FlyBase

XORT- How to Bridge your Database and Application

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Generic Modern Language Database ?

My Parents: hometown dialect

My wife: Mandarine (official form of Chinese)

My son: Plain English

With colleagues: ‘chadoXML’

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Introduction

- An XML-database mapping system for data exchange between DB and XML-driven application
- Developed/Supported by Pinglei Zhou at FlyBase Harvard, 0.007 version now.
- Used: All FlyBase sites
- Written in Perl
- Required perl modules:

  XML::Parser::PerlSAX
  Unicode::String
  XML::DOM
  DBI

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Components

- Database & Schema
- ChadoXML Specification
- DumpSpec collections
- Tools

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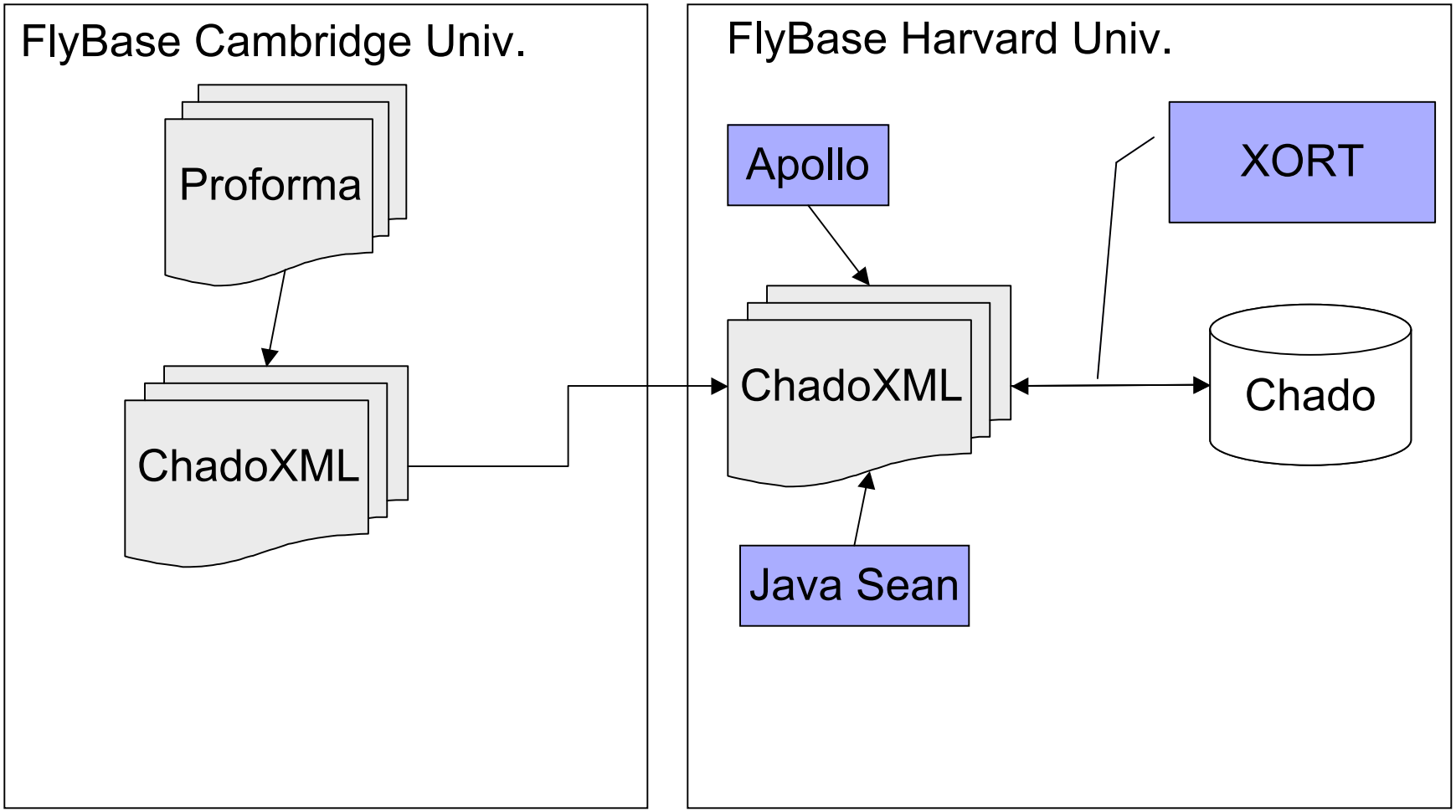
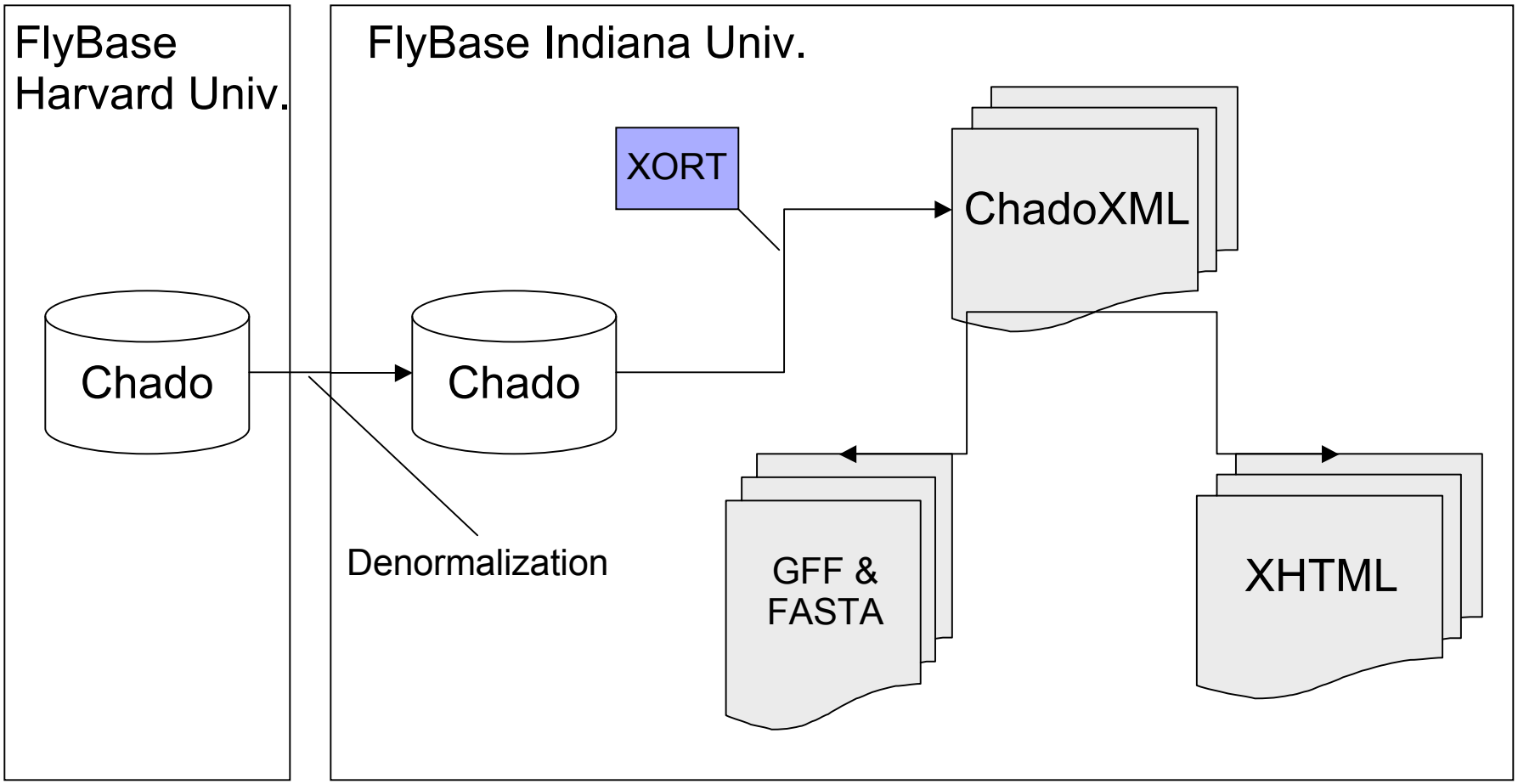
Highlights of Chado XML Specification

- Unique represent of specific database schema
- Get away with those internal primary key value
- Static vs. Operational
- Encoding for non-anscii characters
- Macro mechanism (object reference)

Putting it together: New FlyBase dataflow – Part 1



Putting it together: New FlyBase dataflow – Part 2



FlyBase Data & Report Generation

- Content of all output files is controlled by XML dumpspecs.
  - Dumpspecs are language independent.
  - Easily readable (with knowledge of Chado structure).

- All XML transformation steps are done with XSLT v2.
  - Saxon XSLT (http://saxon.sourceforge.net/)
  - ChadoXML is split into individual chunks before XSLT processing to accommodate large file sizes.
  - Extremely fast. We can process all data for ~60,000 Drosophila genes in under 30 minutes.

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Hibernate & XORT

- Hibernate didn't scale well when dealing with 5,000+ features in bulk.
- Performance tweaks for Hibernate can be quite complicated to setup for bulk operations.
- XORT is currently handling ~6 million features in production with only minor performance problems.
- XORT is much more language independent.

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Support for complex transactions using XORT

Eg:

- Find all records linked to a record using dumpspec

- Merge gene x into y, each with thousands of records attached

1. Dump all data use simple dumpspec

```
<chado>
        <feature dump="all">
                <uniquename test="eq">x</uniquename>
        </feature>
</chado>
```

2. Delete feature x from DB, with triggers to clean orphan records, if necessary
3. Edit the output xml, change uniquename x to y, then load the edited file back to DB

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CHIA
(Chado Interface Application)

Java application organizes SQL and XORT functionality for internal users, eg:

- Dump chado-XML for gene regions for Apollo curation
- Organize and execute “canned” SQL queries
- Serve IDs for curators (in development)
- Dynamic browser Chado without writing SQL statement

CHIA is being designed to be extensible for adding new functionality as needed.

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Limitations

- DB Schema follow certain rules

  All have internal int primary key

  All have unique key(s)

- It may take long path to retrieve certain type of data

  gene->allele->genotype->phenotype via feature_relationship

- Structure not store in memory

  Flush out data as it goes

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Documentation

- Previous presentations
- Using chado to Store Genome Annotation Data

  Current Protocols in Bioinformatics (Baxevanis, A.D., and Davison,D.B., eds) 2,9.6.1-9.6.28.
- XORT specification docs
- XORT draft (unpublished)
- GMOD case demo procedure

  All in the doc directory of XORT package

  http://www.gmod.org

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