A Web-Service Approach for Distributed Access to Methods, Data and Models (I Don't Care Where My Data and Methods Are)

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A Web-Service Approach for Distributed Access to Methods, Data and Models

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Overview

-ub3D

Outline

Overview

Pub3D

Model Exchange

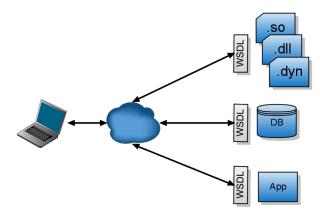
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Local versus Distributed Resources



- Access arbitrary resources (methods, data, applications)
- ▶ All resources look like function calls

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Combining Data & Functionality

- ▶ But what do we mean by "combining" all these resources?
- Different levels of complexity
 - Keep track of new additions to a database via an RSS feed
 - Use Yahoo Pipes to combine and manipulate output easily
 - Write full fledged programs in your language of choice
- Web services allow us to support all these activities in a uniform manner

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Overview

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Web Services - What's Available

Cheminformatics functionality

- Molecular descriptors
- Similarity (2D, 3D)
- Format conversion
- Depictions
- ▶ 3D coordinate generation
- Summarized on <u>ChemBioGrid</u>

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Web Services for Modeling

- Computational web services can be viewed as wrappers around the actual program
- Since predictive models are a common feature in cheminformatics we'd like to support them as well
- This leads to a number of requirements
 - Ability to develop models
 - Store (deploy) models
 - Use the models via the web service infrastructure
- We provide a computational infrastructure based on R which supports
 - Feature selection
 - ► Model development
 - Model deployment
 - Arbitrary R code

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What's Available?

- Regression (OLS, CNN, RF)
- Classification (LDA)
- Clustering (k-means)
- Feature selection (stepwise and exhaustive)
- Automated model generation
 - Load X, Y data, build linear and non-linear models with optional LOO CV
- Deployed models
 - Random forests for 60 NCI DTP cell lines
 - Cytotoxicity
 - Ames mutagenicity

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Web Services - What's Available

Data sources

- We maintain a number of databases
 - PubChem mirror (mainly for local research)
 - Pub3D
- ▶ Directly accessible via queries in SQL
- We also encapsulate specific queries as web service calls

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REST Frontends to SOAP Services

- REST is a network architecture that avoids complex message formats
 - No extra libraries required
 - Access services using URL's
 - Much simpler interface compared to SOAP
- We've been putting REST interfaces onto a number of our SOAP services
- Current REST services include
 - Database (3D structure, PubChem mirror)
 - Molecular descriptors
 - Depictions

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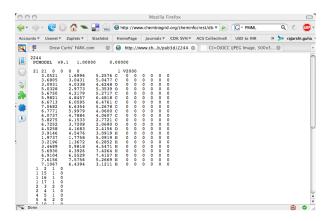
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REST 3D Structure Service

▶ To get a 3D structure for a PubChem CID

http://www.chembiogrid.org/cheminfo/rest/db/pub3d/2244



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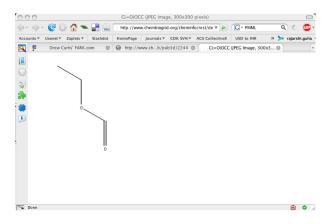
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REST Depiction Service

► To get a 2D depiction for arbitrary SMILES

http://www.chembiogrid.org/cheminfo/rest/depict/C(=0)OCC



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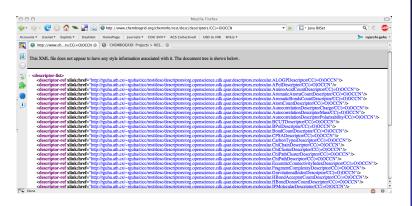
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REST Descriptor Service

► To get descriptors for an arbitrary SMILES string

http://www.chembiogrid.org/cheminfo/rest/desc/descriptors/CC(=0)OCCN



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Pub3D

- A 3D structure database derived from PubChem
- Current version contains a single 3D structure for 17M compounds
 - Structures obtained using MMFF94
 - Not the lowest energy conformer
- Structures can be retrieved in SD format by CID using a web page or web service interfaces
- We also store distance moment shape descriptors allowing us to perform shape similarity searches
- http://www.chembiogrid.org/cheminfo/p3d/

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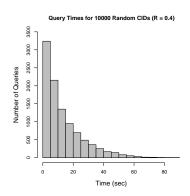
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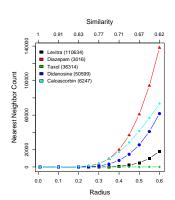
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Pub3D Performance

- Shape searches can be as fast as 5s, for reasonably large result sets
- Fast enough for us to explore the "density of space" around a given query compound





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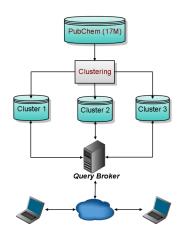
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Pub3D

Pub3D & Clustering

- Indexing gives good performance
- As index size increases, performance degrades
- Could add more RAM
- Clustering the database allows us to scale to significantly larger collection



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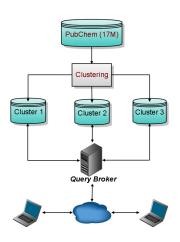
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Pub3D and Conformers

- ► Single, arbitrary conformers aren't too useful
- We have currently generated conformers for a subset of PubChem (4 to 10 heavy atoms)
 - ► 3 Kcal energy window
 - ▶ 243,892 compounds
 - ▶ ≈ 2M conformers
- Clustering will be vital when conformers are considered
 - Allows us to handle arbitrary numbers of conformers
 - ▶ May need to consider some sort of compression
 - Could use cluster information to optimize queries

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Model Exchange

- ▶ The literature contains many published models
- ▶ No way to utilize them unless we manually rebuild them
 - In many cases we will not have access to descriptors
- Difficult to search for models specifically
- ▶ We should be able to do the following
 - Search for models
 - Exchange them
 - Execute them
- ▶ Is this a "format" issue?
 - ▶ To some extent yes

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- Predictive Modelling Markup Language
- A standard supported by the Data Modeling Group
- Allows you to serialize predictive models to XML
 - Linear, logistic regression
 - Tree models
 - Neural networks, Naïve Bayes models
 - Association models
 - Ensemble models (random forests, arbitrary ensembles)
- Supported by a number of platforms
 - ► IBM, Salford Systems
 - SAS, SPSS
 - R

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- ► Since it's XML, it's extensible
- PMML allows us to specify the model itself
- But we need to add extra information to make a model truly searchable
 - Provenance (who made it, when was it made, ...)
 - Property (what is being modeled)
 - Requirements (what are the inputs, how to get them)

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PubsD

Provenance

Easily solved using Dublin Core

Property

- Could be addressed using keywords
- Could reuse pre-existing ontologies

Requirements

- ► This is tricky
- ▶ Need to identify what descriptors were used
- ► What software, version
- ► How to evaluate the descriptors (if possible)

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Summary

- Pub3D is a shape searchable version of PubChem
- Conformers will have to be considered for it to be useful
- ▶ Are searches meaningful? Benchmarks required

- Web services provide one approach to model deployment
- We should be able to search for models explicitly
- ► PMML is one extensible solution the addresses model exchange
- Automated model execution is more challenging

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