



gUSE in CancerGrid project

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The CancerGrid infrastructure



•The general framework components

- WS-PGRADE/gUSE portal
- SZTAKI Private/Local Desktop Grid
- 3GBridge
- Customisation
 - algorithms
 - workflows
 - molecule database
 - resources
- Scenario
- Handling molecules in the database
- Workflow configuration/submission & monitoring

The CancerGrid project

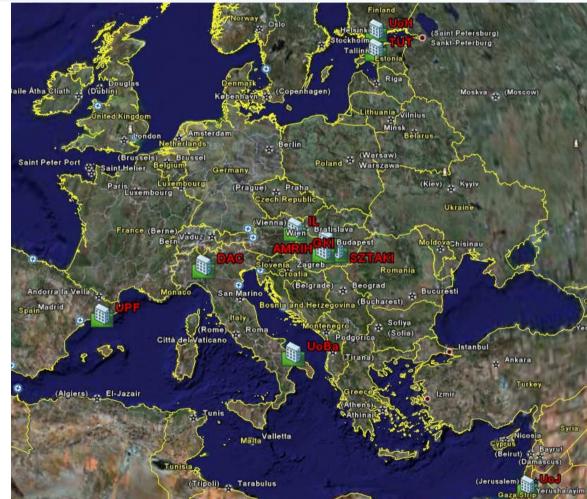


- EU Framework Program 6
- Title: Grid Aided Computer System For Rapid Anti-Cancer Drug Design
- Project period
 - January 1, 2007 December 31, 2009 (June 30, 2010)
- Goals:
 - Developing focused libraries with a high content of anticancer leads, building models for predicting various molecule properties
 - Developing a computer system based on grid technology, which helps to accelerate and automate the in silico design of libraries for drug discovery processes



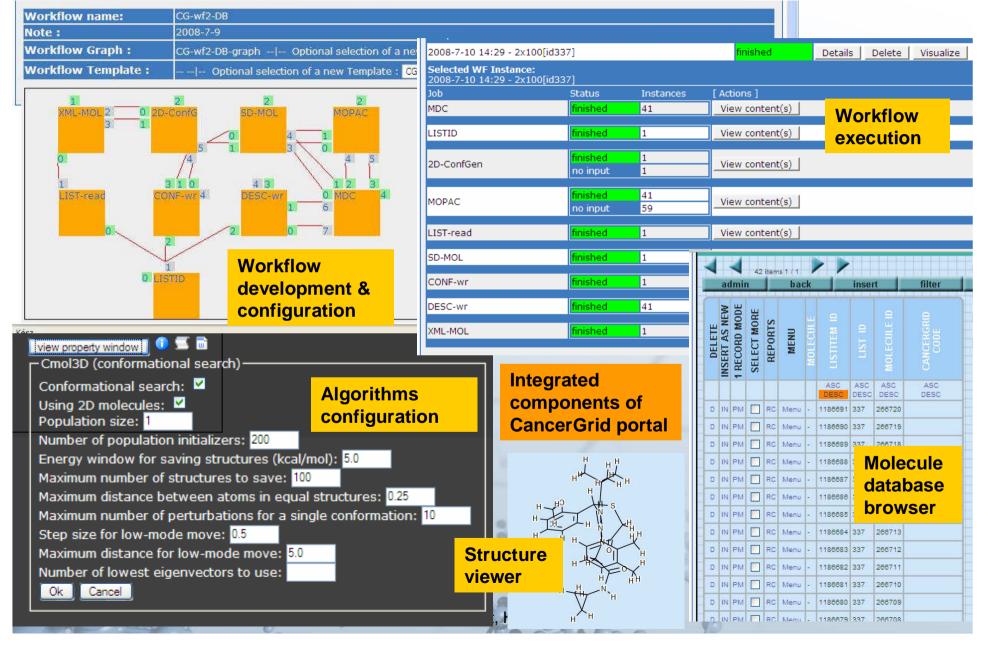
The CancerGrid consortium

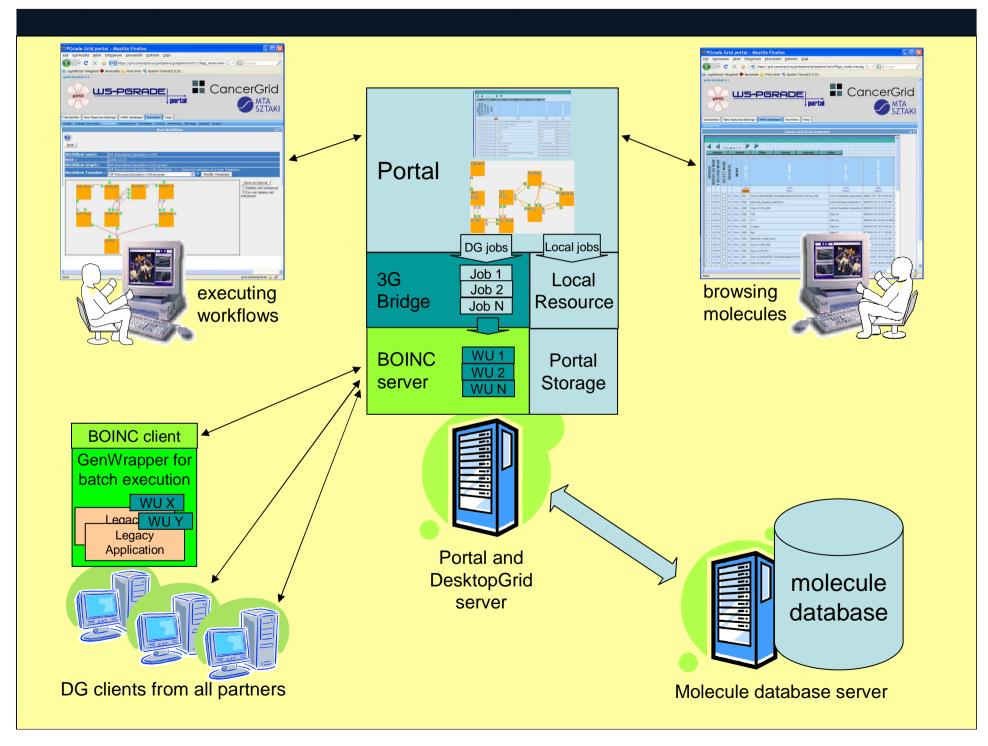
- TargetEx, Inc., Hungary (coordinator) [chemistry]
- AMRI Hungary, Inc., Hungary [chemistry]
- Inte:Ligand, Austria [chemoinformatics]
- Tallinn University of Technology, Estonia [chemoinformatics]
- University of Helsinki, Finland [biotechnology]
- GKI Economic Research, Hungary [economics]
- SZTAKI, Hungary [computer science]
- University of Jerusalem, Israel [chemoinformatics]
- DAC, Italy [biotechnology]
- University of Bari, Italy [chemistry]
- University of Pompeu Fabra, Spain [chemoinformatics]



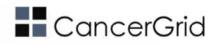
The CancerGrid portal (gUSE & SZTAKI DG)

CancerGrid





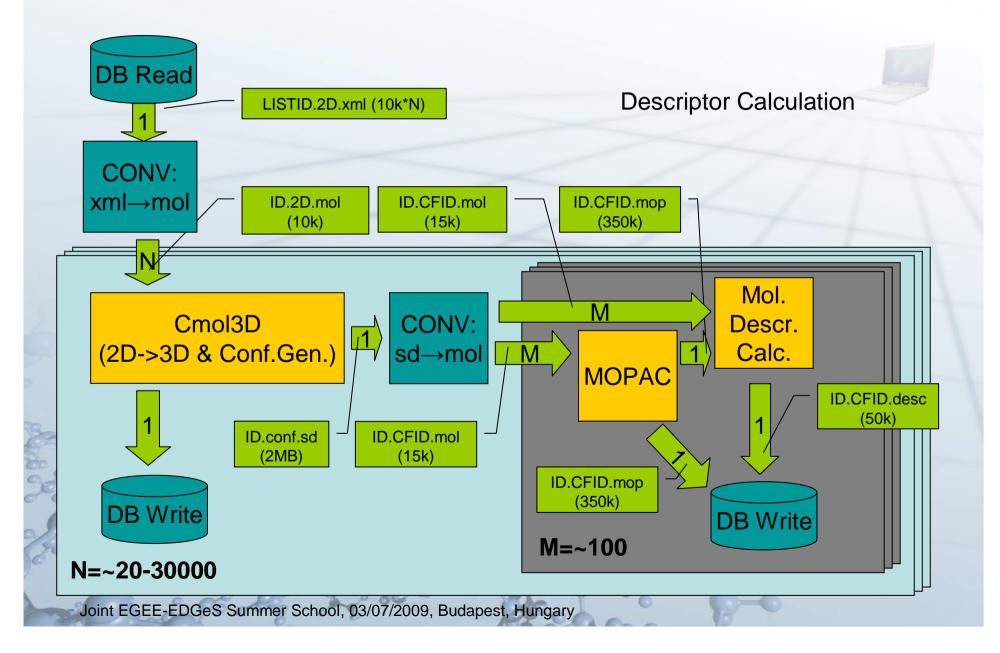
Applications in CancerGrid



- Flexmol is an XML-based molecular language
- Molecule 2D/3D converter (Cmol3D)
- Molecule 3D conformation generator (Cmol3D)
- MOPAC (Molecular Orbital PACkage) is a semiempirical quantum chemistry program based on Dewar and Thiel's NDDO approximation
- Codessa Pro (Comprehensive Descriptors for Structural and Statistical Analysis) is a software suite for developing quantitative structure-activity/property relationships
- Matrix former
- QSAR Model builder **Quantitative structure-activity relationship** (QSAR) is the process by which chemical structure is quantitatively correlated with a well defined process, such as biological activity or chemical reactivity.
- (Chemical) Property Predictor
- File format converters (to integrate the previous tools into a workflow)

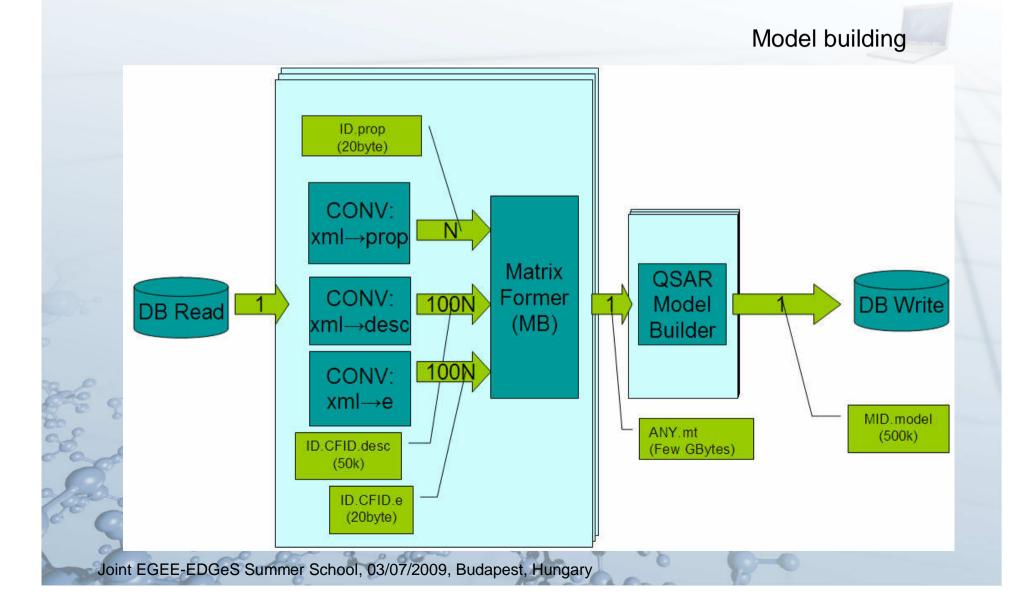
Supported workflow 1/4

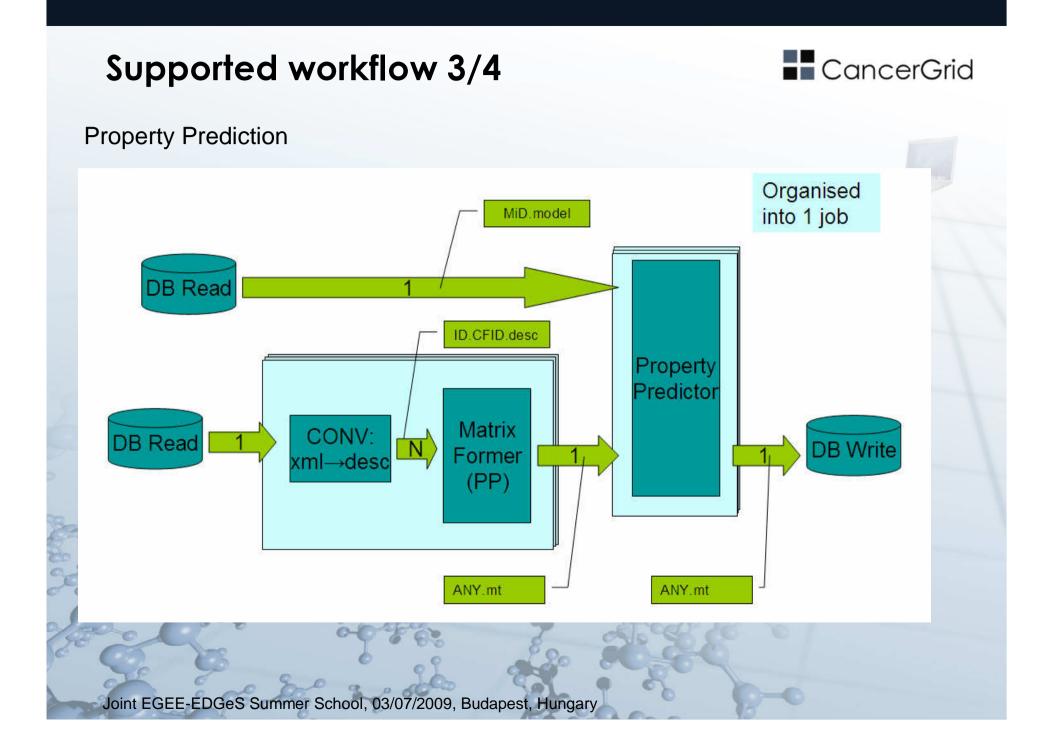




Supported workflow 2/4

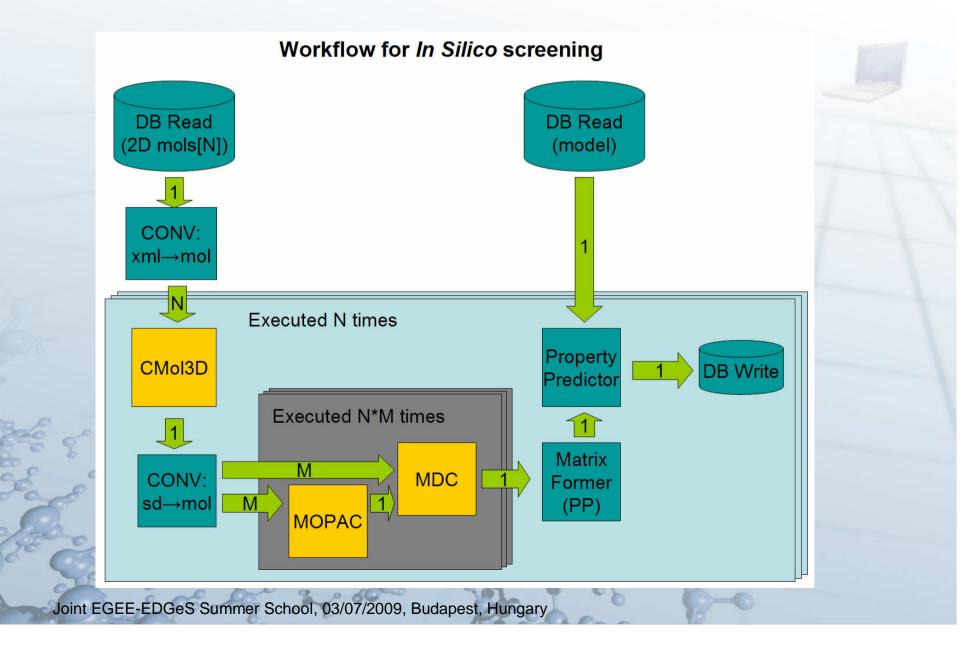


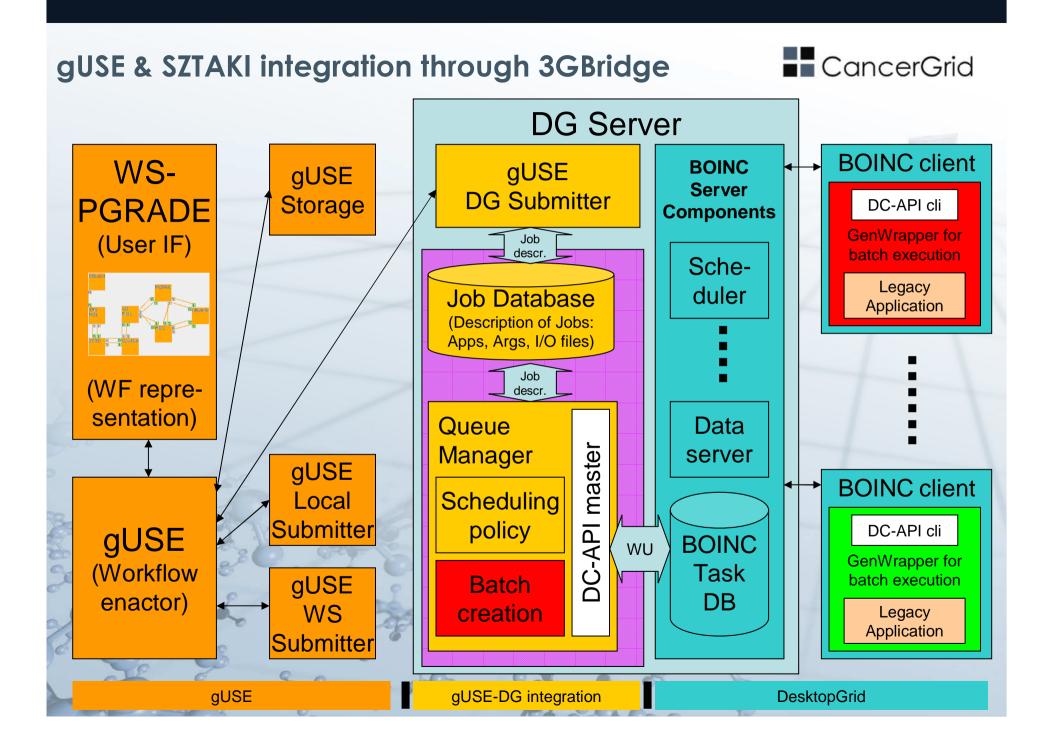




Supported workflow 4/4







Job handling

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Applications: cmol3d, mopac, mdc, fmt, fma, etc.

Various requirements

- Fortran, C, C++
- processing/ memory requirements
- multi-binary applications (already contain some wrappers), libraries
- legacy binaries for Linux and Windows
- config file preparation before execution
- pure logging/ debugging information
- variable number of output files

GenWrapper tool on the client machine Low granularity

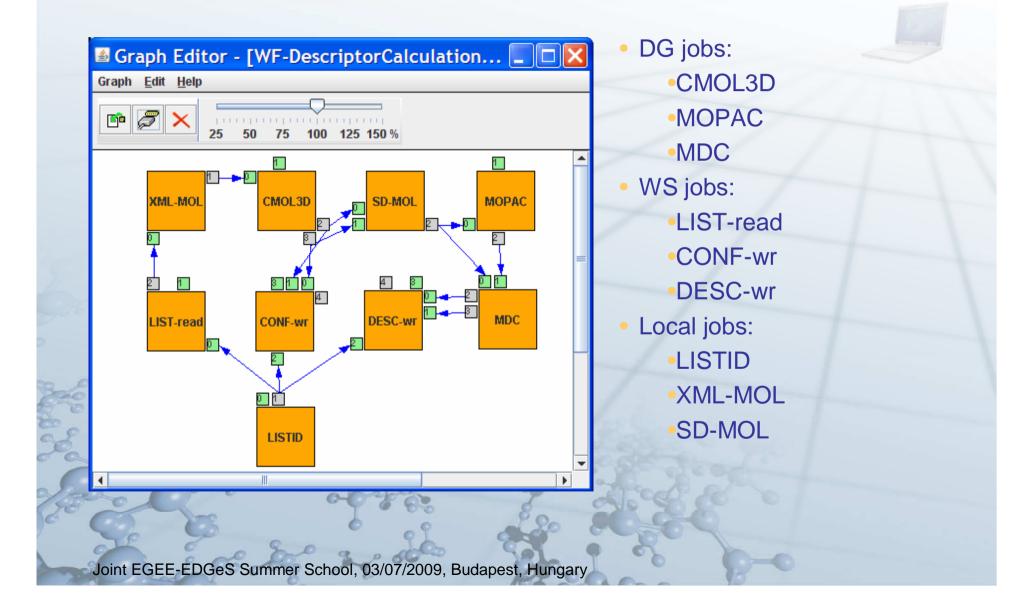
 Execution time is very small (simetimes only a few minutes)

Batch creation plugin in 3GBridge

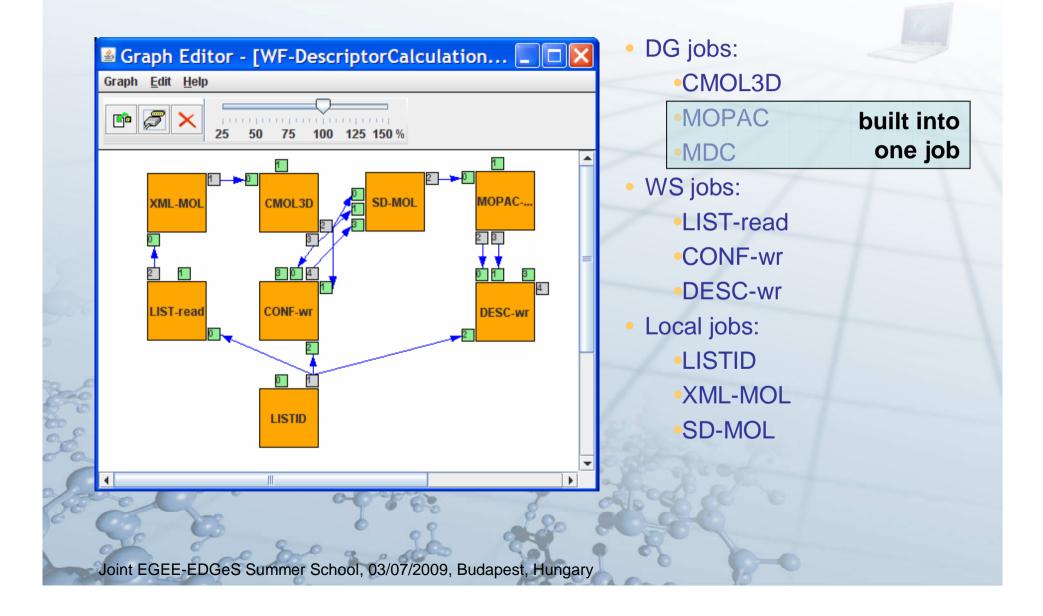
- The workunit contains the shell script that is created to manage the execution of the batch
 - assembled from head, body and tail fragments
 - body part is repeated for each job in the batch
 - may contain macros like
 %{name}

Descriptor calculation workflow in gUSE





Optimised descriptor calculation workflow in gUSE



High-level scenario



- Initial state: molecules/structures stored in DB, organised into lists
- User selects list of molecules/structures
- User selects/downloads a workflow from repository
- User configures the workflow to take the list as input
- User optionally updates parameters of the modules
- Submits workflow
- Optionally monitors the status
 - When workflow finished, results are stored in the DB

Molecule lists

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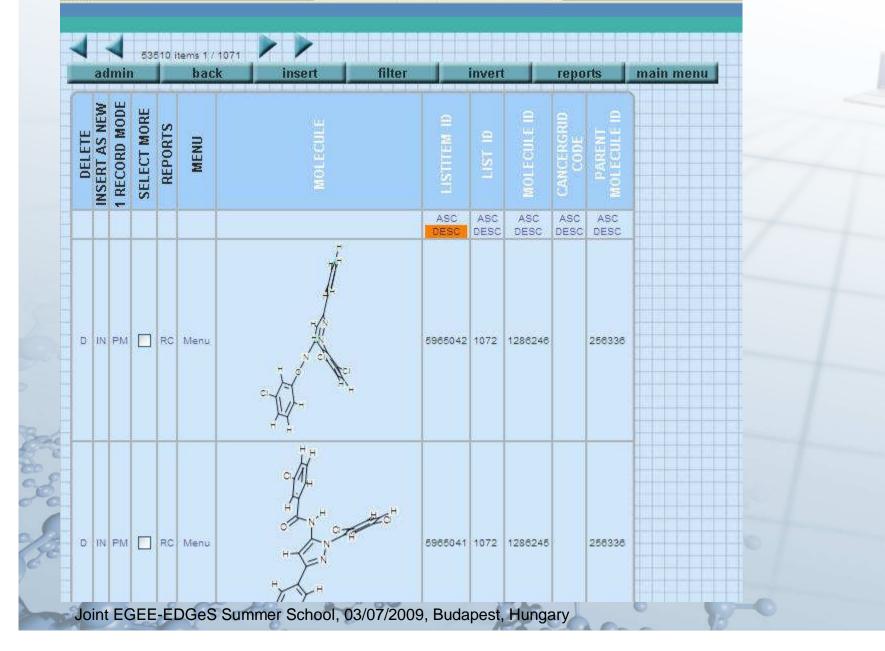
Listitems view

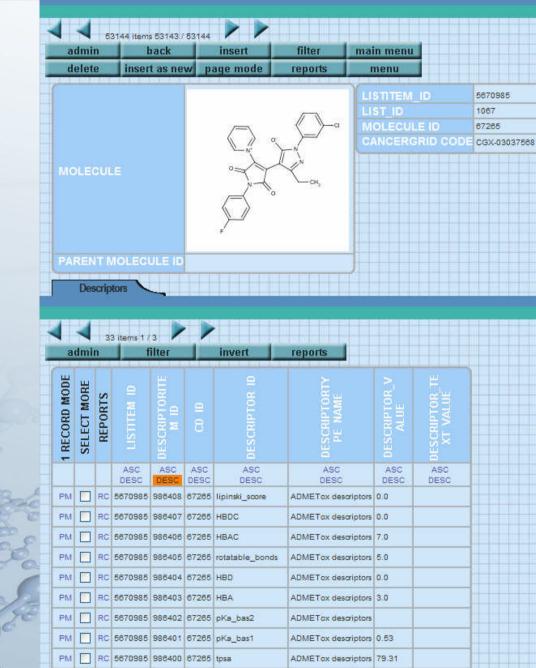
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Molecule viewer







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Inspecting molecules one by one...

Manipulating the lists



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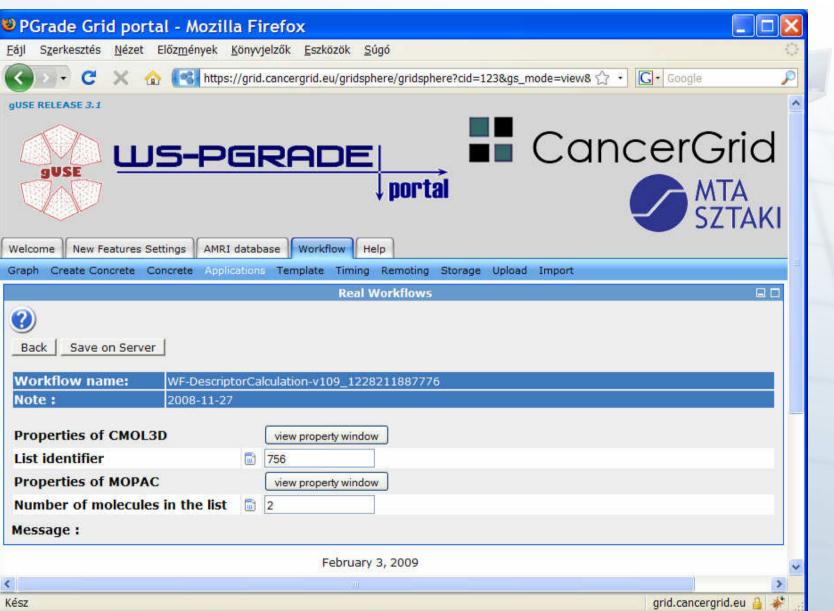
Downloading workflow from repository CancerGrid

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School, Scottzoos, Budapest, Hungary

Joint

Workflow configuration



CancerGrid

John LOLE-LOGE Summer School, 03/07/2003, Dudapest, Hungary

Cmol3D property settings



Cmol3D (conformational search) Conformational search:	V
Using 2D molecules:	
Population size:	100
Number of population initializers:	200
Energy window for saving structures (kcal/mol):	5.0
Maximum number of structures to save:	10
Maximum distance between atoms in equal structures:	0.25
Maximum number of perturbations for a single conformation:	10
Step size for low-mode move:	0.5
Maximum distance for low-mode move:	5.0
Number of lowest eigenvectors to use:	10

List of workflows (Novice user view)



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Status monitor

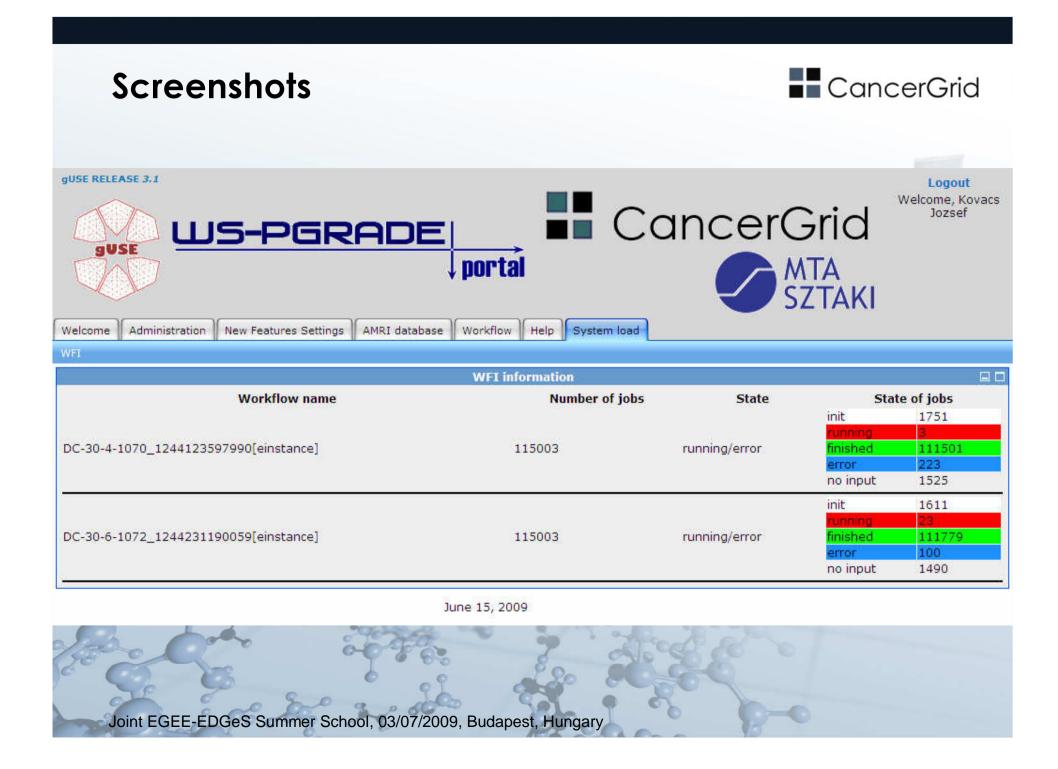
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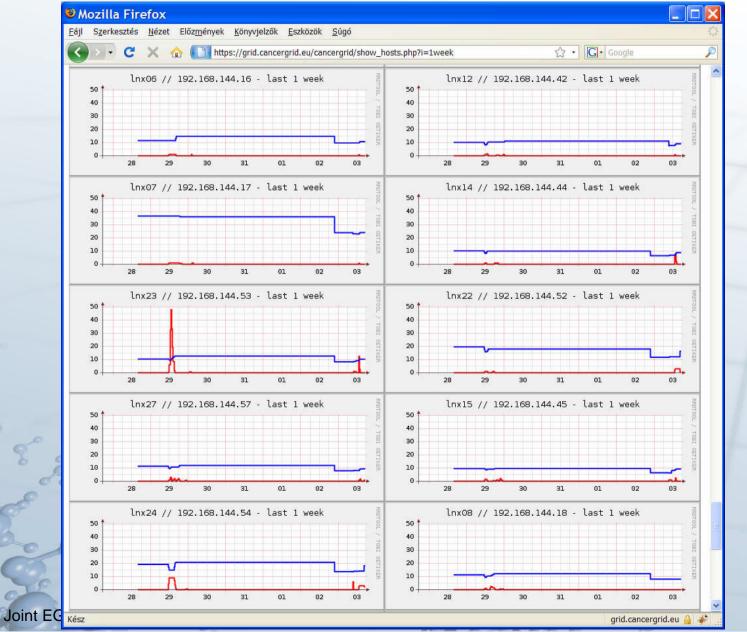
Job statuses of a workflow (Advanced view)

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CMOL3D	finished 3754 waiting 12 submitted 1234	View finished View waiting View submitted	View all content(s)
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5D-MOL	finished 250	View finished	View all content(s)
		View finished	View all content(s)



Monitoring the clients





The system in numbers...



Statistics

- Currently 70 machines are integrated into the system, the goal is to have about 200 machines
- Requires only 1 central server to be maintained (clients needs no maintenance!)
- 13 algorithms has been integrated
- 4 workflows are available
- 5-6 partners from the consortium have used it for different purposes

Peak performance

 Description calculation for 30.000 compounds (with 10 conformers) takes 5 days (executing the combination of CMOL3D, MOPAC and MDC tools from CODESSA using 3D descriptors). With 1 PC it could be a year...

Note: there are faster algorithms, but Grid is worth applying only for computationally intensive algorithms (like the ones above)

By decreasing the number of conformers and by increasing the number of machines, the calculation can be even 100 times faster i.e. millions of compounds can be processed within 1 week. This is our current direction...

Summary & Future plan



- Any community that has several computational intensive algorithms can easily execute them on a SZTAKI DesktopGrid (SZDG) system:
 - the community can create its own institutional SZDG project
 - can simply attach the available PC computers as resources
 - can insert the algorithms in their SZDG project
 - can easily combine these components into more complex workflow applications, if necessary
- Such a system
 - has been prototyped for the Cancer Research community within the CancerGrid projects
 - can be specialized for any community requirements
- SZTAKI is ready to support other communities with this technology
- In the future
 - we plan to continue extending the CancerGrid portal with more algorithms, workflows and PC resources
 - we plan to create an open portal where various algorithms from the field of computational chemistry and bioinformatics will be supported, which will be publicly available
 - we plan to integrate ZINC database
 - Joint EGEE-EDGeS Summer School, 03/07/2009, Budapest, Hungary



If you need more detailed (technical) information, email to <u>desktopgrid@lpds.sztaki.hu</u> or visit www.desktopgrid.hu



Thank you for your attention!

Questions?





Acknowledgement:

CancerGrid EU FP6 project (FP6-2005-LIFESCTHTALTH-7)

http://www.cancergrid.eu