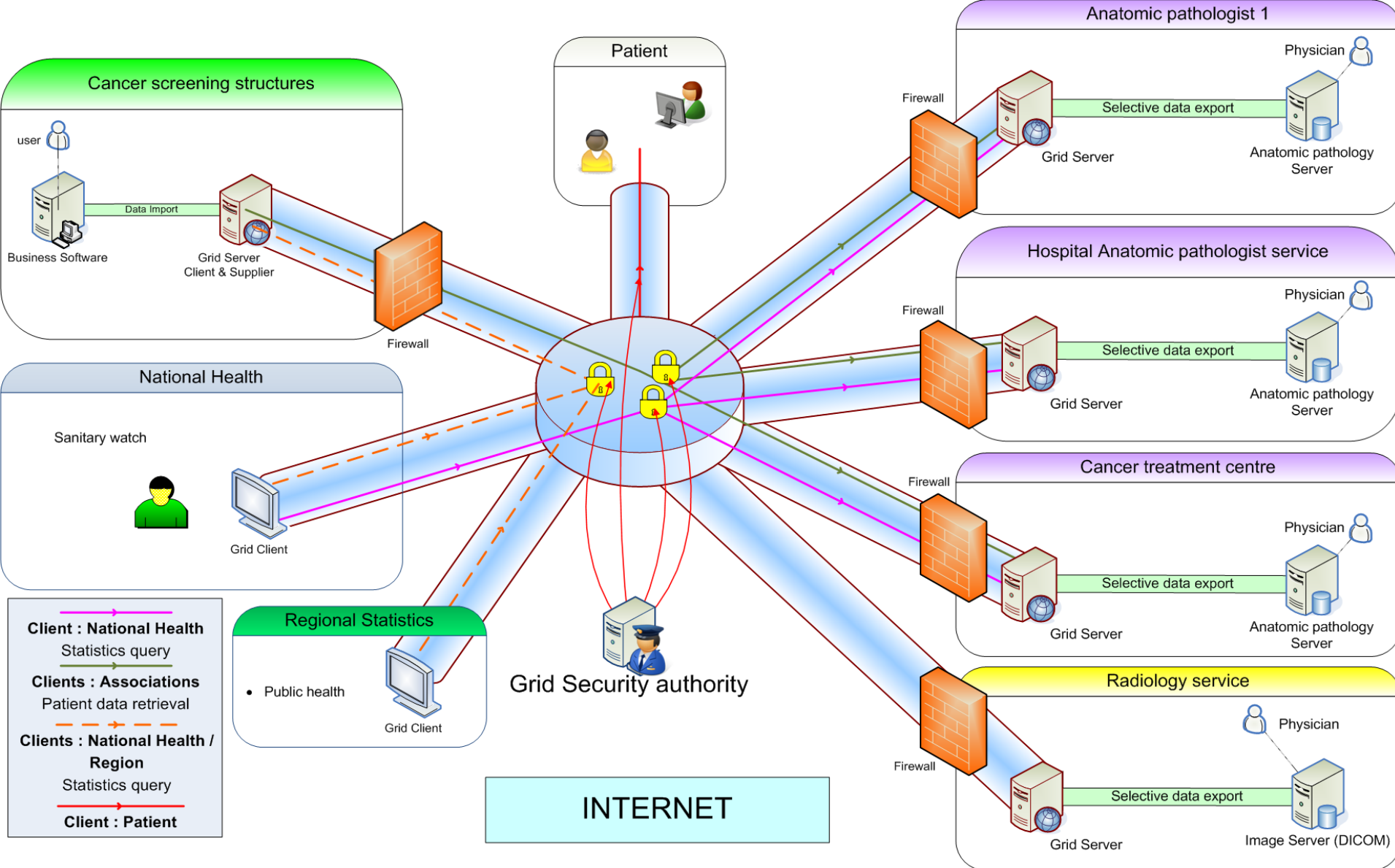
Sentinel network

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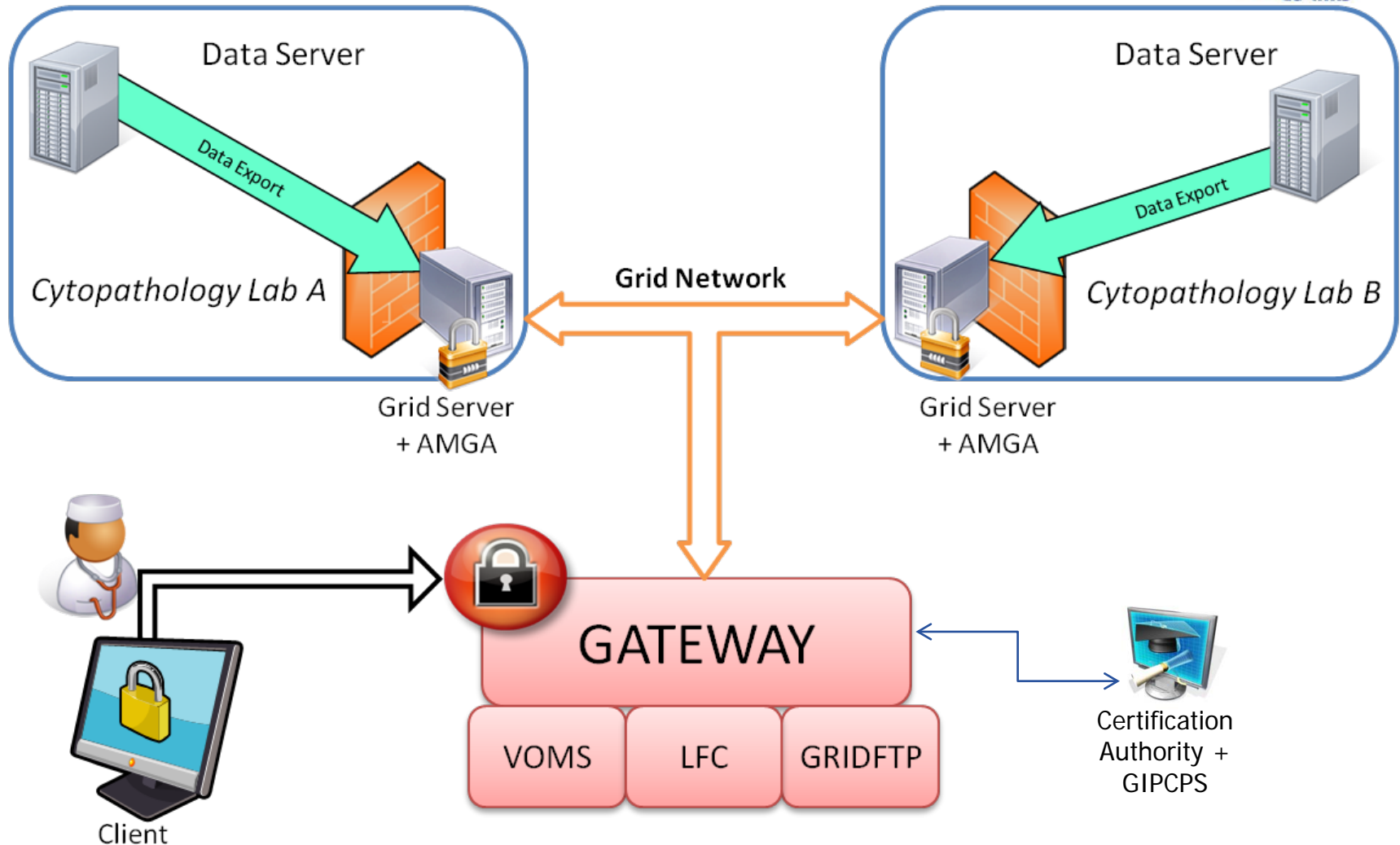
Architecture

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Technical architecture

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*Grid-enabled sentinel network for cancer surveillance,
Proceedings of Healthgrid conference 2009
Studies in Health Technology and Informatics*

Collaboration: CNRS – MAAT - RSCA

- **Coupling of grid data management and computing services allows continuous**
 - Data collection
 - Data analysis
 - Updated modeling
 - Towards decision making
- **Use cases**
 - Tsunami alert system
 - Flood alert system
 - Epidemiology

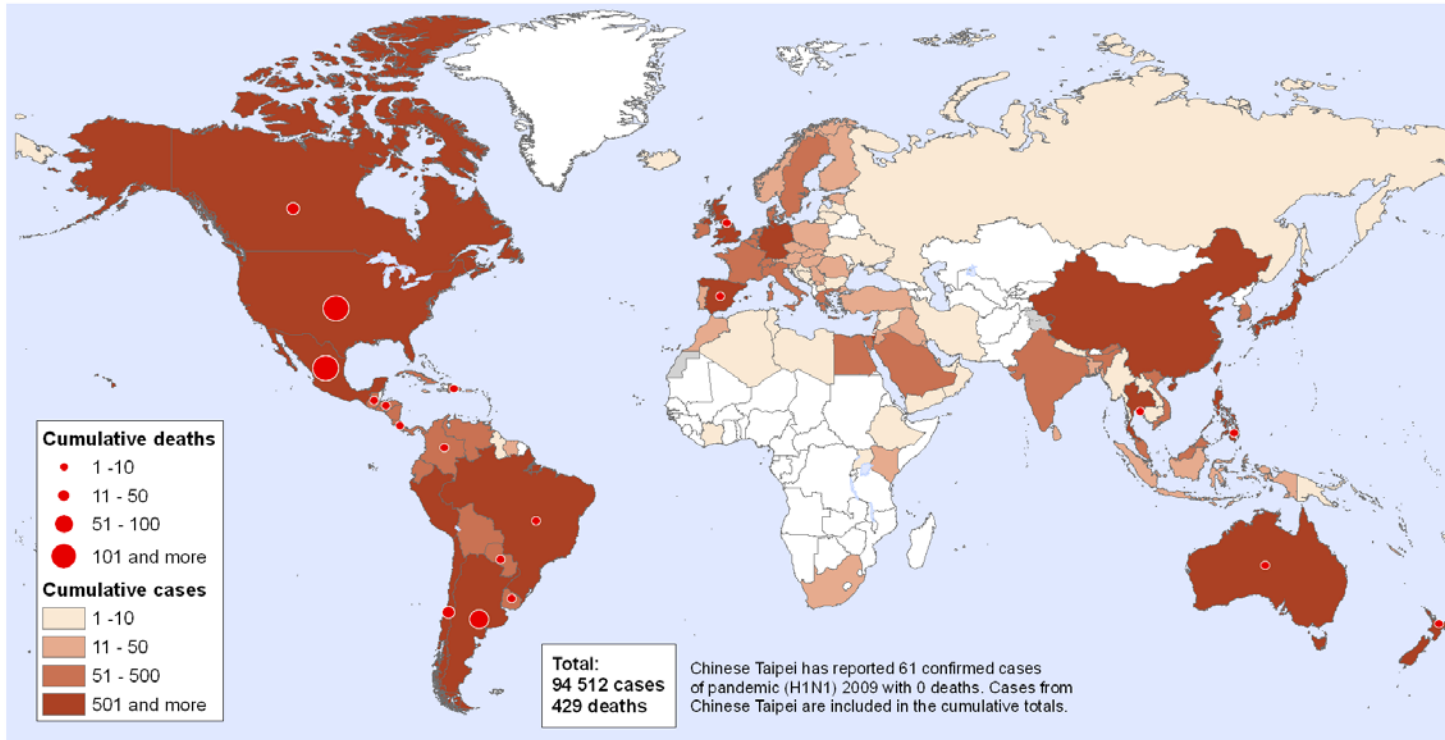
Grid-enabled influenza surveillance network

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Pandemic (H1N1) 2009,
Number of laboratory confirmed cases as reported to WHO

Status as of 06 July 2009
09:00 GMT



The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Map produced: 06 July 2009 09:00 GMT

Data Source: World Health Organization
Map Production: Public Health Information
and Geographic Information Systems (GIS)
World Health Organization



World Health
Organization

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> Is there a way to improve the response to emerging diseases using grids ?

> Elements for Epidemiologists

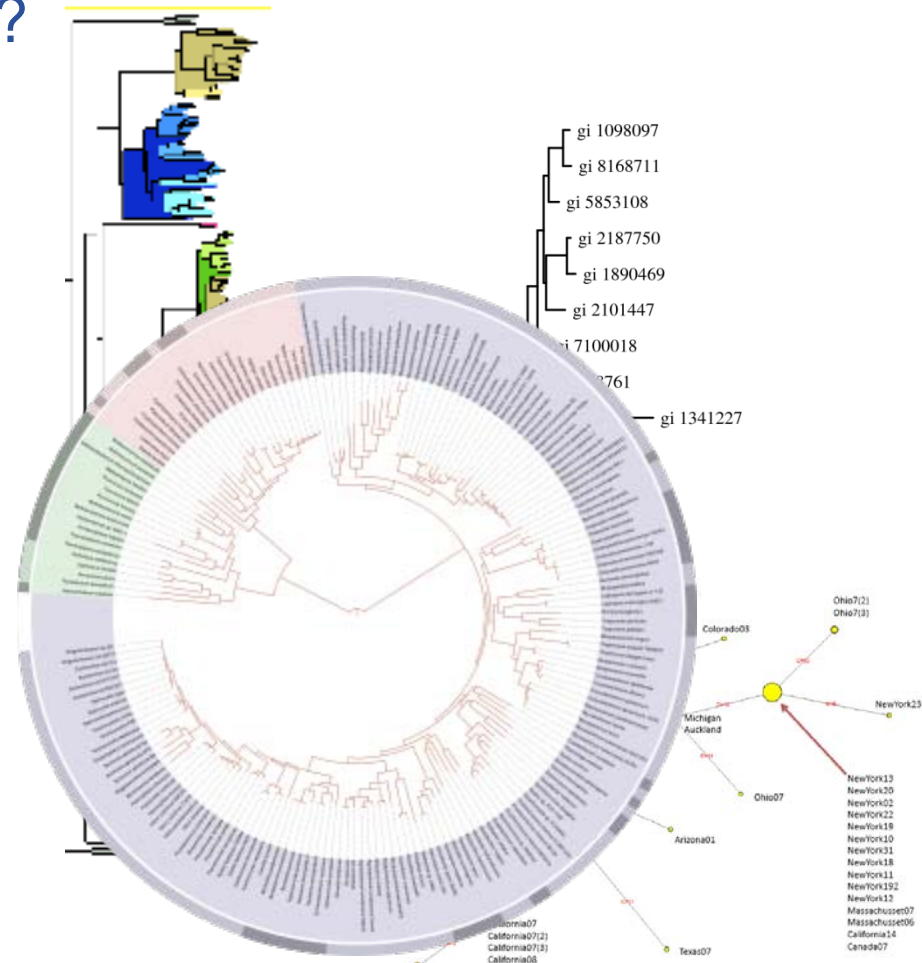
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- Where does the virus come from?
- How does the virus spread?
- How does the virus evolve?



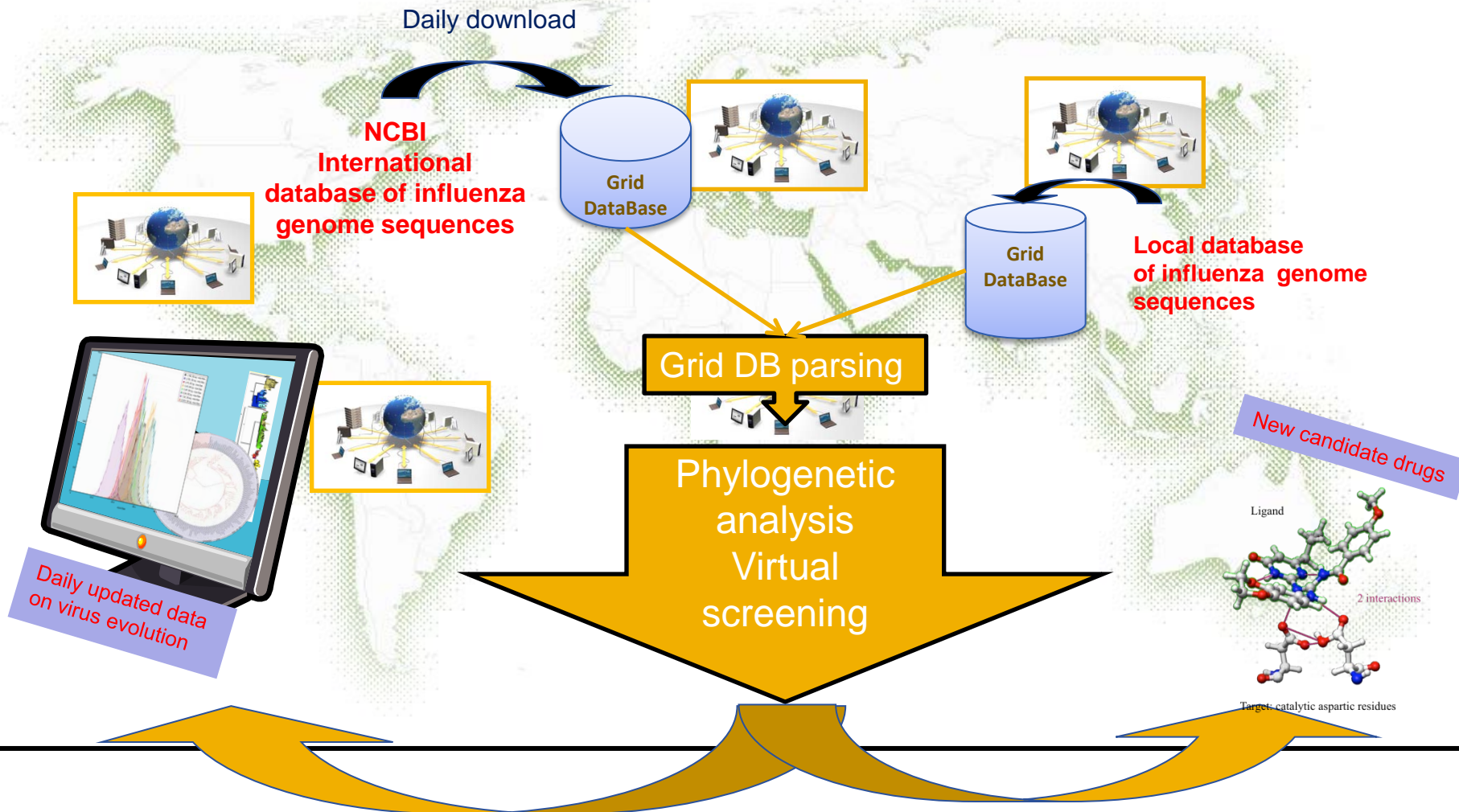
Epidemiologist



« The only way to track down a virus history
Is through its imprint on the viral genome »

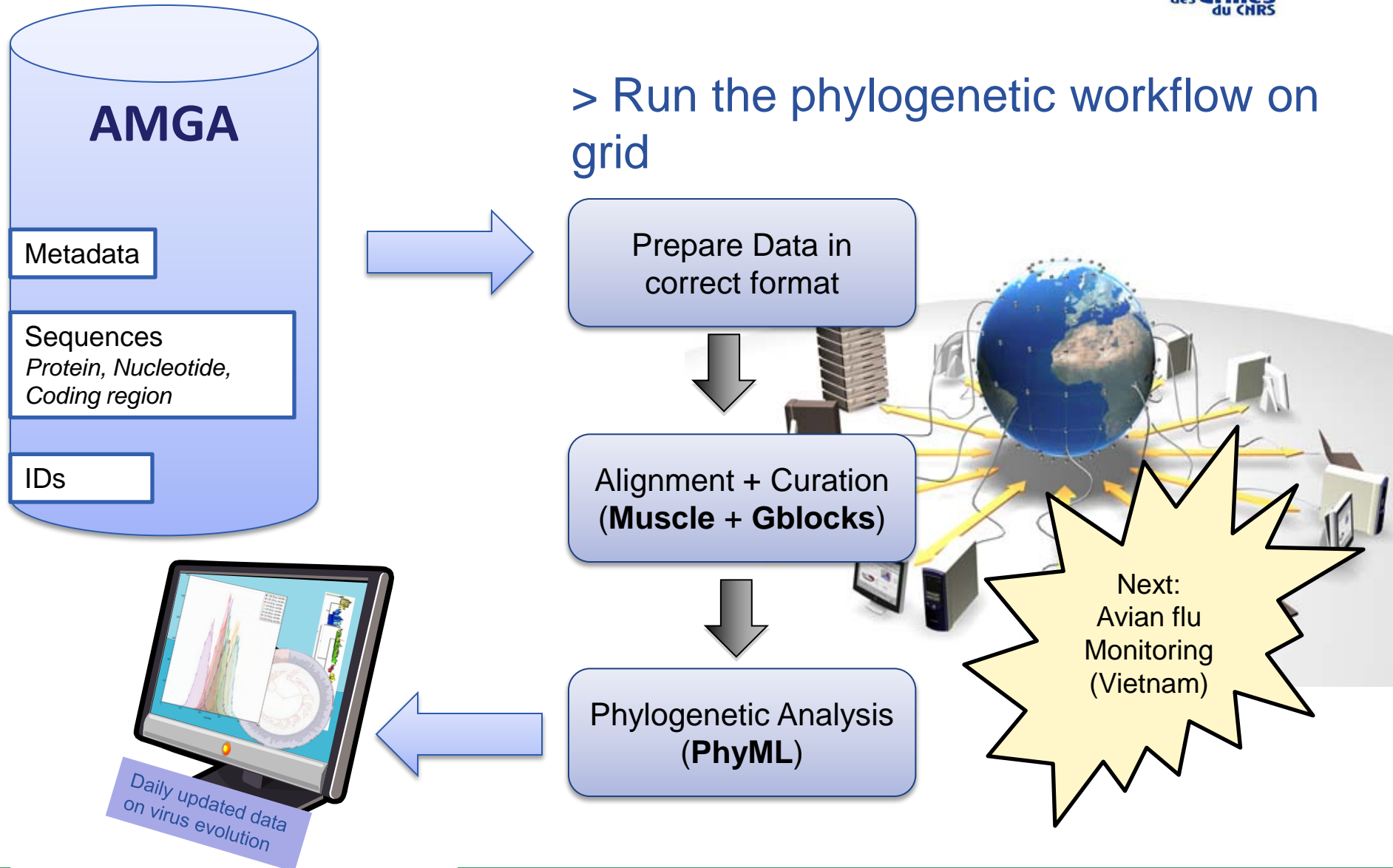
Monitoring the evolution of influenza viruses

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Molecular epidemiology pipeline to monitor influenza A virus

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- **Grid services are better than they have ever been**
 - Opportunities to do science differently or at a larger scale
- **Many opportunities for collaboration in the field of life sciences**
 - Virtual Screening
 - Surveillance networks (influenza)
- **HealthGrid conference 2010**
 - Paris, June 28-30 2010
 - Program-registration: <http://paris2010.healthgrid.org>