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## Advanced Strategies for Efficient Workflow Management with GridWay

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## **CD-HIT**

- "Cluster Database at High Identity with Tolerance"
- Protein (and also DNA) clustering
  - Compares protein DB entries
  - Eliminates redundancies
- Example: Used in UniProt for generating UniRef data sets
- Our case: Widely used in the Spanish National Oncology Research Center (CNIO)
  - Input DB: 504,876 proteins / 435MB
- Infeasible to be executed on single machine
  - Memory requirements
  - Total execution time



## 2. Parallel Execution of CD-HIT (cd-hit-para)

## cd-hit-para

- Execute cd-hit in parallel mode
- Idea: divide the input database to compare each division in parallel
  - Divide the input db
  - Repeat
    - Cluster the first division (cdhit)
    - Compare others against this one (cd-hit-2d)
  - Merge results
- Speed-up the process and deal with **larger databases**
- Computational characteristics
  - Variable degree of parallelism
  - Grain must be adjusted





## 2. Parallel Execution of CD-HIT (cd-hit-para)





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## 4. Results

# Grid Infrastructure

## **BIOMED** sites



Site	Processor	Nodes	Speed
BIFI	Intel P4	56	3.2GHz
CESGA	Intel PIII	16	500MHz
CGG	Intel PIII	58	1.2GHz
CIEMAT	Intel Xeon	226	3.2GHz
GRIF	Intel P4	14	2.8GHz
JINR	Intel PD	30	2.8GHz
LHEP	Intel P4	374	3GHz
PNPI	Intel P4	60	3GHz
RAL	Intel P4	62	2.8GHz
RALPP	Intel PIII	1064	1GHz
ScotGRID	Intel Xeon	6	2.8GHz
SINP	Intel Xeon	94	2.8GHz

4. Results





Expected: without considering either queue wait times or job failures Max: taking into account just the *critical path* 

### 5. Current Work

## cd-hit-grid

- Larger database 4,186,284 proteins (1.7 GB) from CNIO
- Improve the efficiency of the workflow execution with redundancy and agglomeration





# Thank you for your attention!