GeneDB

- GeneDB is the organism data resource and annotation database for the Pathogen Sequencing Unit (PSU) at the Sanger Institute, UK
- Contains 37 organisms, which is expected to grow to 62
- Currently migrating to chado schema
- Java API with two engines Hibernate & iBatis
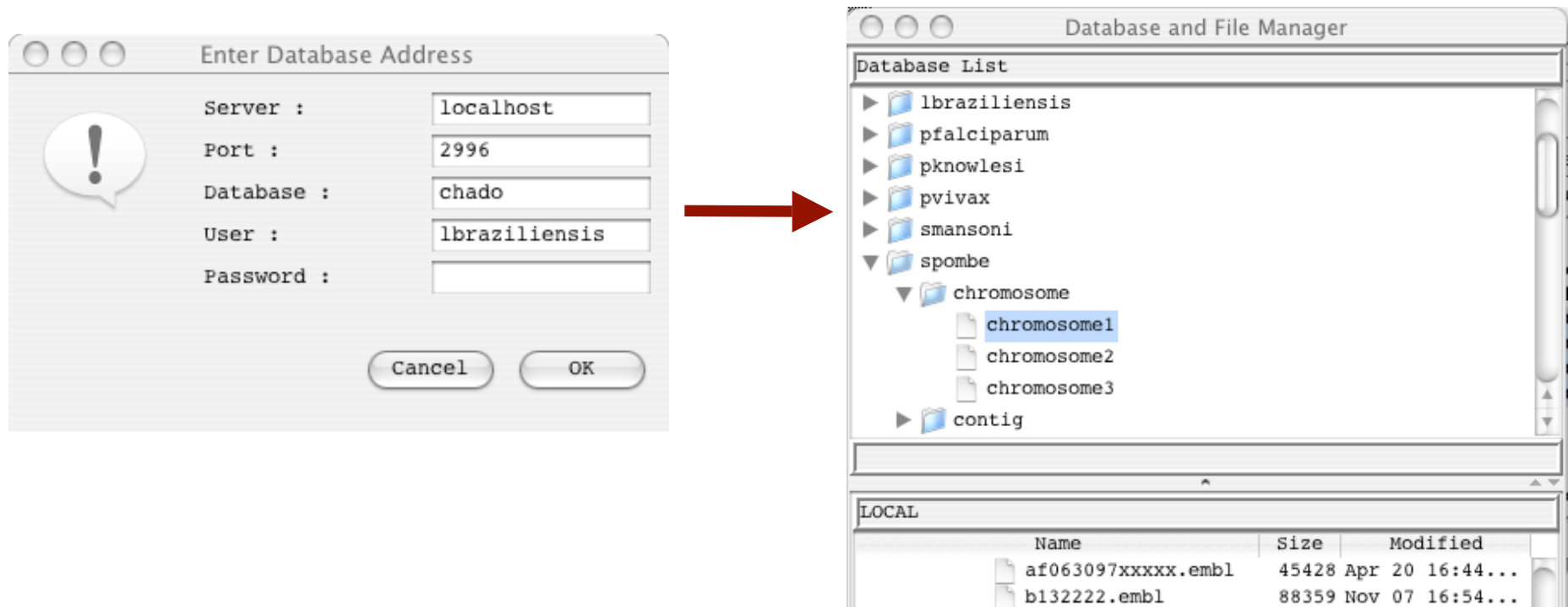
Technical - Connections

- Connections are configured in the Spring configuration file

  `<bean id="dataSource" class="org.apache.commons.dbcp.BasicDataSource">`

  `<property name="driverClassName" value="org.postgresql.Driver" />`

  `<property name="url" value="jdbc:postgresql://holly.sanger.ac.uk:5432/chado" />`

  `<property name="username" value="DELIBERATELY_BOGUS_NAME"/>`

  `<property name="password" value="WIBBLE" />`

  `</bean>`

- Uses a connection pool

- Connection to the database is specified graphically, so the iBatis configuration file has variables for the location:

  `<property name="JDBC.Driver" value="org.postgresql.Driver"/>`

  `<property name="JDBC.ConnectionURL" value="jdbc:postgresql://${chado}"/>`

  `<property name="JDBC.Username" value="${username}"/>`

  `<property name="JDBC.Password" value="${password}"/>`

- provide database location, username & password
- select from scrollable list of feature with residues (organisms in separate Postgres schemas) what to open in Artemis

Technical - Code Generation

- The shared interface and hibernate implementation were originally generated

- There's no explicit code generation (although the Spring and Hibernate runtimes may use them behinds the scenes)

Technical - Transactions

- Transactions are fully supported

- There's no explicit code generation (although the Spring and Hibernate runtimes may use them behind the scenes)

Demo – Sample Problem

CvTerm - gene

→ Creating a gene

genes[0] = new Feature(ORG, GENE, "xfile", false, false, now, now);

Organism - gmod1

    genes[0].setSeqLen(1029);

    sequenceDao.persist(genes[0]);

    FeatureLoc loc = new FeatureLoc(SOURCE_FEATURE, genes[0], 13691, false, 14720, false, (short)1, 0, 0

,0);

    sequenceDao.persist(loc);

    addFeatureProp(genes[0], "description", "A test gene for GMOD meeting");

    addSynonymsToFeature(genes[0], "mulder", "scully");

    createExon("exon1", genes[0], 13691, 13767, now, 0);

createExon("exon2", genes[0], 14687, 14720, now, 1);

→ Retrieve a gene

Feature f = sequenceDao.getFeatureByUniqueName("xfile");

displayGene(f);

→ Update a gene

genes[0].setUniqueName("x-file");

sequenceDao.merge(genes[0]);

Demo – Sample Problem

```
private Feature createExon(String name, Feature gene, int min, int max, Timestamp now, int rank) {

        Feature exon = new Feature(ORG, EXON, name, false, false, now, now);
        exon.setSeqLen(max-min);
        sequenceDao.persist(exon);

        FeatureLoc loc = new FeatureLoc(SOURCE_FEATURE, exon, min, false, max, false,
                                        (short)1, 0, 0 ,0);
        sequenceDao.persist(loc);

        return exon;

    }
```

GeneDB

Gene: xfile

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Pathogen Sequencing Unit

▾ Naming

Symbol: xfile

Synonyms:
    mulder,scully
Type:
    gene

▾ Exons

Exon	Start	End
exon1	13691	13767
exon2	14687	14720

▾ Residues

ATGGCGTTAGTATTCATGGTTACTGGTTTCGCTACTGATATCACCCAGCGTGTAGGCTGTGGAATCGAACACTGGTATTGTATAAATGTTTGTGAATACACTGAGAAATAA

Hosted by the Sanger Institute   Curator feedback   Technical feedback

```
<st:section name="Naming" id="gene_naming" collapsed="false" collapsible="false"
hideIfEmpty="true">
  <dl>
      <dt><b>symbol:</b></dt>
      <dd>${feature.uniqueName}</dd>
  </dl>
  <db:synonym name="synonym" var="name" collection="${feature.featureSynonyms}">
    <br /><b>Synonym:</b> <db:list-string collection="${name}" />
  </db:synonym>
  <dt><b>Type:</b></dt>
  <dd>${feature.cvTerm.name}</dd>

<st:section name="Exons" collapsed="false" collapsible="true" hideIfEmpty="true">
      <display:table name="exons" uid="tmp" pagesize="30" class="simple" cellspacing="0"
cellpadding="4">
            <display:column property="uniqueName" title="Exon"/>
            <display:column property="featureLocsForSrcFeatureId.fmin" title="Start"/>
            <display:column property="featureLocsForSrcFeatureId.fmax" title="end"/>
      </display:table>
</st:section>

<st:section name="cds" collapsible="true">
      <b>${feature.residues}</b>
</st:section>
```