Object Modeling for Semantic Meaning

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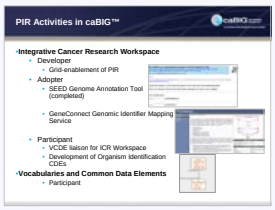
Protein Information Resource (PIR)

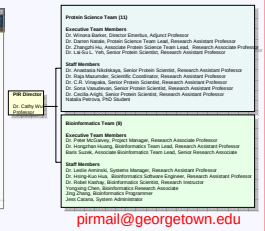


http://cagrid-portal.nci.nih.gov/

http://www.uniprot.org

http://pir.georgetown.edu

http://pir.georgetown.edu/proteomics



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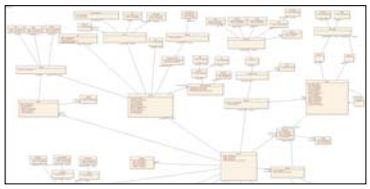
Iterative Information Model Development

First Model

Problems:
- Record modeling -> Limited semantics and scientific meaning
- XML schema constraints -> A lot of objects without attribute
- Unidirectional associations, association names missing -> Limited navigability

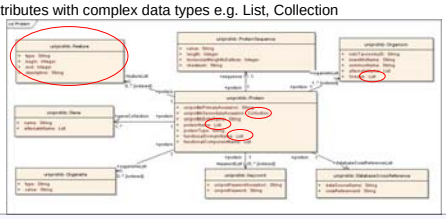


A model reverse engineered from UniProtKB XSD

Applied domain modeling for core components and reused parts of available models e.g. caBIO

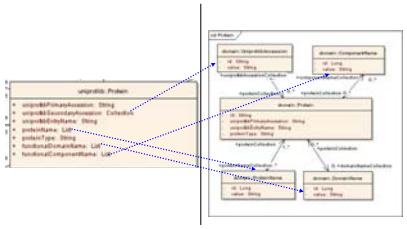
Second Model

Problems:
- Semantics needed improvement; better class naming, removal of type attributes
- Attributes with complex data types e.g. List, Collection



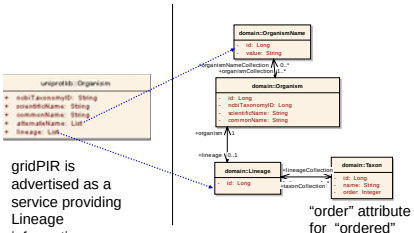
Towards Final Model

Removing Complex Data types



Towards Final Model

Removing Complex Data types / Improving Semantics



gridPIR is advertised as a service providing Lineage information

"order" attribute for "ordered" collection

Towards Final Model

Improving semantics

Protein sequence annotation
- Regions or sites of interest in the sequence
- Posttranslational modifications
- Binding sites
- Enzyme active sites

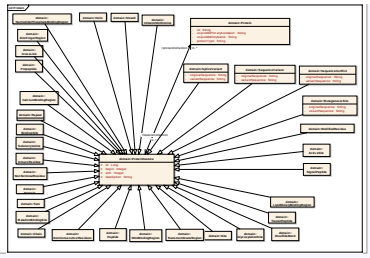
Problems:
- Using "type" hides the semantic value such Protein annotation
- Can't meet use cases such as:

Find me all the proteins which "Calcium Binding Region" or "Zinc Finger Region"

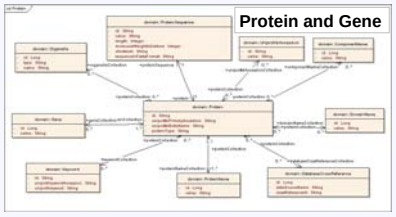
Towards Final Model

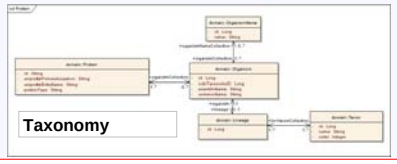
Improving semantics

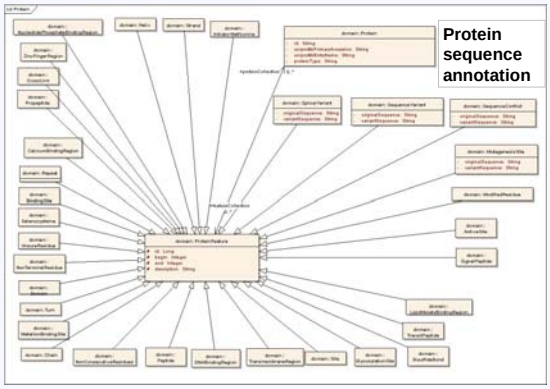
One object for each Protein Feature type



Final Model







Conclusion

- ❑Better advertisement and discovery of gridPIR data service
  - ❑gridPIR as a Gene/Protein resource
  - ❑gridPIR as a Protein Annotation resource
  - ❑gridPIR as a Taxonomy information resource
- ❑Better understanding of scientific content of the service
- ❑Better usability:
  - ❑Retrieve proteins for a gene
  - ❑Retrieve sequence for a protein
  - ❑Retrieve proteins containing calcium binding sites
  - ❑Retrieve proteins containing zinc finger regions
  - ❑Retrieve proteins for a taxon in taxonomy tree