

# g-INFO portal

Doan Trung Tung

Aurélien BERNARD, Ana Lucia DA-COSTA, Vincent BLOCH,  
Thanh-Hoa LE, Yannick LEGRE, Lydia MAIGNE, Jean  
SALZEMANN, Hong-Quang NGUYEN, Vincent BRETON



# Outline

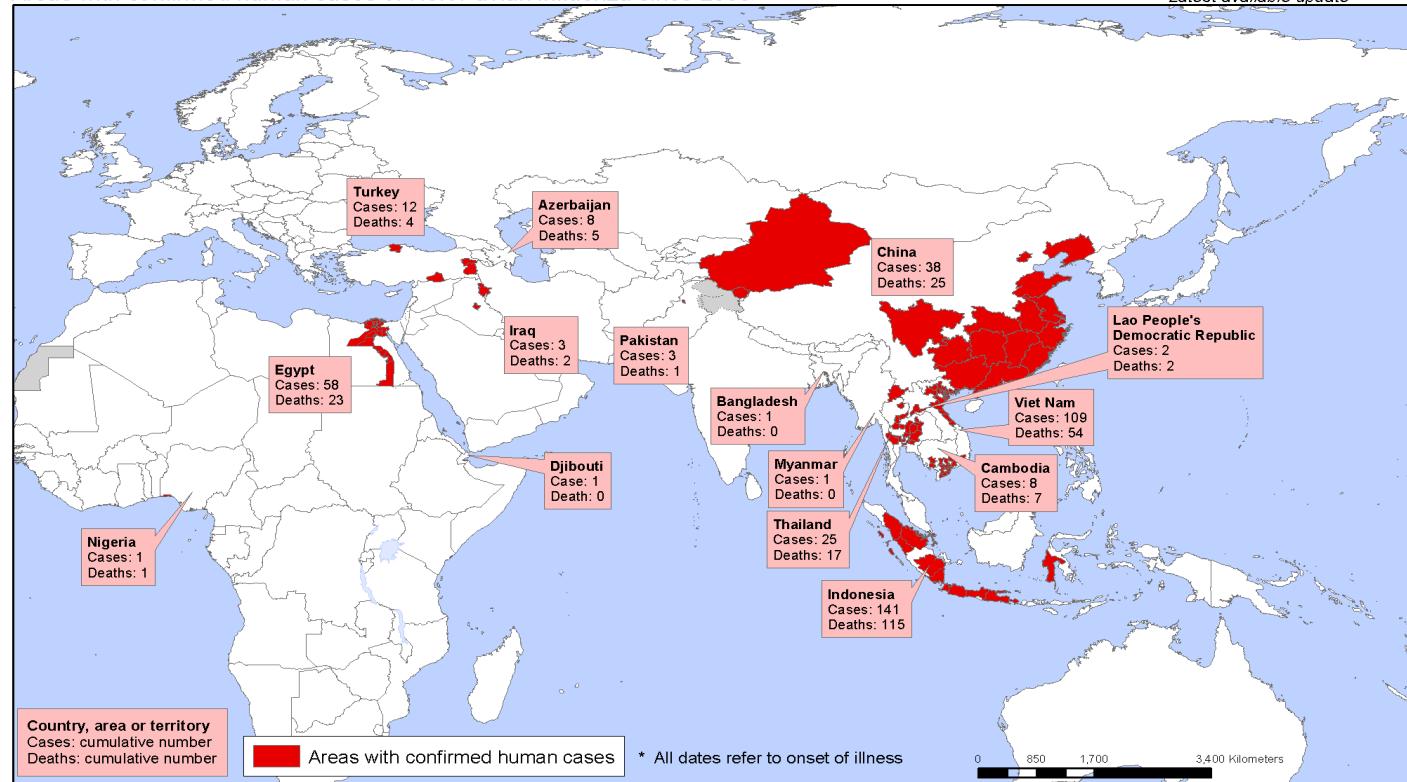
- ❖ Introduction
- ❖ Overview of g-INFO
- ❖ Implementation of g-INFO
- ❖ Conclusions and perspectives

# Why g-INFO?

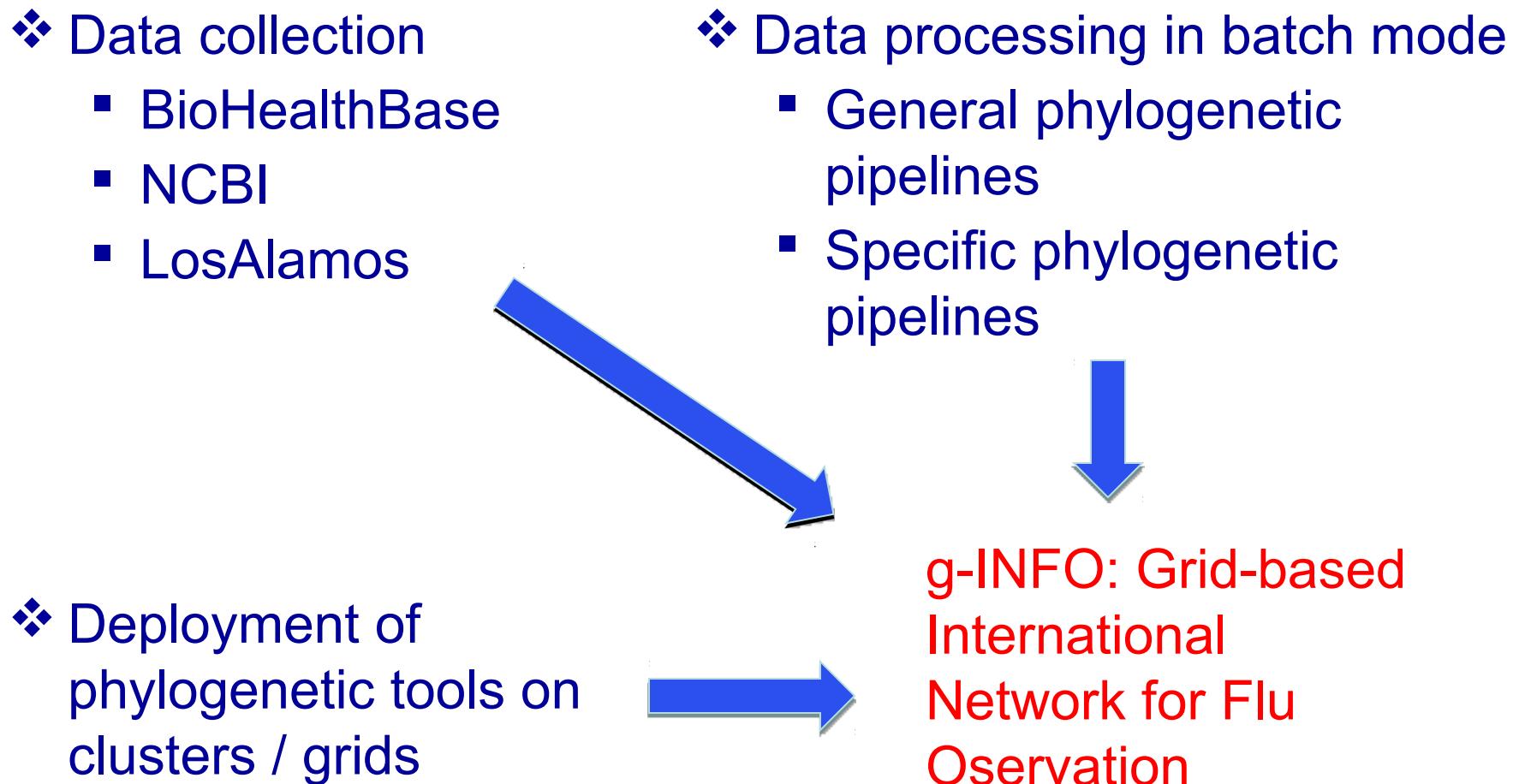
## ❖ H5N1 (avian flu)

Areas with confirmed human cases of H5N1 avian influenza since 2003 \*

Status as of 11 March 2009  
Latest available update



# Influenza surveillance

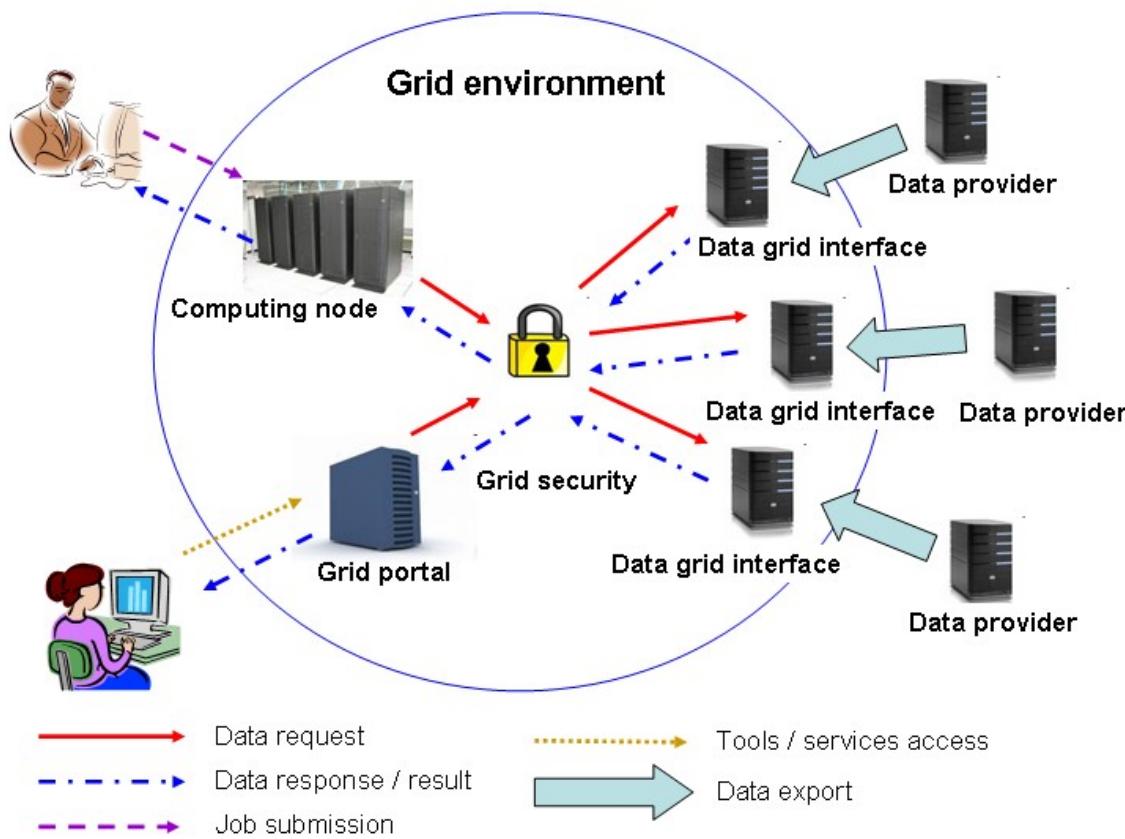


# **g-INFO's overview**

# g-INFO's goals

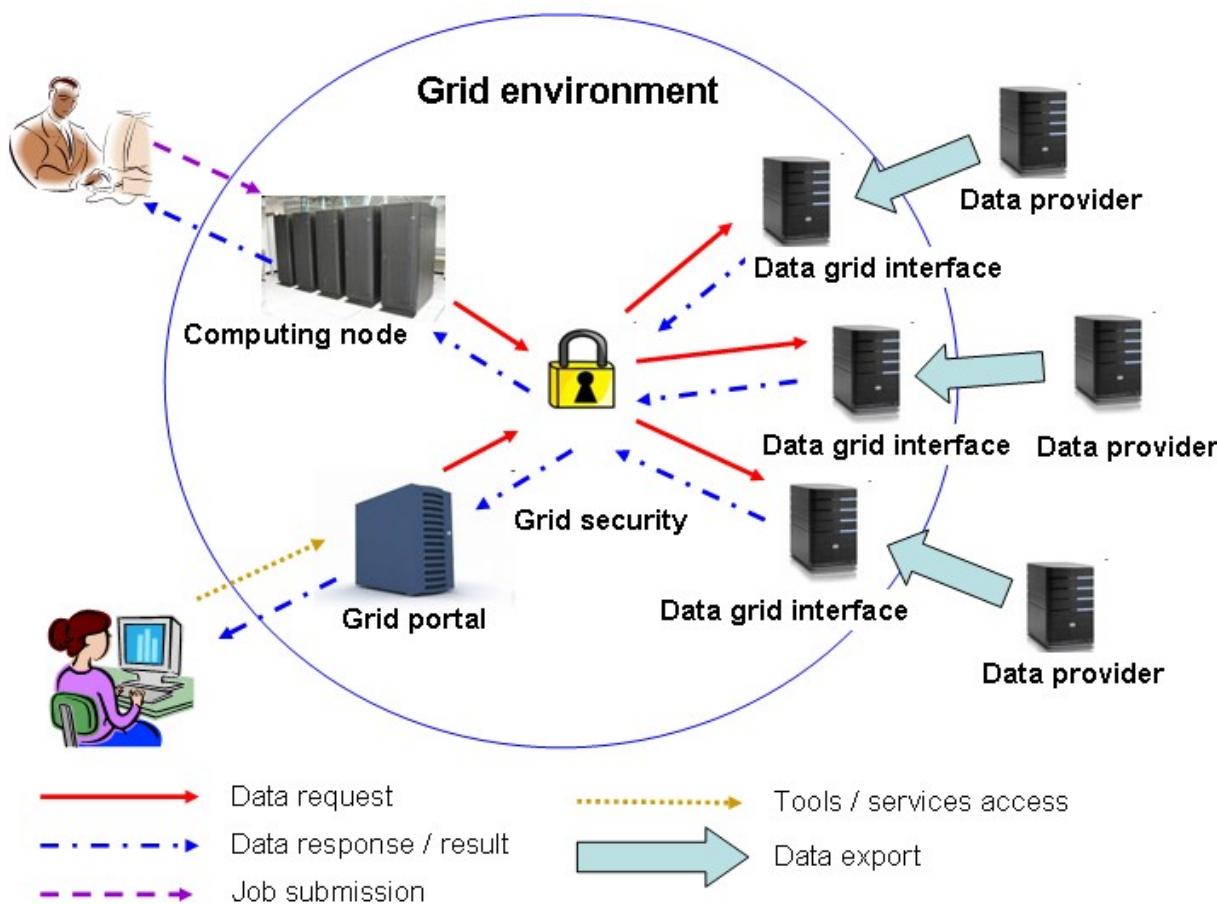
- ❖ Integration of influenza virus data sources into a federation of databases
- ❖ Automatic phylogenetic pipelines
- ❖ Specific molecular epidemiology studies

# Architecture of g-INFO system



- Each data provider has its own server(s) to store his data
- Data provider export only selected data to a data grid interface server
- The data exported is integrated in a common schema on the interface servers
- Providers can keep the privilege of granting access rights to their data

# Architecture of g-INFO system



- Epidemiologic pipelines will be deployed on the grid
  - ❖ BLAST
  - ❖ Alignment
  - ❖ Phylogenetic trees
  - ❖ Visualisation
  - ❖ ... and more

# g-INFO's implementation

# Data collection

>ABV25634

```
MKAILLVLLCAFAATNADTLCIGYHANNSTDVTDTVLEKNVTVTHSVNLLED SHNGKL CRLGGIAPLQLG  
KCNIAGWLLGNPEC DLLTVSSWSYIVETSNSDNGTCYPGFIDYEELREQLSSVSSFEKFEIFPKTSSW  
PNHETTRGVTAACP YAGASSFYRNLLWLVKKENSYPKLSKS YVNNKGKEVLV LWGVHHPTSTDQOSLYQ  
NADAYVSVGSSKYD RRFTEIAARP KVRGQAGR MNYYWTLL EPGDTITFEATGNLVAPRYA FALNRGSES  
GIITS DAPVHD CDTK CQT PHGAIN SLPF QNIHP VTIGECP KVKST KLRM VTLR NIPSI QSRGLFGAI  
AGFIEGGWTGLIDGWGYHHQNGQGSYAADQKSTQNAIDGITNKVN SIEKMNTQFTVVGKFNNLERR  
IKN LNKKVDDGF LDVWTYNAELL VLLENERTL DFHD SNVKN LYEKAR SQRNNAKEIGN GCFEFYHKCDD  
ACME SVRNGTYDYP KYSEES KLNREE IDGVKLES MMVYQILAIYSTVASS L VLLVSLGAISFWMC SNGSL  
QCRICI
```

## FTP NCBI

Index de <ftp://ftp.ncbi.nih.gov/genomes/INFLUENZA/updates/2009-07-16/>

Vers un rép. de plus haut niveau

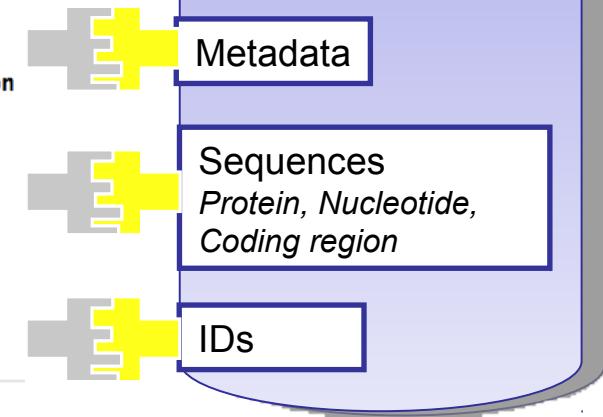
### Nom

- genomeset.dat
- influenza.cds
- influenza.dat
- influenza.faa
- influenza.fna
- influenza\_aa.dat
- influenza\_na.dat

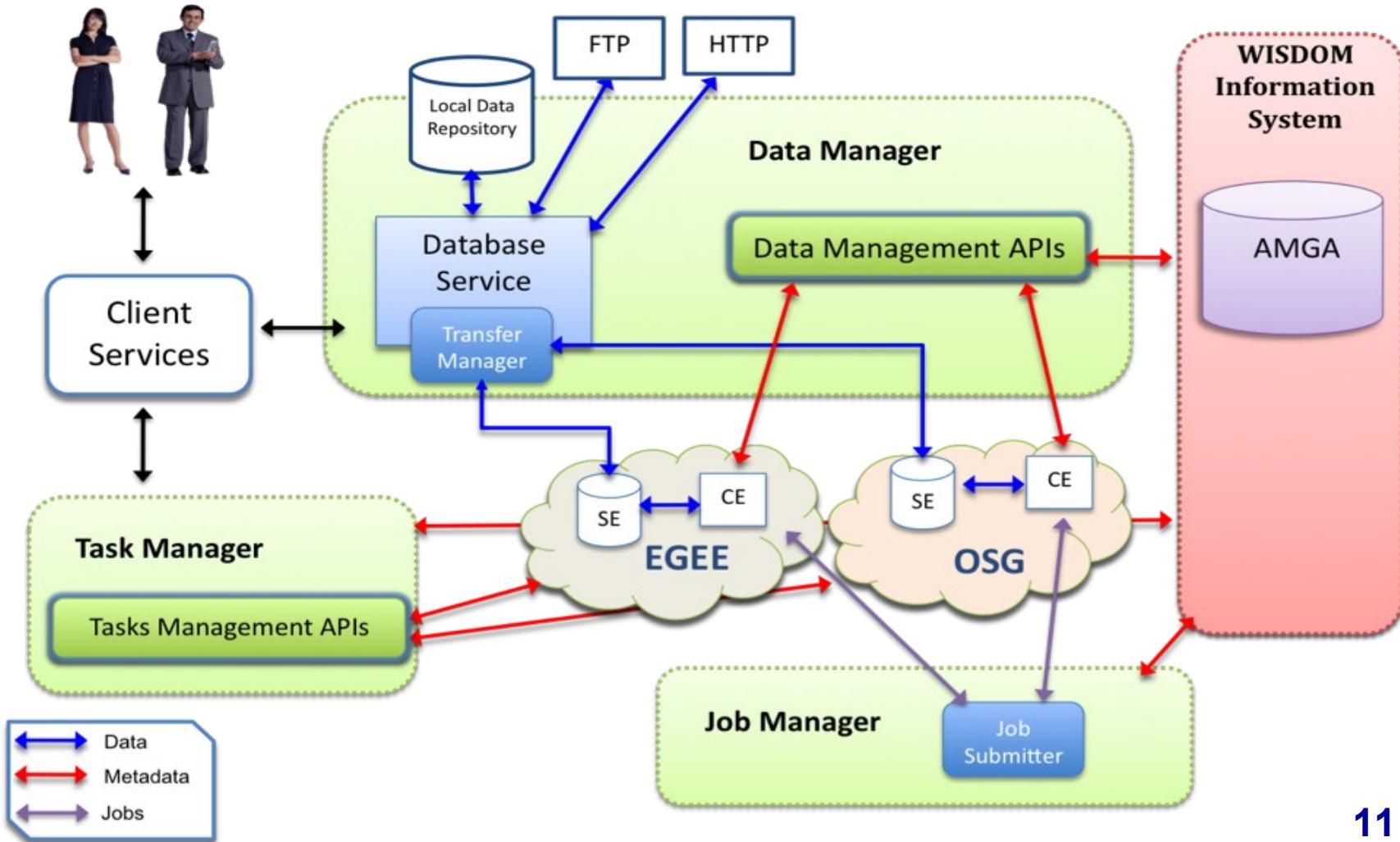


### Taille      Dernière modification

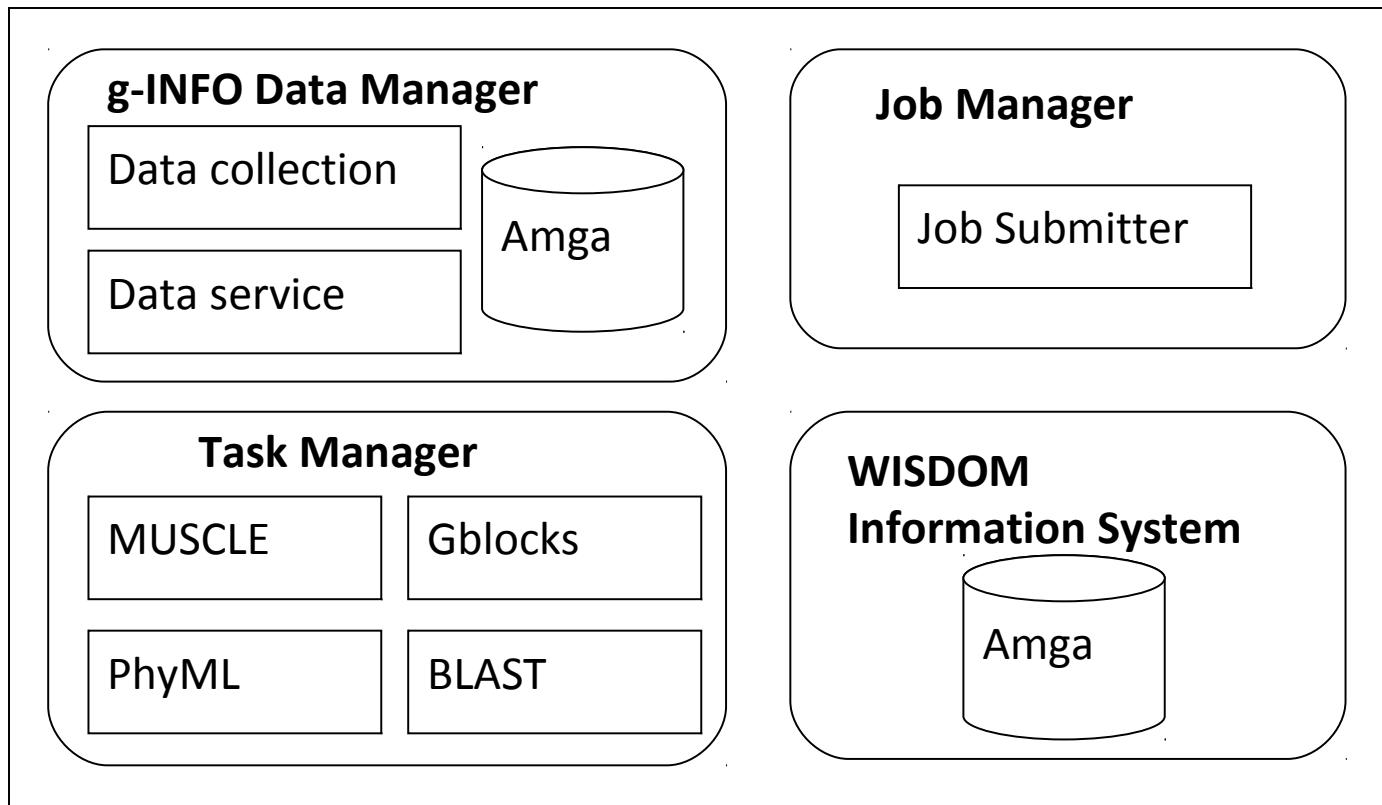
105 KB	16/07/09	08:04:00
5 KB	16/07/09	08:04:00
42 KB	16/07/09	08:04:00
97 KB	16/07/09	08:04:00
13 KB	16/07/09	08:04:00
9 KB	16/07/09	08:04:00



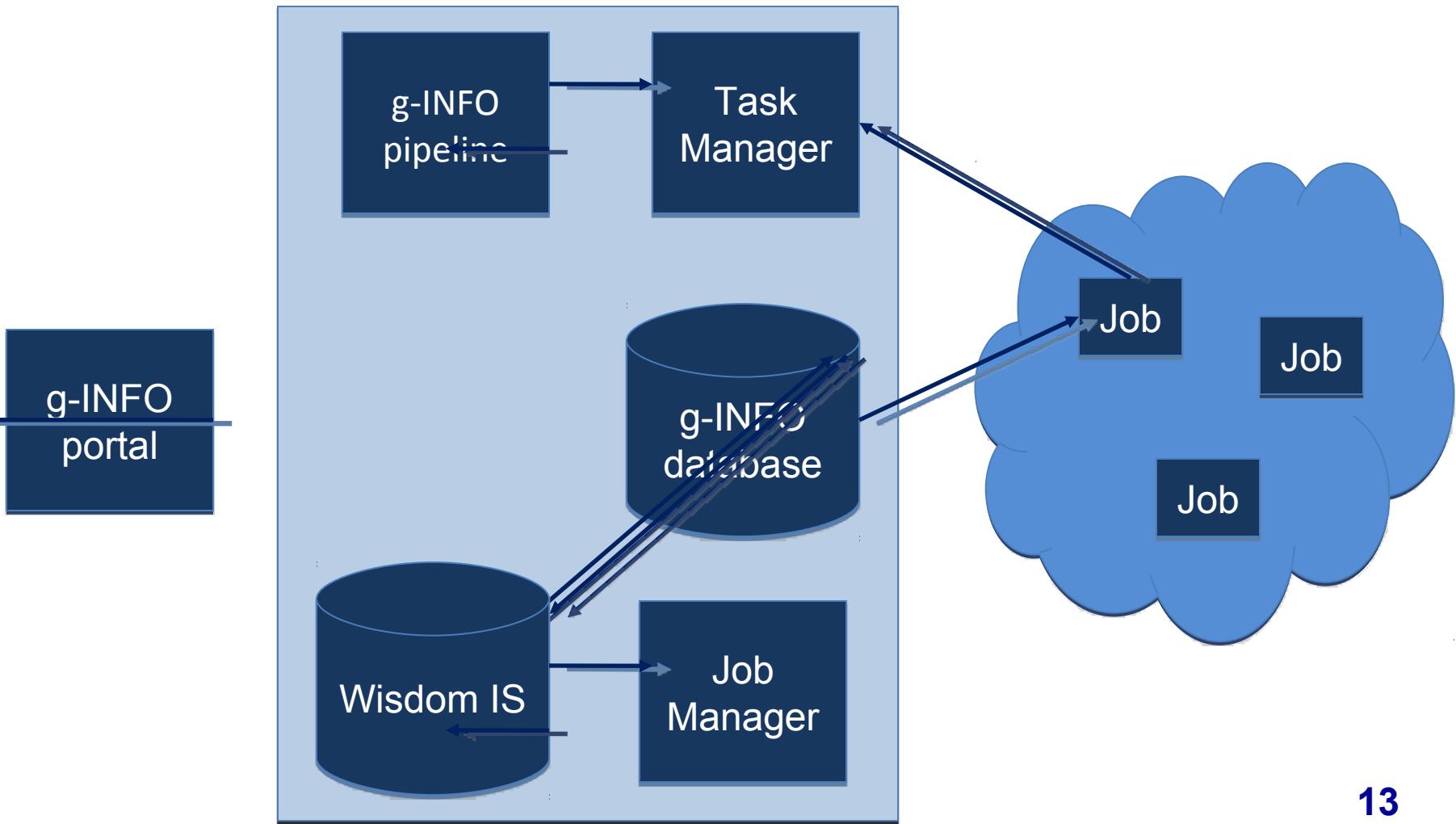
# WISDOM Production Environment



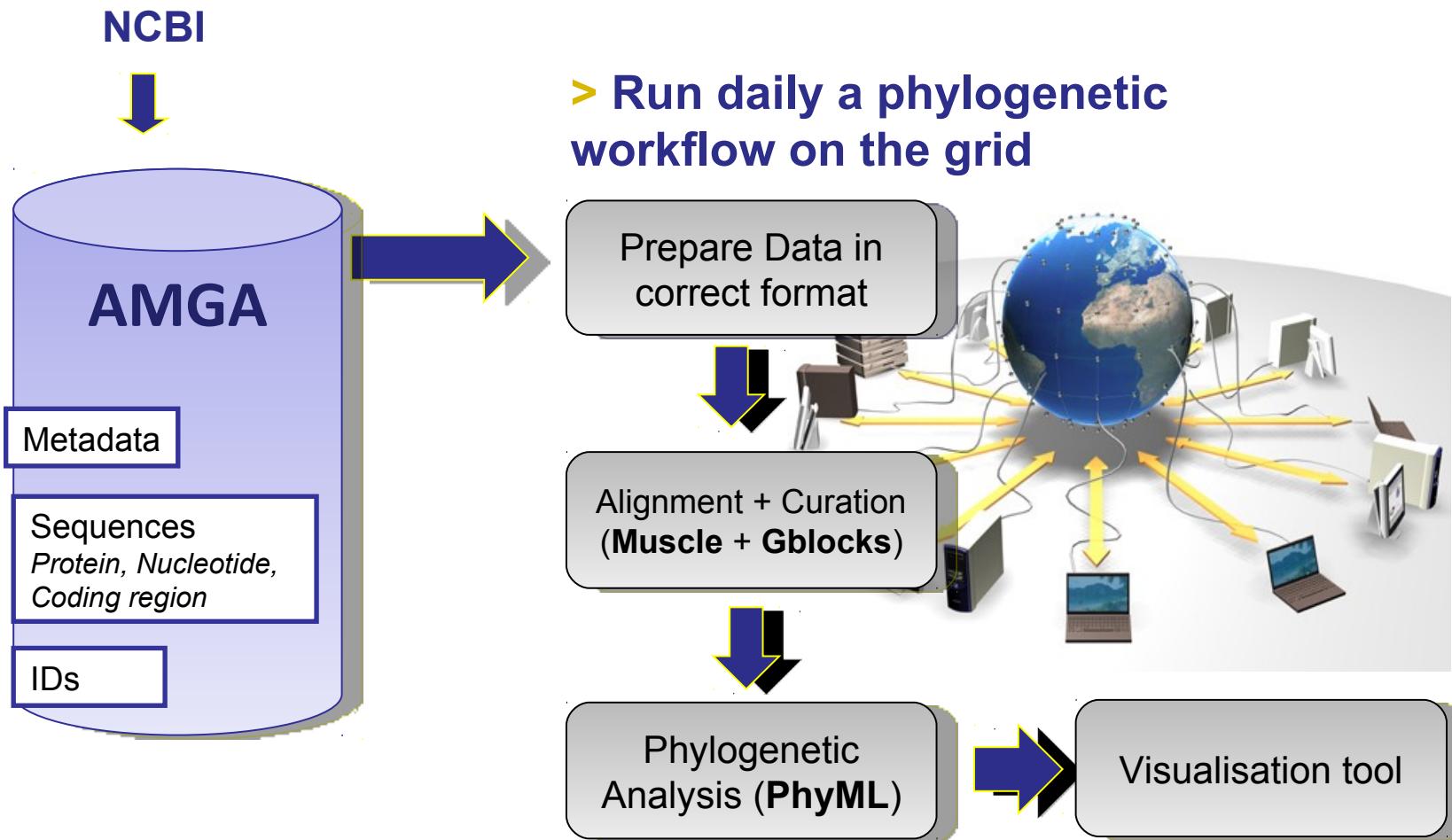
# Integration of g-INFO into WPE



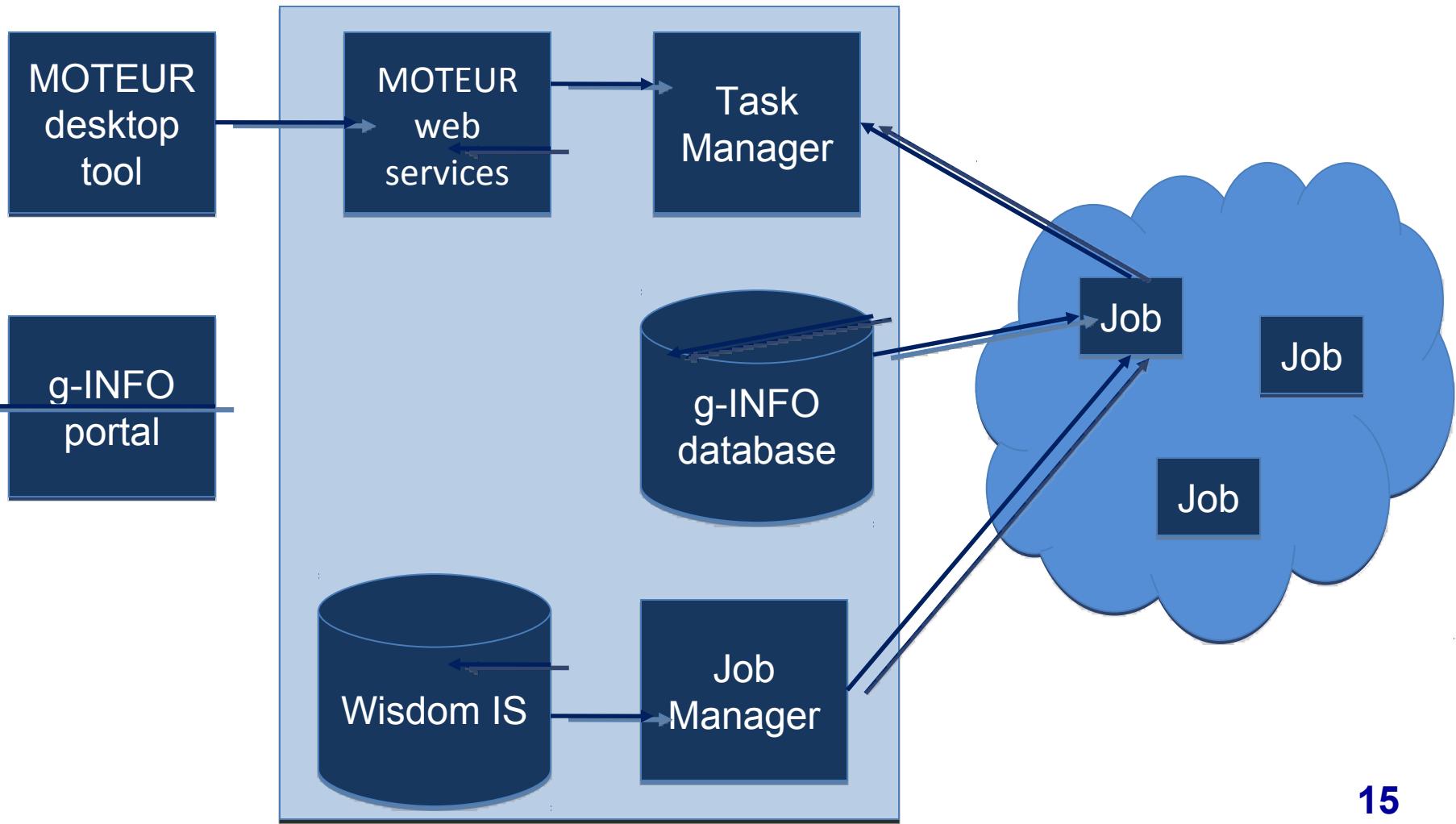
# Automatic phylogenetic pipeline



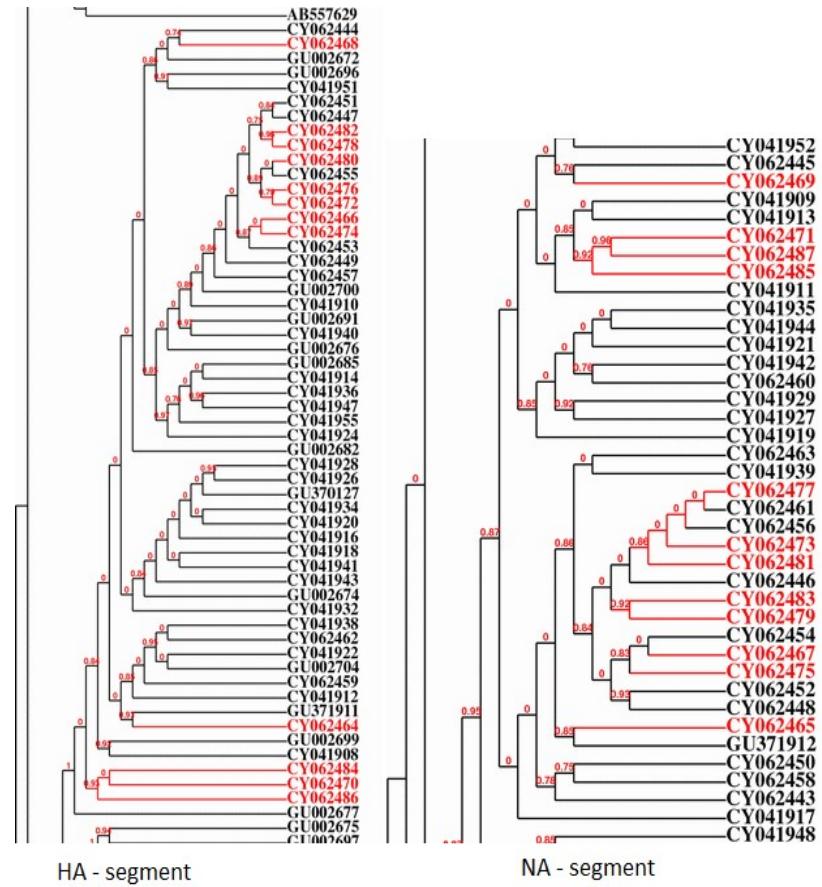
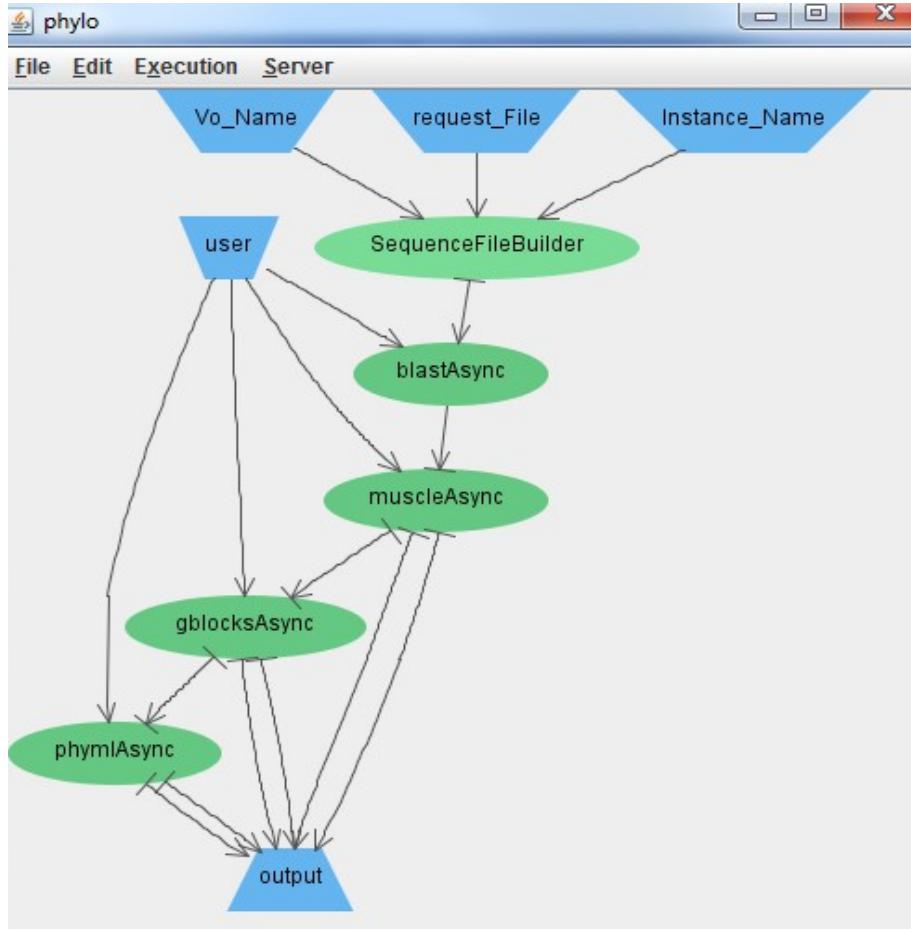
# Automatic phylogenetic pipeline



# Manual phylogenetic workflow



# Workflow execution example

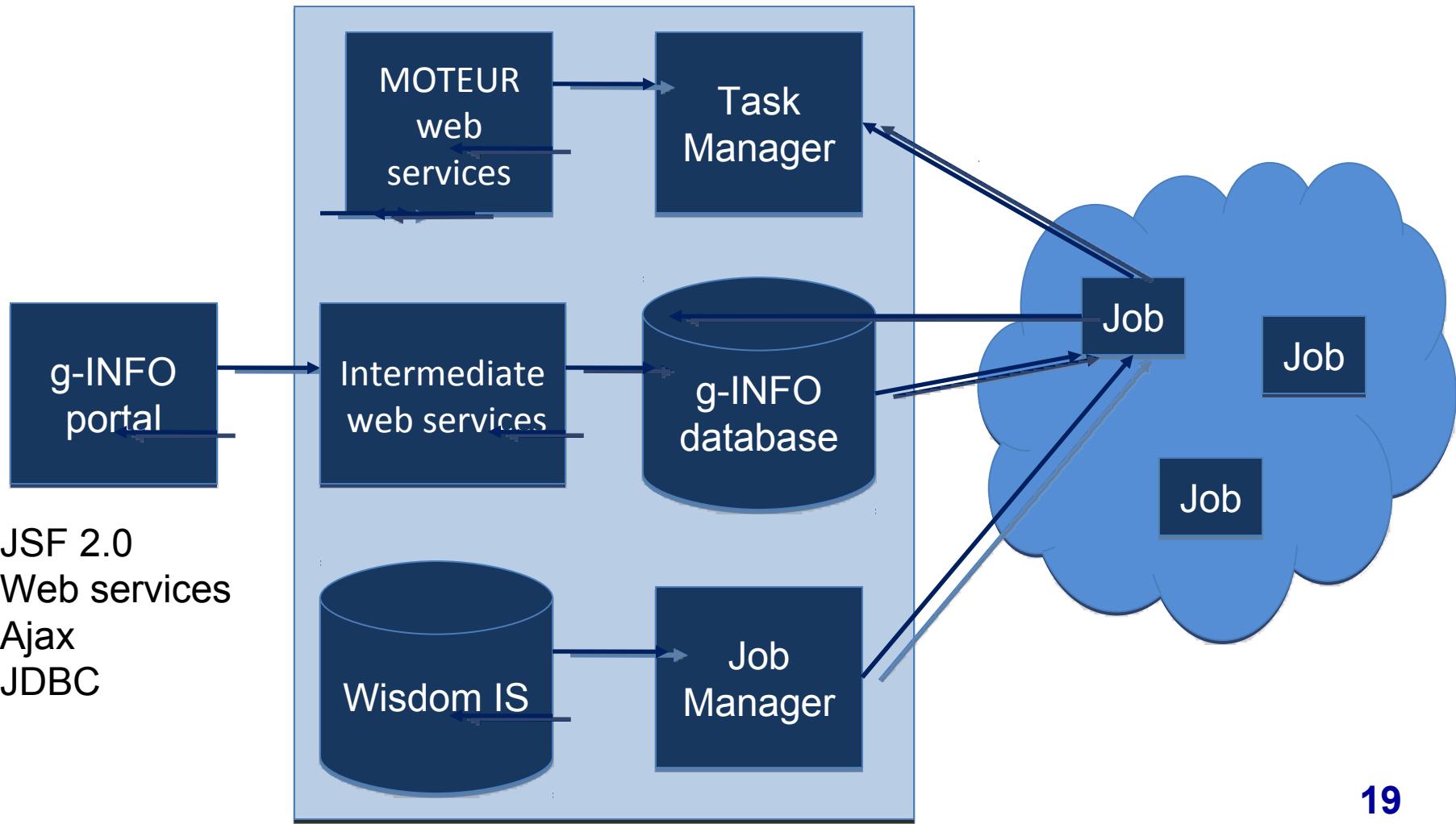


# **g-INFO portal**

# g-INFO portal

- ❖ Collaboration among IFI, IOIT and HPC:
  - ❖ IFI: web services to interact between the portal and the system
  - ❖ IOIT: design and develop the portal
  - ❖ HPC: visualization tool
- ❖ Technologies:
  - ❖ JSF 2.0, Ajax, web services, Java applet, ...

# g-INFO portal



# g-INFO portal – home page

grid-based  
International  
Network for  
Flu  
Observation

**g-INFO: Home**

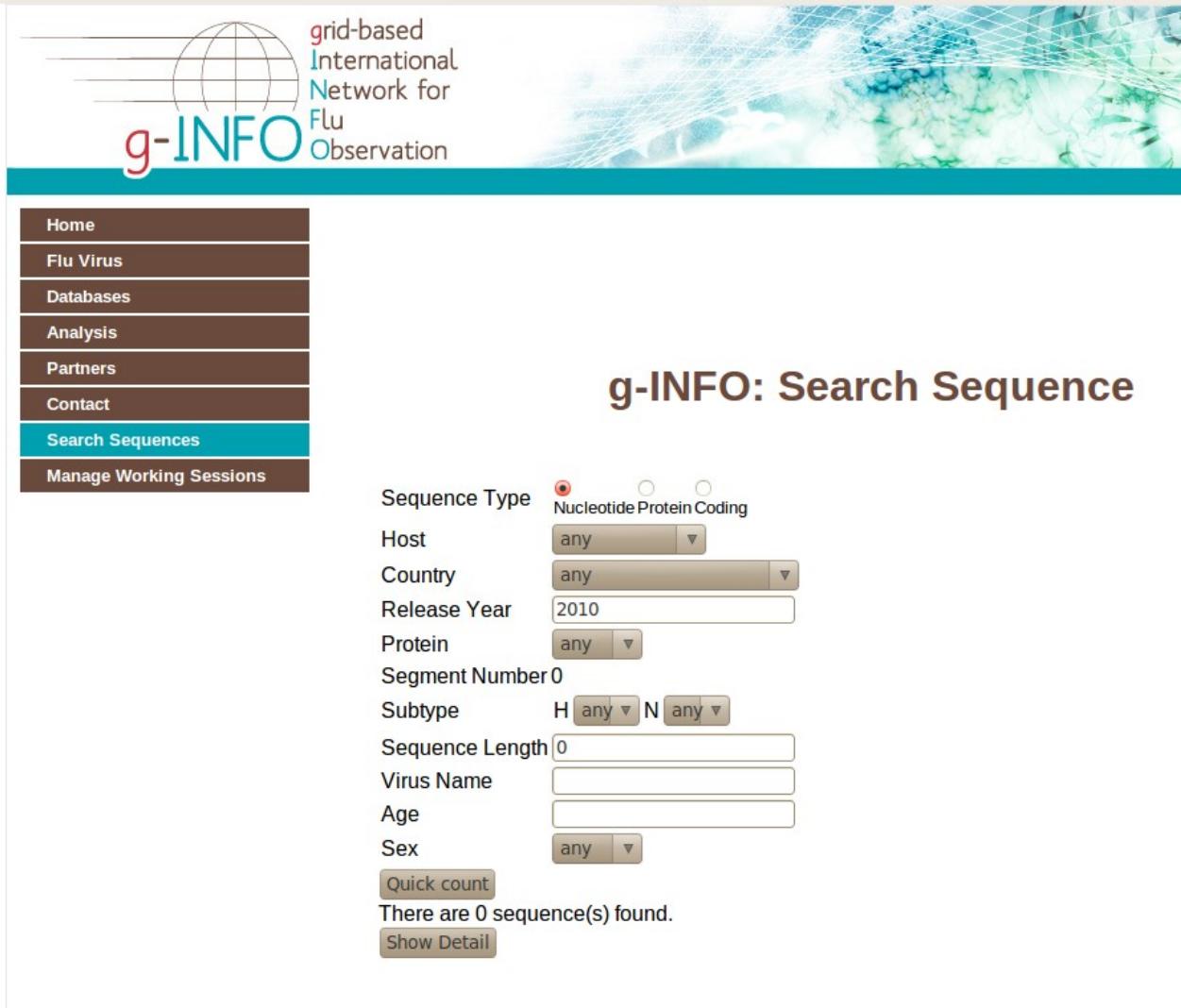
Recent years have seen the emergence of diseases which have spread very quickly around the world, either through human travel, like SARS and SIV(H1N1), or animal migration, like avian flu (H5N1) or more recently, the swine flu outbreak that has been classified as a "pandemic" by WHO in response to its world-wide geographic Spread.

Among the biggest challenges from emerging infectious diseases, is the relation to early detection and surveillance of the diseases, as new cases can appear anywhere. This is due to the globalization of exchanges and the circulation of people and animals around the world, as recently demonstrated by the avian flu epidemics. An international collaboration of research teams in Europe and Asia has been exploring some innovative *in silico* approaches to better tackle flu, taking advantage of the very large computing resources available on international Grid infrastructures. Based on current H1N1 pandemic example, it is expected to have an impact by adding a new weapon to researchers' arsenal: the grid.

Existing data sources have been integrated towards a global surveillance network for molecular epidemiology, based on Service Oriented Architecture (SOA) and Grid technologies. The idea is to dynamically analyze the molecular biology data, made available on public databases using computing, storage and automatic updating services offered by grid technology.

Design HealthGrid | Valid XHTML | Valid CSS | CC-BY-SA

# g-INFO portal - search



The image shows the g-INFO portal search interface. At the top left is the g-INFO logo with the text "grid-based International Network for Flu Observation". To the right is a decorative background image of a virus structure. A vertical navigation menu on the left includes links for Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences (which is highlighted in blue), and Manage Working Sessions.

**g-INFO: Search Sequence**

Sequence Type  Nucleotide  Protein Coding

Host

Country

Release Year

Protein

Segment Number

Subtype H  N

Sequence Length

Virus Name

Age

Sex

There are 0 sequence(s) found.

# g-INFO portal – search results



The image shows the g-INFO portal interface. At the top left is the g-INFO logo, which includes a stylized globe icon and the text "grid-based International Network for Flu Observation". To the right of the logo is a decorative banner featuring a green and white abstract design. On the left side, there is a vertical navigation menu bar with the following items: Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences (which is highlighted in blue), and Manage Working Sessions.

## g-INFO: Nucleotide List

There are 156 Nucleotide(s) found.  
[Select All](#) | [None](#) sequences found  
(Select All may take a long time at the first run depend on the number of sequences found)

[Select All](#) | [None](#) sequences in this page

[Download Fasta](#) / Run Working session with selected input 1..10/156 [Next](#)

Nucleotide ID	Host	Country	Release Year	Segment Number	Sequence Length	Virus Name	Select
GU562459	Human	Russia	2010	7	1002	Influenza A virus (A/Karasuk/01/2010(H1N1))	<input type="checkbox"/>
GU562462	Human	Russia	2010	8	865	Influenza A virus (A/Karasuk/01/2010(H1N1))	<input type="checkbox"/>
GU562458	Human	Russia	2010	4	1752	Influenza A virus (A/Karasuk/01/2010(H1N1))	<input type="checkbox"/>
GU562456	Human	Russia	2010	4	1016	Influenza A virus (A/Karasuk/01/2010(H1N1))	<input type="checkbox"/>

# g-INFO portal – search results

Analysis  
Partners  
Contact  
**Search Sequences**  
Manage Working Sessions

## g-INFO: Nucleotide Detail

Nucleotide ID GU562462

Host Human

Country Russia

Release 2010

Year 2010

Segment 8

Number 8

Sequence Length 865

Virus Name Influenza A virus (A/Karasuk/01/2010(H1N1))

>GU562462  
GTGACAAAAACATAATGGACTCCAACACCAGTCAAGCTTCAGGTAGACTGTTTCTTGGCATATCC  
CAAGCGATTGAGACAATGGATTGGGTGATGCCATTCTGATCGGCTCCGCCAGAGATCAAAGT  
TTAAAGGAAGAGGAACACCCCTGGCCTCGATATCGAAACAGCCACTCTGTTGGAAACAAATCGT  
AATGGATCTTGAAGAGGAATCCAGCGAGACACTTAGAATGACAATTGATCTGACACTTCGCGC  
CCTTCTGACATGACCTCGAGGAATGTCACGGAGACTGGTCATGCTCATGCCATTGGCAAAGATAA  
GGCCCTTTGCGTCGATTGGACCAGGCATATGGAAAAGAACATAGTACTGAAAGCGAACCTCAG  
TAATTTAACCGATTAGAGACCTTGATACTACTAAGGGCTTCACTGAGGAGGGAGCAATAGTGGAC  
AATTCACCATTACCTTCTTCCAGGACATACTTATGAGGATGTCAAAATGCAGTTGGGTCTCAT  
GGAGGACTTGAATGGAATGGTAACACGGTTCGAGTCTCTGAAAATATACAGAGATTGCTTGGAGAAA  
GTGATGAGAATGGGAGACCTTCATTACCTCCAGAGCAGAAATGAAAAGTGGCGAGAGCAATTGGGACA  
AATTTGAGGAATAAGGTGGTTAATTGAAGAAATGCGGCACAGATTGAAAGCGACAGAGAAATAGTTCC  
ACAAATAACATTATGCAAGCCTTACAACACTGCTTGAAGTAGAACAGAGATAAGAGCTTCTCGTT  
CAGCTTATTAATGATAAAAAACAC

[Download Fasta](#)

/ Run Working session with selected input

# g-INFO portal – working sessions

The screenshot shows the g-INFO portal interface. At the top left is the logo: a globe icon with the text "g-INFO" below it, followed by "Flu-based International Network for Flu Observation". To the right is a decorative background image of a network or virus structure. A navigation menu on the left includes links for Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences, and Manage Working Sessions (which is highlighted in blue). The main content area is titled "g-INFO: Working Sessions". Below this, a message states "This is your current working session list:" followed by a table with columns for Working Session ID, Status, Start Date, and End Date. The table lists 17 working sessions, all of which are currently running.

Working Session ID	Status	Start Date	End Date
WS03	running	2010-11-10 11:10:42	
WorkingSession03	running	2010-11-11 10:19:41	
WS04	running	2010-11-11 11:03:14	
WorkingSessionAbc	running	2010-11-15 03:05:04	
WorkingSessionGogogo	running	2010-11-15 10:53:18	
hieu01	running	2010-11-16 08:59:12	
WorkingSession_19Oct	running	2010-11-26 11:20:03	
WorkingSession 29Oct	running		
WorkingSession01	running		
WorkingSession04	running		
November 11	running		
phien lam viec	running		
nov 15	running		
TestWS	running		
abc	running		
WorkingSession05	running		

# g-INFO portal – define working session template

The screenshot shows the g-INFO portal homepage with a sidebar menu and a central form for creating a new workflow template.

**g-INFO Logo:** grid-based International Network for Flu Observation

**Menu (Sidebar):**

- Home
- Flu Virus
- Databases
- Analysis
- Partners
- Contact
- Search Sequences
- Manage Working Sessions

**Central Content:**

## g-INFO: Create New WorkFlow Template

WorkFlow Template Name

[Next](#)

Design HealthGrid | Valid XHTML | Valid CSS | CC-BY-SA



# g-INFO portal – define working session template

The screenshot shows the g-INFO portal interface. At the top left is the logo: "grid-based International Network for Flu Observation" with "g-INFO" in red and blue. To the right is a decorative background image of a virus structure. A vertical navigation menu on the left includes links: Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences, and Manage Working Sessions (which is highlighted in teal). The main content area has a teal header "g-INFO: Select Tool". Below it, a form is displayed for creating a workflow template named "sample wft". The form fields are: Component1 (dropdown menu set to "blast"), Tool1 (dropdown menu set to "blast"), Argument1 (text input field containing "-p blastn -b 20 -a|4 -e 0.001"), and Save (button). At the bottom of the page is a teal footer bar with the text "Design HealthGrid | Valid XHTML | Valid CSS | CC-BY-SA".



# g-INFO portal – define working session template

The screenshot shows the g-INFO portal homepage. The header features the g-INFO logo with the text "grid-based International Network for Flu Observation". Below the header is a navigation menu with links: Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences, and Manage Working Sessions. The "Manage Working Sessions" link is highlighted with a teal background. The main content area is titled "g-INFO: Select Tool". It displays a "WorkFlow Template Name" input field containing "sample wft". Below it are dropdown menus for "Component2" (set to "alignment") and "Tool2" (set to "muscle"). A text input field for "Argument2" contains "-maxiters 10". A "Save" button is located at the bottom left of this section. At the very bottom of the page is a footer bar with the text "Design HealthGrid | Valid XHTML | Valid CSS | CC-BY-SA".

# g-INFO portal – define working session template

The screenshot shows the g-INFO portal interface. At the top, there is a logo with a globe icon and the text "grid-based International Network for Flu Observation". Below the logo is a navigation menu with links: Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences, and Manage Working Sessions (which is highlighted). The main content area has a title "g-INFO: Checkout WorkFlow Template" and a message "You have create a new WorkFlow Template". It shows a table for defining workflow steps:

Tool Position	Tool	Args	Edit	Remove
1	blast	-p blastn -b 20 -a 4 -e 0.001	Edit	Remove
2	muscle	-maxiters 10	Edit	Remove

Below the table are links "More toolFinish". At the bottom of the page is a footer bar with the text "Design HealthGrid | Valid XHTML | Valid CSS | CC-BY-SA".

# g-INFO portal – run working session

**Databases**  
**Analysis**  
**Partners**  
**Contact**  
**Search Sequences**  
**Manage Working Sessions**

## g-INFO: Working Sessions

Upload Fasta:

```
>GU562462
GTGACAAAAACATAATGGACTCCAACCCATGTCAGCTTCAAGTAGACTTTCTTGCGATATCCG
CAAGGGATTGCAGACAAATGGATTGGTGTATGCCCATCCCTGATCGCTCCGGAGATCAAAGTC
TTAAAAGGAAGGGCAACCTTGGCTCGATATCGAACAGCCACTCTTGGAAACAAATCGTGG
AATGGATCTTGAAGAGGAACCTCAGCGAGACACTAGAAATGACAATTGATCTGTACCTACTTCCGCTA
CTTCTGACATGACCTCGAGGAATGTCAGAGACTGGTCATGTCATCCTAGGAAAGATAATA
GGCCCTTTCGTCGATTGGACCAAGGGCATGATGGAAAAGAACATAGTACTGAAGCGAACCTCAGTG
TAATCTTAAAGGATTAGAGACCTTGATACTAAAGGGCTTCACTGAGGAGGGAGCAATAGTTGGAGA
AATTTCACCAATTCTTCTTCCAGGACATACTTATGAGGATGTCAAAATGCACTGGGTCCTCATC
GGAGGACTTGATGGAATGGTAAACCGTTGAGCTCTGAAAATATACAGAGATTGCGTTGGAGAAACT
GTGATGAGAATGGAGACCTTCATTACCTCCAGAGCAGAAATGAAAGTGGCAGAGCAATTGGGACAGA
AATTGGAGAATAAGGGTTAATTGAAGAAATCGGGCACAGATTGAAGGGACAGAGAATAGTTTCA
ACAAATAACATTATGCAAGCTTACAACACTGCTGAGTAGAACAGAGATAAGAGCTTCTCGTT
CAGCTTATTAATGATAAAAAACAC
```

Enter new working session Name:

User's existing workflow template list:

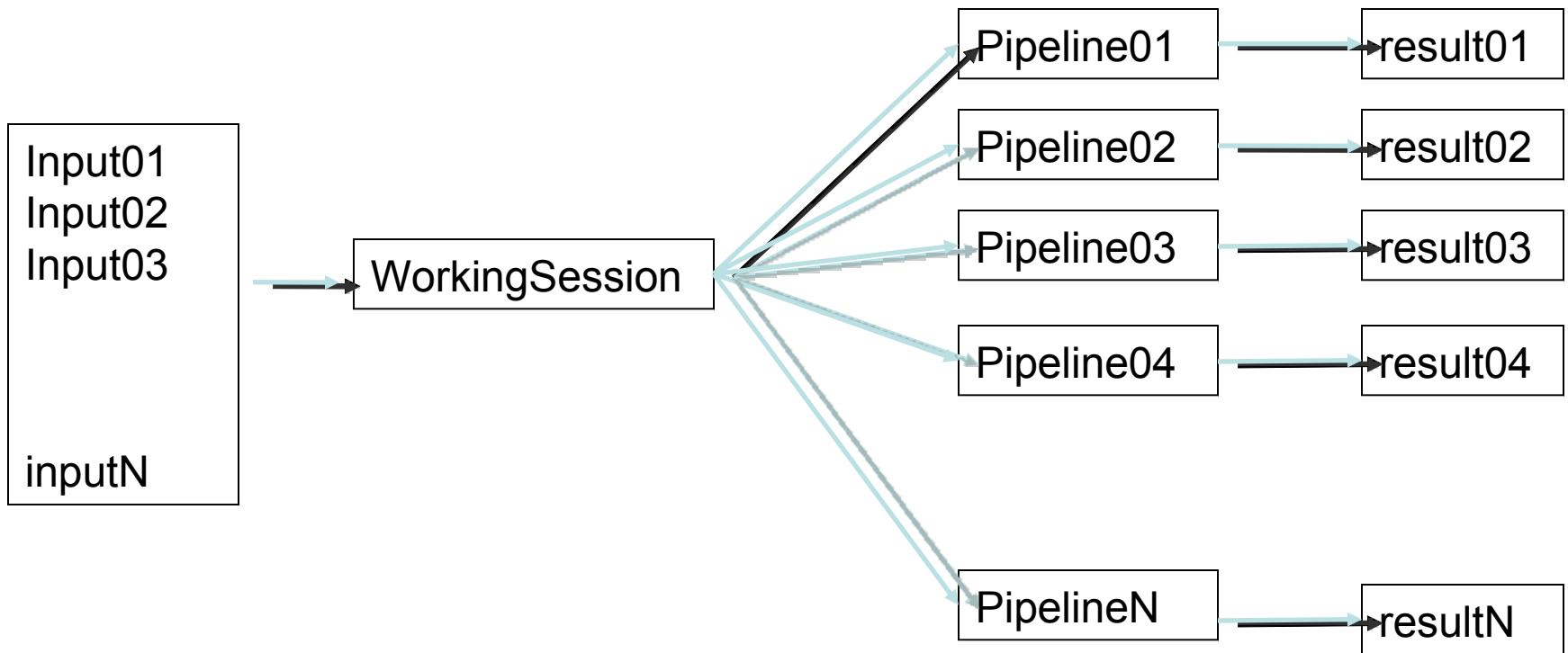
sample wft 1

Tool Position	Tool	Args
1	blast	-p blastn -b 20 -a 4 -e 0.001
2	muscle	maxiters 10

sample wft 2

Tool Position	Tool	Args
1	blast	-p blastn -b 20 -a 4 -e 0.001

# g-INFO portal – run working session



# g-INFO portal – visualization

The screenshot displays the g-INFO portal visualization interface. At the top left is the g-INFO logo with the text "g-INFO: Global-based International Network for Flu Observation". The main menu on the left includes links for Home, Flu Virus, Databases, Analysis, Partners, Contact, Search Sequences, and Manage Working Sessions (which is highlighted in green). The central area features a phylogenetic tree titled "IFI-Phylo-Applet" with nodes labeled ADH2, ADH1, ADHX, ADHY, ADH4, ADH3, ADH2, and ADH1. To the right of the tree is a "Clipboard" window containing phylogenetic tree data in Newick format. Below the clipboard is a "Node Info" section with fields for Username (admin), Working-Session (WorkingSession01), Pipeline (Pipeline01), Component (phylogeny), Filename (rvf.nw), and Type (n). A "Load Data" button is also present.

g-INFO: Working Sessions

IFI-Phylo-Applet

File View Search:

ADH2  
ADH1  
ADHX  
ADHY  
ADH4  
ADH3  
ADH2  
ADH1

Clipboard:

```
((ADH2:0.1144,ADHX:0.11,ADH1:0.0514,ADHY:0.1214,ADH4:0.1114,ADH3:0.1114,ADH2:0.1114,ADH1:0.1114);)
```

Node Info:

Username:	admin
Working-Session:	WorkingSession01
Pipeline:	Pipeline01
Component:	phylogeny
Filename:	rvf.nw
Type:	n

Load Data

# Conclusions

- ❖ A success in terms of international collaboration
- ❖ An example of developing grid application in Vietnam
- ❖ A complementary service for the public health research community

# Perspectives

- ❖ Provide more tools and pipelines
- ❖ Import other database resources
- ❖ Improve system's performance
- ❖ We are expecting the research community to contribute with more useful tools
- ❖ Can be applied for other emerging diseases

# Thank you!