

***EGEE Conference 2006***

***swissPIT***  
***a usecase for proteomic software***  
***on the SwissBioGrid***  
***infrastructure***

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# Project overview

swissPIT = Swiss **P**rotein **I**dentification **T**oolbox

...tries to analyze mass spectrometry data with different programs.

*(more details by Patricia Hernandez on Thursday)*

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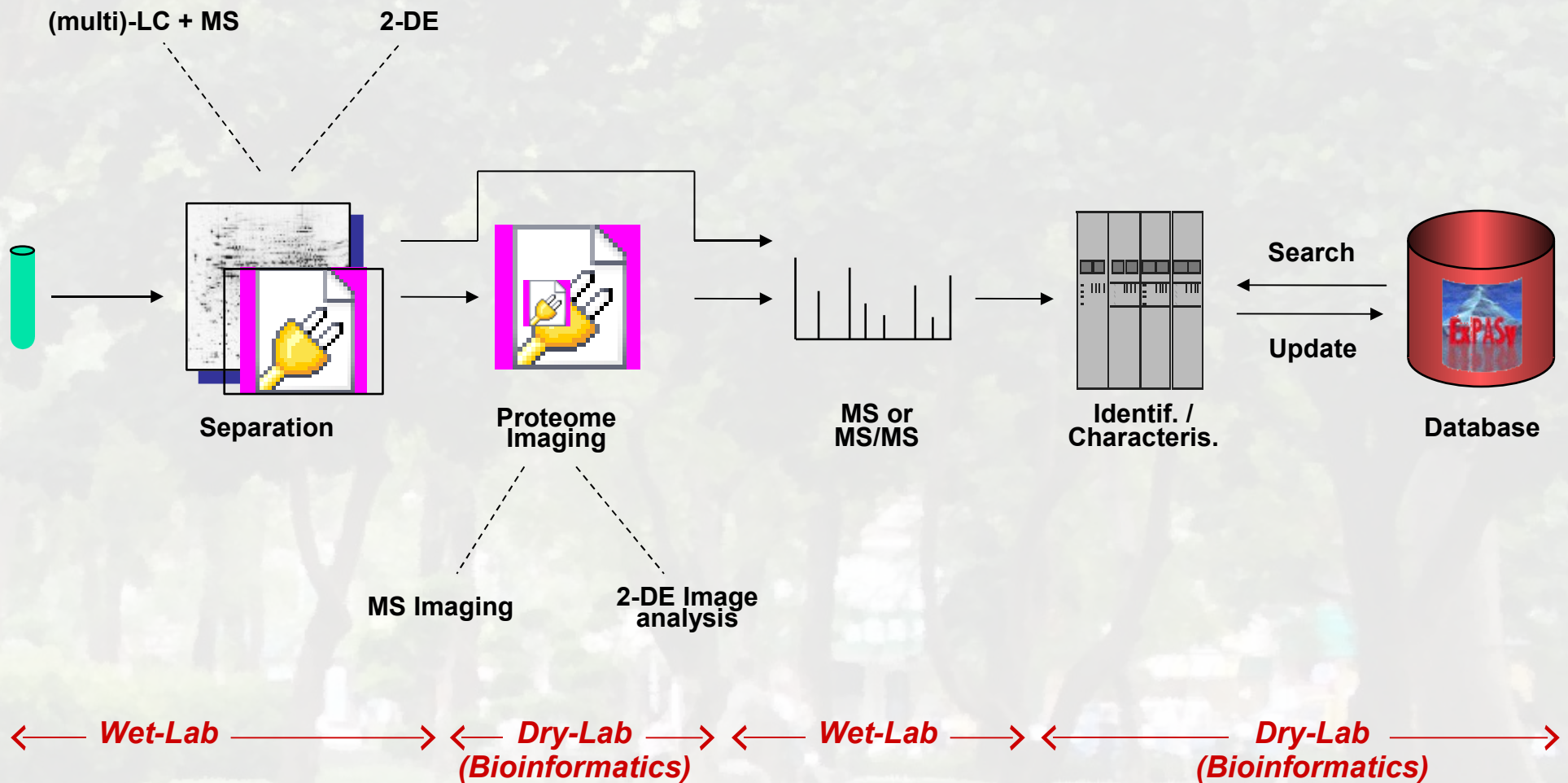
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I am sure some of you think:

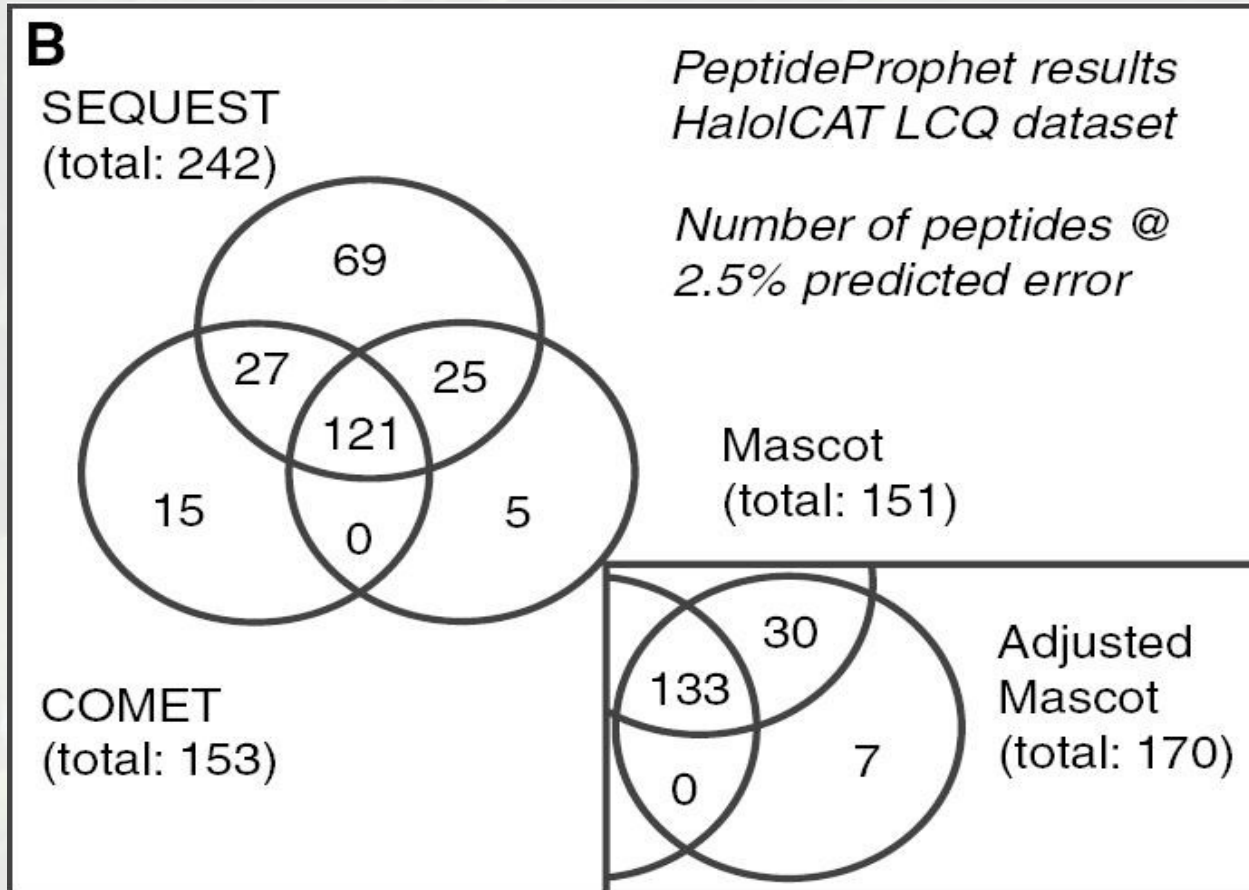
*“What does this guy want? This is the EGEE Conference 2006 and not some classes in biology...?!?”*

# Proteomics workflow



by Ron D. Appel

# Problem in MS/MS data analysis



# Scope of the user

- The Biologist:
  - Semi-automatic system to analyze MS-MS data
    - Easy to understand and simple to use
    - The results if possible yesterday
- The Bioinformatician/Statistician/experienced Biologist:
  - Benchmarks
    - How to improve the identification process ?
      - Which strategy/program for which data?
      - Which parameter set?
  - Data analysis across projects and groups
    - How meaningful are the results ?
      - Comparison and Validation?

# swissPIT and the big computers

Can I install swissPIT on my own computer?

...yes, but you do not become happy with it, because...

- Pierre-Alain Binz (GeneBio SA):
  - Data files up to 300MB packed binary ~ 2GB raw data
  - Computing time up to 32h (depending on parameter + CPU's)
- Paul Jenoe (Biozentrum Basel):
  - Sequest is 10x slower in comparison to Phenyx (GeneBio SA)

# Goals of swissPIT

1. Compare available software
2. Implementation of analysis workflows
3. Unified interface for different programs

Where to start first:

- Web interface
  - Data management
  - Parameter sharing + standardization between programs
  - Unified result visualization
- Automatic system to execute programs in parallel



# What do we need from the community

- Automatic certificate handling
- Distributed DB's and version controlling
- User space + data sharing
- Data backup
- New licensing models for commercial software
- Automatic workflow control
- Job monitoring
- Support to optimize software for distributed computing

**End of the talk**

***Thank you for your attention!***