



# Computational Challenges at EMBL-Grenoble

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*ESRFUP WP11 Workshop on*

Exploiting the GRID

ESRF, Grenoble, France

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# EMBL ?







# EMBL Facts



- 21 Member Countries
- 5 Facilities (Heidelberg, Hamburg, Cambridge, Rome, Grenoble)
- ~100 Research Groups
- >1440 Employee from 60 nations
- Ranking as the highest non-US institute in research performance by ISI Science Indicator for 1992-2002



# EMBL Units



- **Cell Biology**- Heidelberg
- **Biophysics** - HD
- **Developmental Biology** - HD
- **Gene Expression** - HD
- **Computational Biology** - HD
- **Structural Biology** – HD, HH, GR
- **Bioinformatics** - Cambridge
- **Mouse Biology** - Rome
- **Center for Disease Mechanisms**
- **Center for High Throughput Functional Genomics**
- **Center for Molecular and Cellular Imaging**





# EMBL Facilities



- Advanced Light Microscopy, Genomics, Proteomics, Protein Expression and Purification, Electron Microscopy, Flow Cytometry, Monoclonal Antibody and Chemical Biology
- Microcomputing and data acquisition (detector electronics for high speed time-resolved synchrotron radiation scattering experiments; use of microstructures to carry out work on single cells; and image processing methods for biological applications)



# EMBL Software Solutions

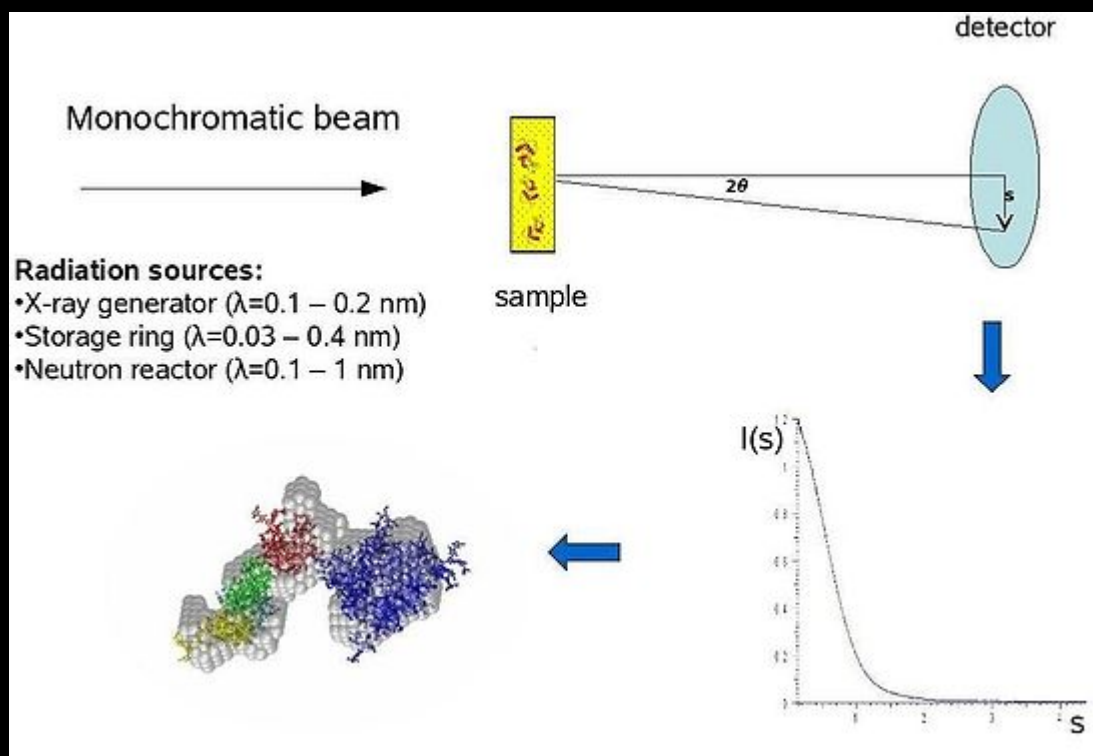


- EMBL-EBI Dbs: EMBL-Bank – *DNA/RNA sequence*;  
UniProt – *protein sequence*;  
Ensemble – *genomes*;  
EMSD – *wwPDB*;  
ArrayExpress – *gene expression*
- EMBL-EBI Tools: >200, eg: SMART; STRING; ELM; Harvester;...
- Hamburg Tools: ABRA – *EXAFS*;  
ARP/wARP; Autow-Rickshow; BEST; XREC – *MX*;  
ATSAS – *SAX*;
- Heidelberg Tools: BLAST2GENE;  
4DXpress;  
MEPD;  
SIRW;  
Genes2Diseases  
...

# Job Types

- Small data – long run:  
SAX iterations

*ideal for job submission*







# Job Types



- Huge DB + small data – long(?) run: *dedicated servers with fast DB access*  
(*DB replica/indexing for job submission?*)  
sequence search; Molecule Replacement

```
AAB24882 TYHMCQFHCERYVNNHSGEKLYECNERSKAFSCPSHLQCHKRRQIGEKTHEHNQCGKAFPT 60
AAB24881 -----YECNQC GKAF AQHSSLKCHYRTHIGEKPYECNQC GKAFSK 40
          ****: .***: * **:* * :****.:* *****..

AAB24882 PSHLQYHERTHTGKPYECHQCGQAFKKCSLLQRHKRTHTGKPYE-CNQC GKAF AQ- 116
AAB24881 HSHLQCHKRTHTGKPYECNQC GKAF SQHGLLQRHKRTHTGKPYMNVINMVKPLHNS 98
          **** *:*****:***:**.: .*****: *.: :
```

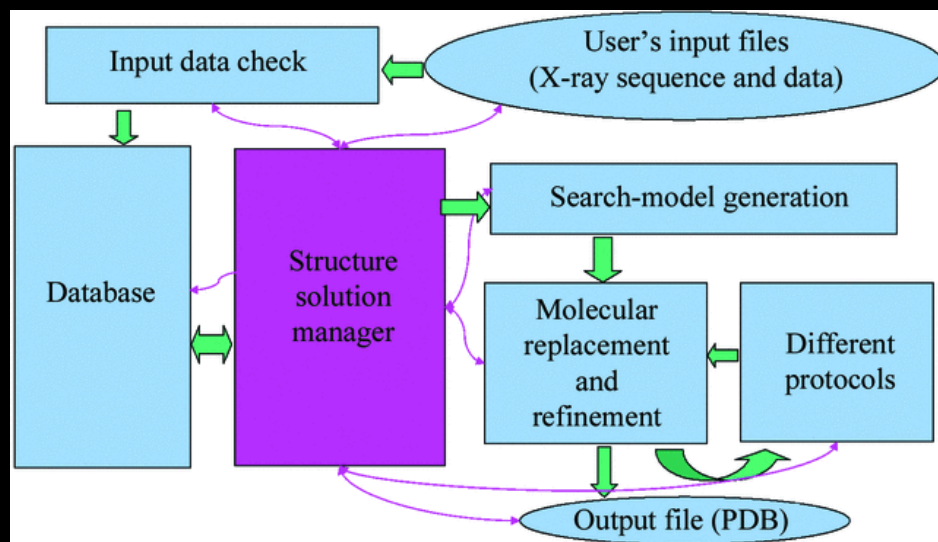
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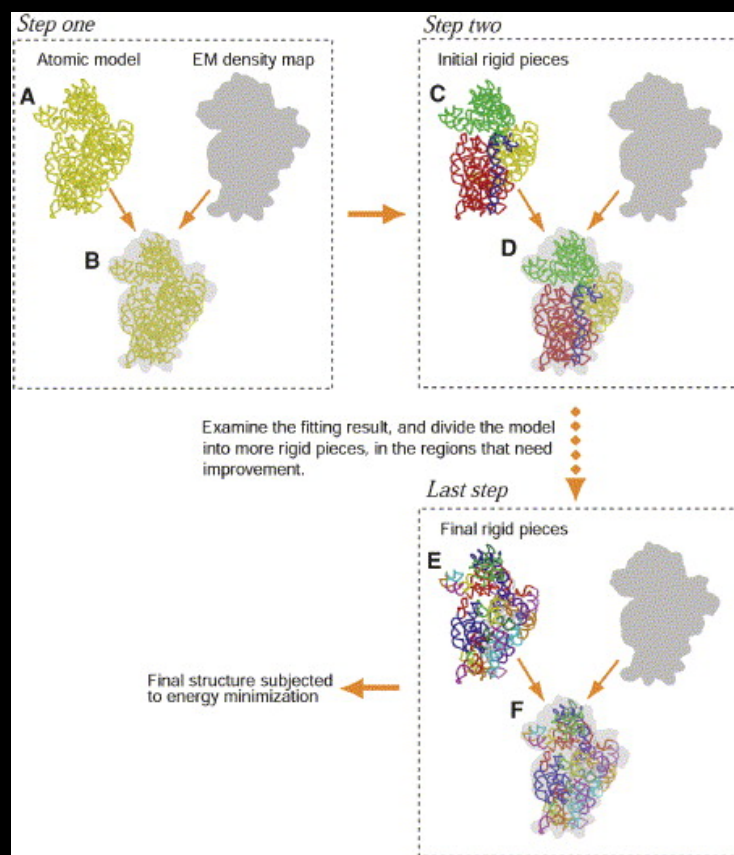
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                ****: .***: * **:* * :****.:* *****..

AAB24882      PSHLQYHERTHTGKPYECHQCGQAFKKCSLLQRHKRTHHTGKPYE-CNQCCKAFAQ- 116
AAB24881      HSHLQCHKRTHHTGKPYECNQCCKAFSQHGLLQRHKRTHHTGKPYMNVINMVKPLHNS 98
                **** *:*****:****:**.: .*****: *.: :
  
```



# Job Types

- Modest data – long run: *good for job submission*  
Rigid Body Fitting; EM classification / reconstruction

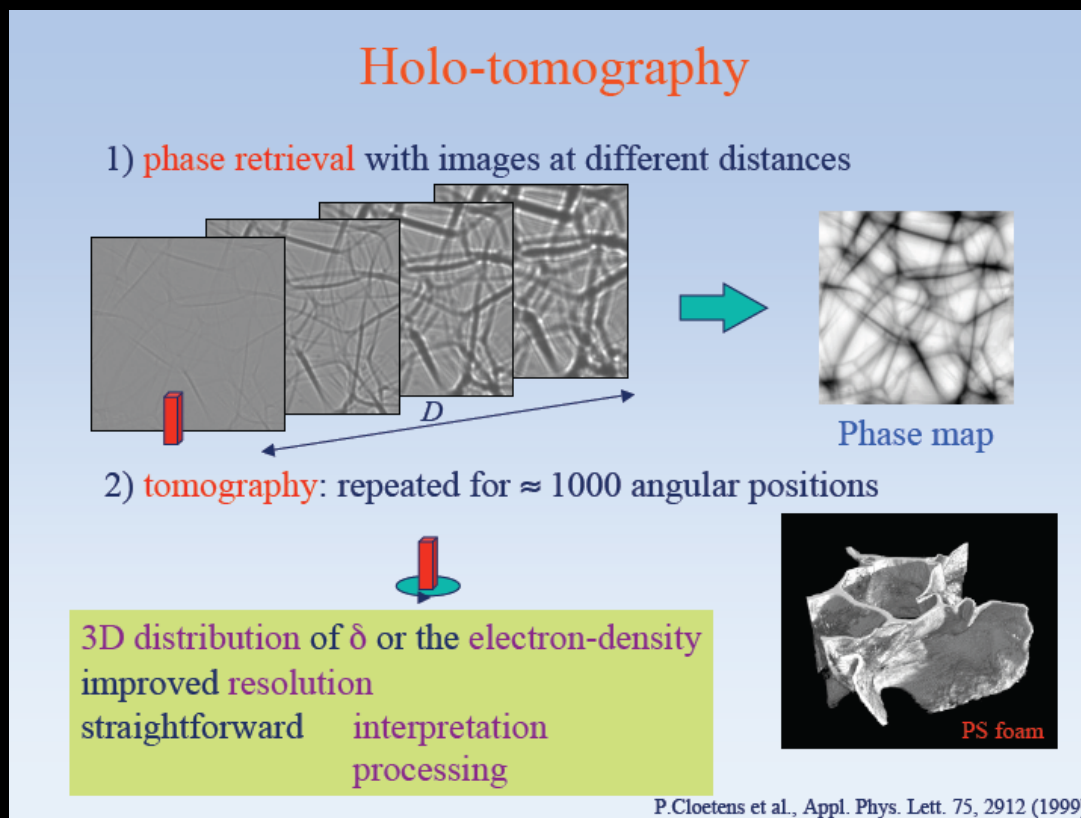


[http://www.sciencedirect.com/science?\\_ob=ArticleURL&\\_udi=B6VSR-4FNDMYJ-9&\\_user=656670&\\_rdoc=1&\\_fmt=&\\_orig=search&\\_sort=d&view=c&\\_acct=C000035638&\\_version=1&\\_urlVersion=0&\\_userid=656670&md5=537687f9b56129e077f50e1657aae8f8](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6VSR-4FNDMYJ-9&_user=656670&_rdoc=1&_fmt=&_orig=search&_sort=d&view=c&_acct=C000035638&_version=1&_urlVersion=0&_userid=656670&md5=537687f9b56129e077f50e1657aae8f8)

# Job Types

- Big data – long run:  
Holo-; NanoScan-Tomography

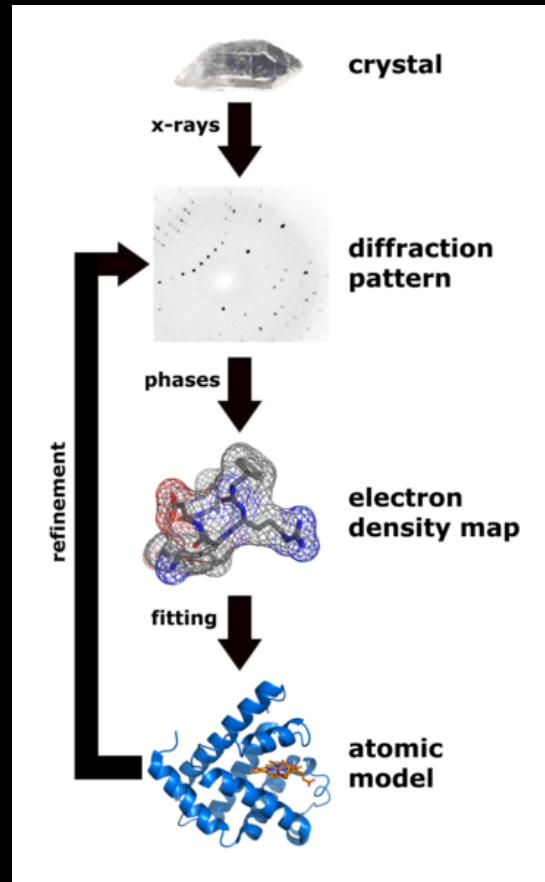
*good for job submission*



# Job Types

- (Modest) data – SHORT RUN:  
MX data processing

*must be submitted!*





# Job Types



- Small data – long run: *ideal for job submission*  
SAX iterations
- Huge DB + small data – long(?) run: *dedicated servers with fast DB access*  
(*DB replica/indexing for job submission?*)  
sequence search; Molecule Replacement
- Modest data – long run: *good for job submission*  
Rigid Body Fitting; EM classification / reconstruction
- Big data – long run: *good for job submission*  
Holo-; NanoScan-Tomography
- (Modest) data – SHORT RUN: *must be submitted!*  
MX data processing





Thank you for your attention!

