

# Moby, Legacy Apps and the Semantic Web

**Web Services BioHackathon 2008**

**Paul Gordon**

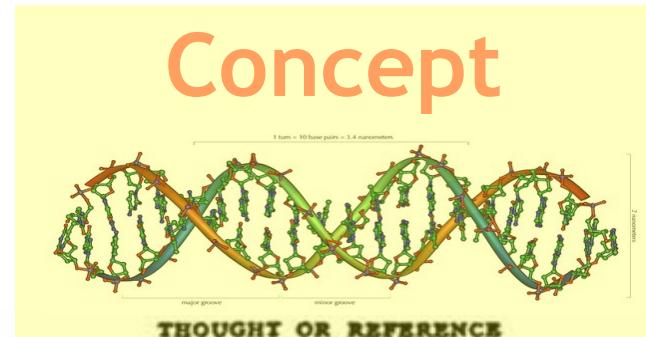
**Sun Center of Excellence for Visual Genomics  
University of Calgary**

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# Motivation & Goals

- Interoperability of maximum number of autonomous resources (databases & analysis programs)
- Minimal overhead of implementation
- Flexibility for bioinformaticians
- Usability for biologists

# What are Semantics?

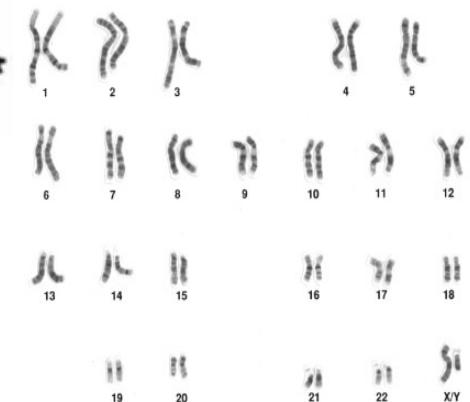


# Words

# DNA, D.N.A., Deoxyribonucleic Acid ADN (French)

脱?核糖核酸, 国防部核子局  
(Simplified Chinese)...

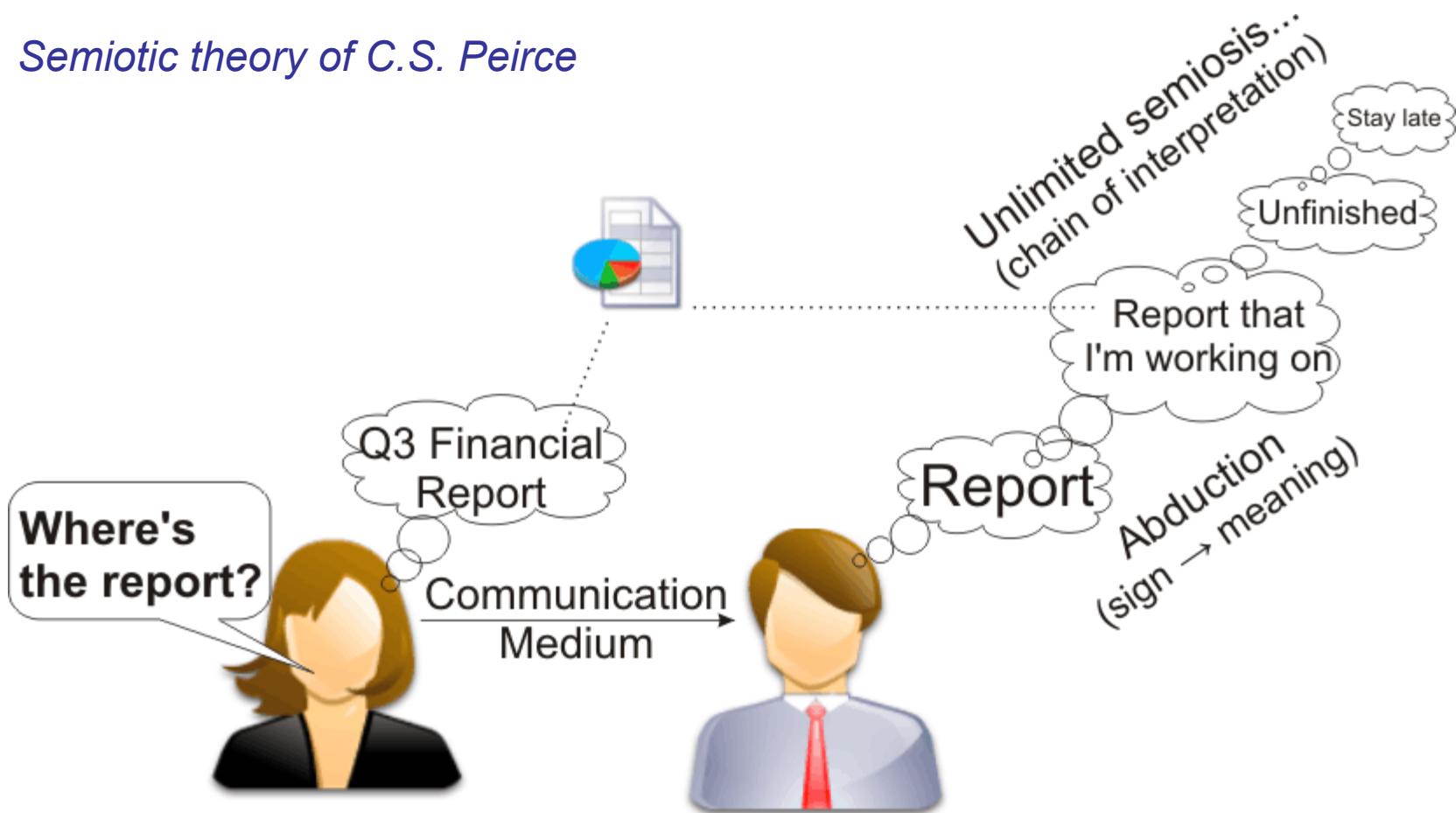
# Things



## Semantic Triangle from *The Meaning of Meaning* (1923)

# Words have no fixed meaning in normal conversation

Semiotic theory of C.S. Peirce



Computers don't generally work this way, their interpretation of input is **strict**

# Paul's Pragmatic Maxims

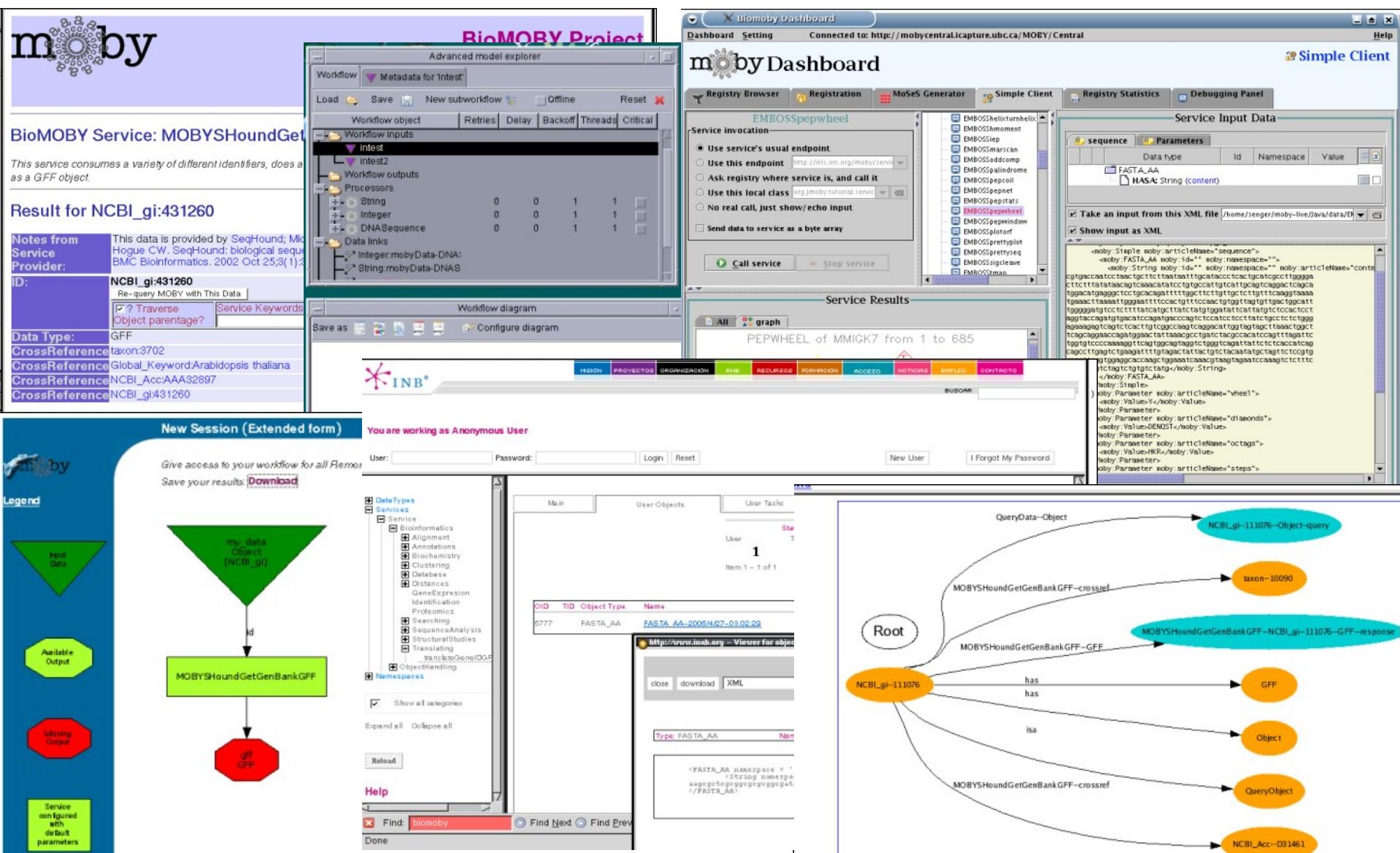
- You cannot get rid of work
- Redistribute work amongst parties
  - Who's most motivated?
  - Who's most knowledgeable?
- Avoid repetition of work
  - Accessibility of code
  - Reusability of code



The limits of my language are the limits of my mind. All I know is what I have words for.

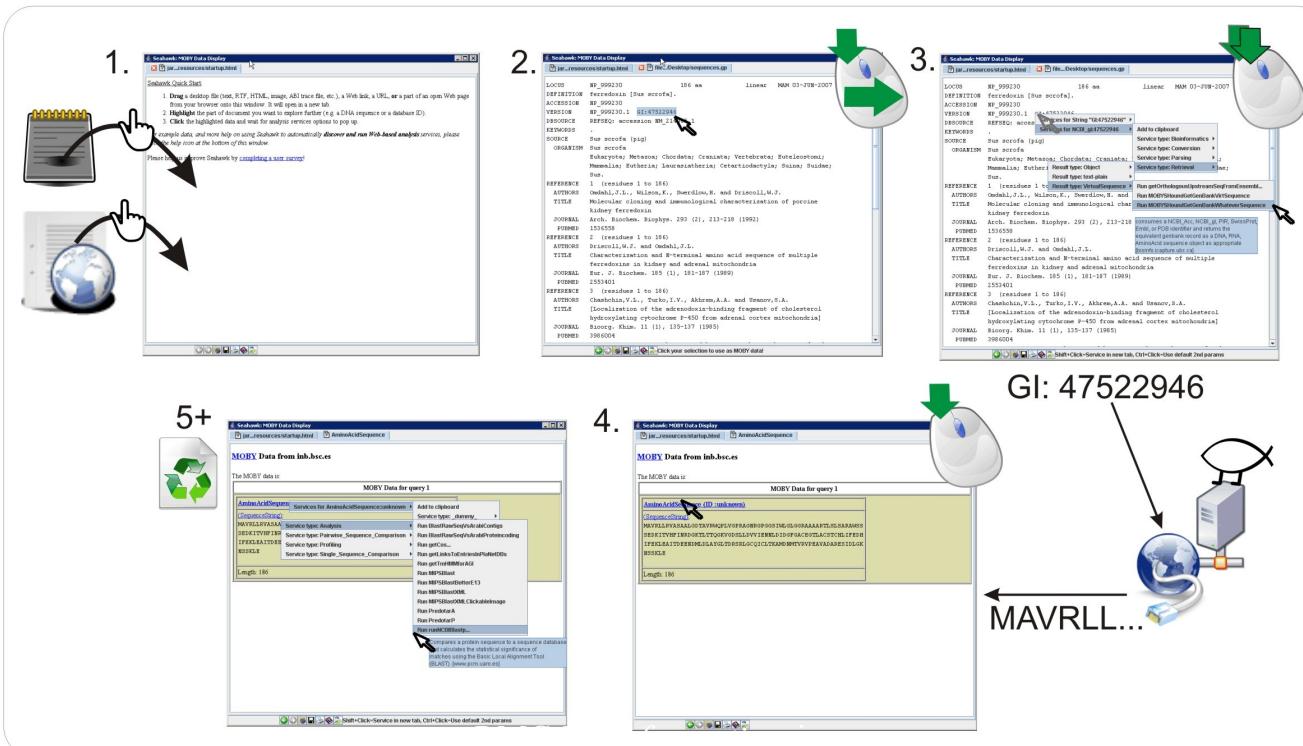
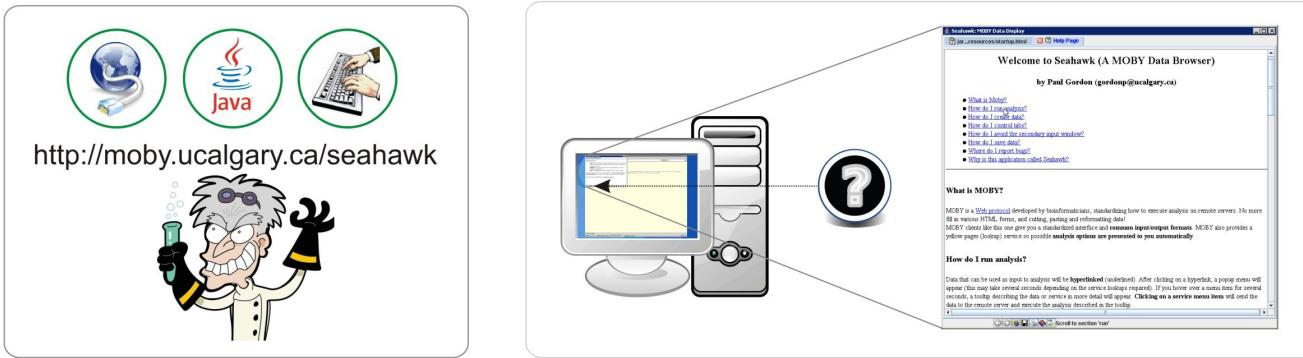
*Ludwig Wittgenstein*

# Many MOBY Clients...



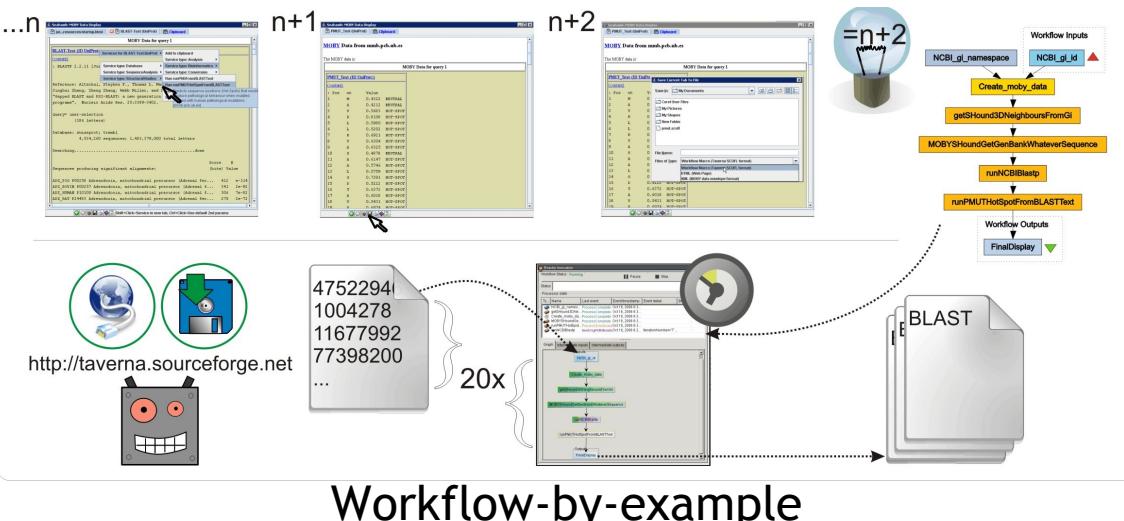
# Seahawk: MOBY Client for Biologists

Drag ‘n’ drop, highlight existing data for use with MOBY Services



# Service Provision Model

- Make existing computational resources available as MOBY services
- Build new platform tools as MOBY services
- Make it easier for biologists to create and run MOBY workflows for repetitive analysis



Workflow-by-example

The screenshot shows two web-based interfaces for workflow execution:

- bioewp: a Workflow Enactment Portal for Bioinformatics**: A Java-based application window showing a user profile and a list of available results.
- bioinformatics.ijs.si: bioewp: Workflow Results**: A web browser window displaying execution details, workflow inputs, and results lists for two different workflow executions.

The results lists include various bioinformatics tasks such as "Cell Lines Catalogues", "Text lines separator", and "Extract IDs by matching catalogues names".

Workflow Execution Web Portals

# MOBY Service Provision: Java

```
import org.biomoby.shared.MobyDataType;
import org.biomoby.shared.data.*;
import org.biomoby.service.*;

@mobyService(name="ConvertAAtoFASTA_AA",
    type="FormatConversion",
    provider="moby.ucalgary.ca",
    author="gordonp@ucalgary.ca",
    in={"inseq:AminoAcidSequence"},
    out={"outseq:FASTA_AA"},
    description={"Converts amino acid objects into FastA formatted records,
        "primarily to increase inter-service compatibility"})

public class ConvertAAtoFASTA_AA extends MobyServlet{

    public void processRequest(MobyDataJob request, MobyDataJob result)
        throws Exception{

        // The input parameter for this method is registered as "inseq"
        MobyDataComposite aaSeqObj = (MobyDataComposite) request.get(" inseq");

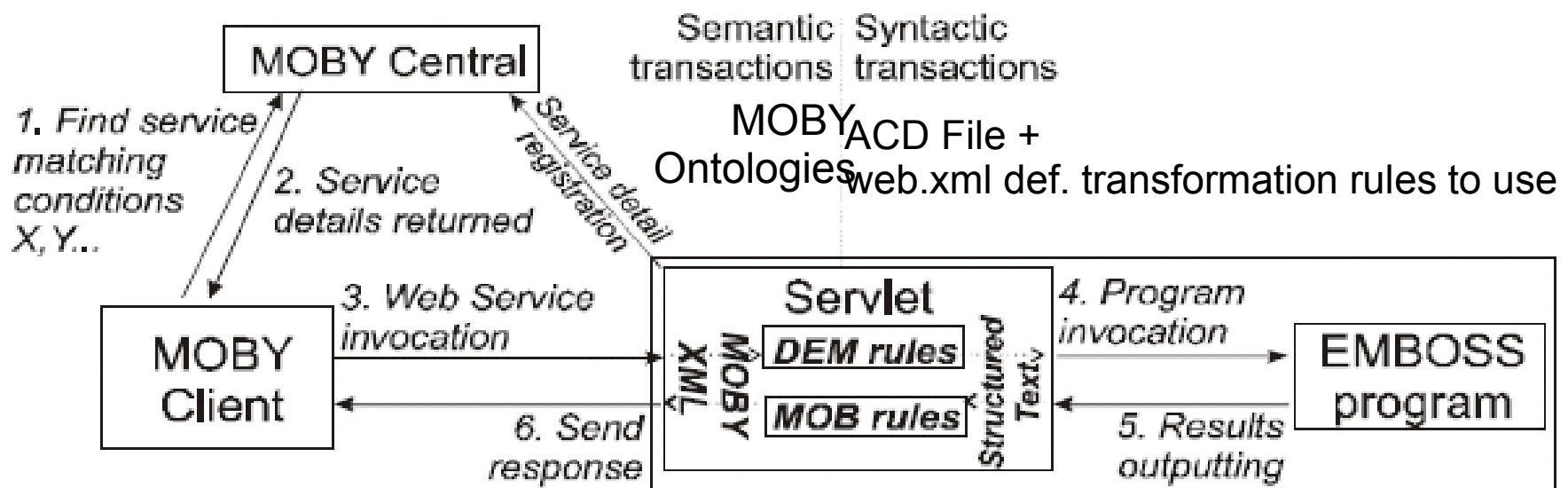
        // SequenceString is a member of incoming AminoAcidSequence object
        MobyDataString aaStringObj = (MobyDataString) aaSeqObj.get(" SequenceString");
        String aaString = aaStringObject.toString();

        ...
    }
}
```

# MOBY Service Provision Legacy

**Legacy non-XML apps (by MOBY Service provider)**

EMBOSS = declarative “MOB” and “DEM” rules  
+ web.xml + ACD file spec



Gordon P.M.K., Kawas E., Wilkinson M.D., Sensen C.W. (2007) Using a novel data transformation technique to provide the EMBOSS software suite as Semantic Web Services. [To appear](#) in Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine (San Jose, California), November 2-4, 2007.

# MOB Rules

## Formatted EMBOSS text

```
CHARGE of HBB_HUMAN from 1 to 146: window 5

Position Charge
1 0.100
2 -0.100
3 -0.400
4 -0.200
5 -0.200
6 -0.200
7 0.000
8 0.200
9 0.000
10 0.000
...
142 0.400
```

↓ MOB rule (regex+XML)

```
<ProteinChargeTable articleName="" namespace="" id="">

<String articleName="caption">CHARGE of HBB_HUMAN from 1 to 146: window 5</String>

<tableRow articleName="header">
  <String articleName="cell">Position</String>
  <String articleName="cell">Charge</String>
</tableRow>

<tableRow articleName="row">
  <String articleName="cell">1</String>
  <String articleName="cell">0.100</String>
</tableRow>
...
<tableRow articleName="row">
  <String articleName="cell">142</String>
  <String articleName="cell">0.400</String>
</tableRow>
</ProteinChargeTable>
```

MOBY XML

# DEM Rules

## MOBY XML

```
<DNASequence namespace="NCBI_gi" id="146411799">
  <String articleName="SequenceString" id="">TAGGCAT...GATGT</String>
  <String articleName="Length" id="">252</String>
</DNASequence>
```

## DEM rule (XSLT)

```
>NCBI_gi | 146411799
TAGGCATTACCTACCAACTAACTAATGTTCCGCACCC
CCATTTTAAGTGAAGCTGTGAAGCTCCTTCTATTAC
...
GATGT
```

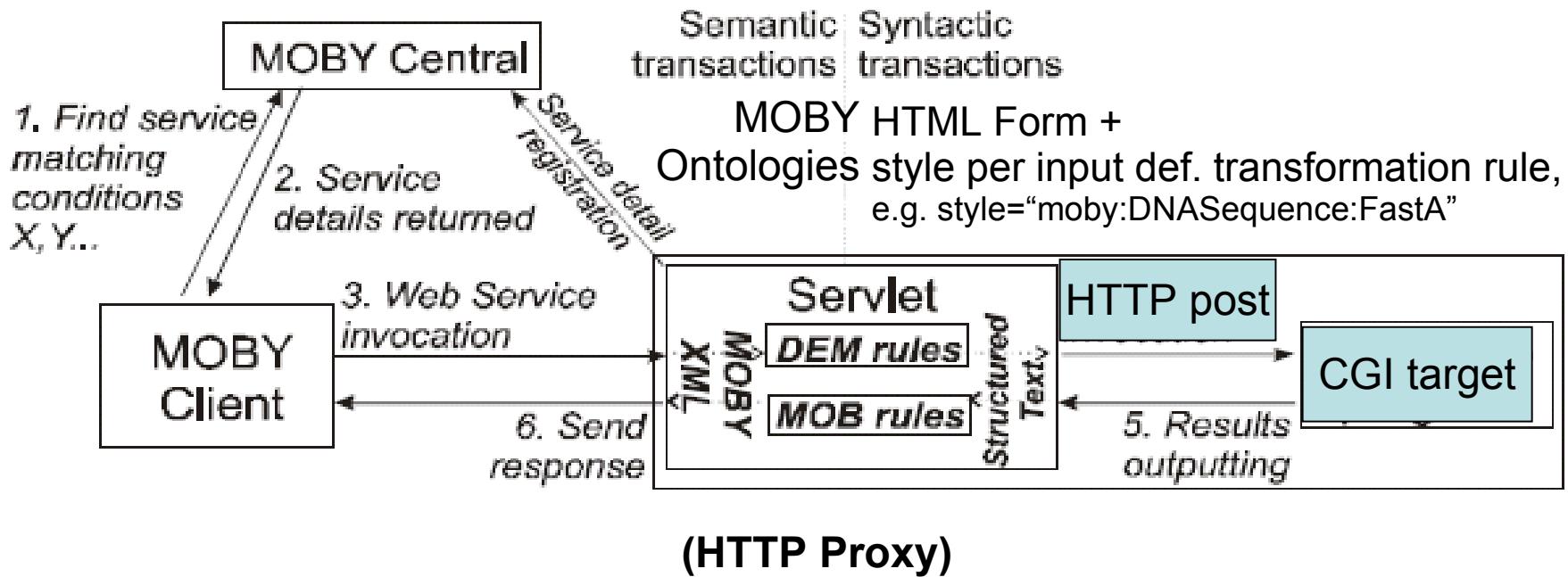
## FASTA-formatted text

```
<xsl:template match="moby:GenericSequence"
  name="GenericSequence.1" mode="seqall">...
</xsl:template>
```

# MOBY Service Provision

**Legacy non-XML apps (by Web site authors)**

HTML = declarative “MOB” and “DEM” rules  
+ HTML form spec



# Wrapping CGIs

File Edit View History Bookmarks Tools Help

file:///home/gordonp/moby-live/Java/src/main/ca/ucalgary/services/util/test/o Google

University of Calgary Webma... Osprey: PCR Product Oli...

**Target Sequence Data**

This should be one DNA template sequence that is the target for PCR amplification.

Choose one of:

1. Paste in DNA sequence (FastA/Pearson format preferred, other formats may parse with less confidence):
2. Upload a target DNA sequence file (max 10MB):

Upload a secondary binding DNA sequence file, e.g. other transcripts from the same species (max 10MB):

**Core Parameters**

Perfect duplex melting temperature (Celsius)

Minimum  Allowable difference for the pair  Maximum

Oligonucleotide length

Minimum  Optimal  Maximum

Na<sup>+</sup> concentration (molar)  (standard PCR is typically 0.05M)

**Other Parameters**

PCR product length: Minimum  Optimum  Maximum

Product must include the following target position or interval

- ◆ (e.g. 314 or 100-200, separate multiple products with commas):
- ◆ or specified as a tab-delimited file:
- ◆ or have a  5' or  3' bias

DNA concentration (molar)

Done

# Semantic Markup via CSS

```
<head>

<meta name="moby:service"
      scheme="http://moby.ucalgary.ca/moby/MOBY-Central.pl"
      content="Primers,moby.ucalgary.ca,CalcPCRPrimers: Takes a DNA sequence
              and calculates PCR probes satisfying given conditions" />

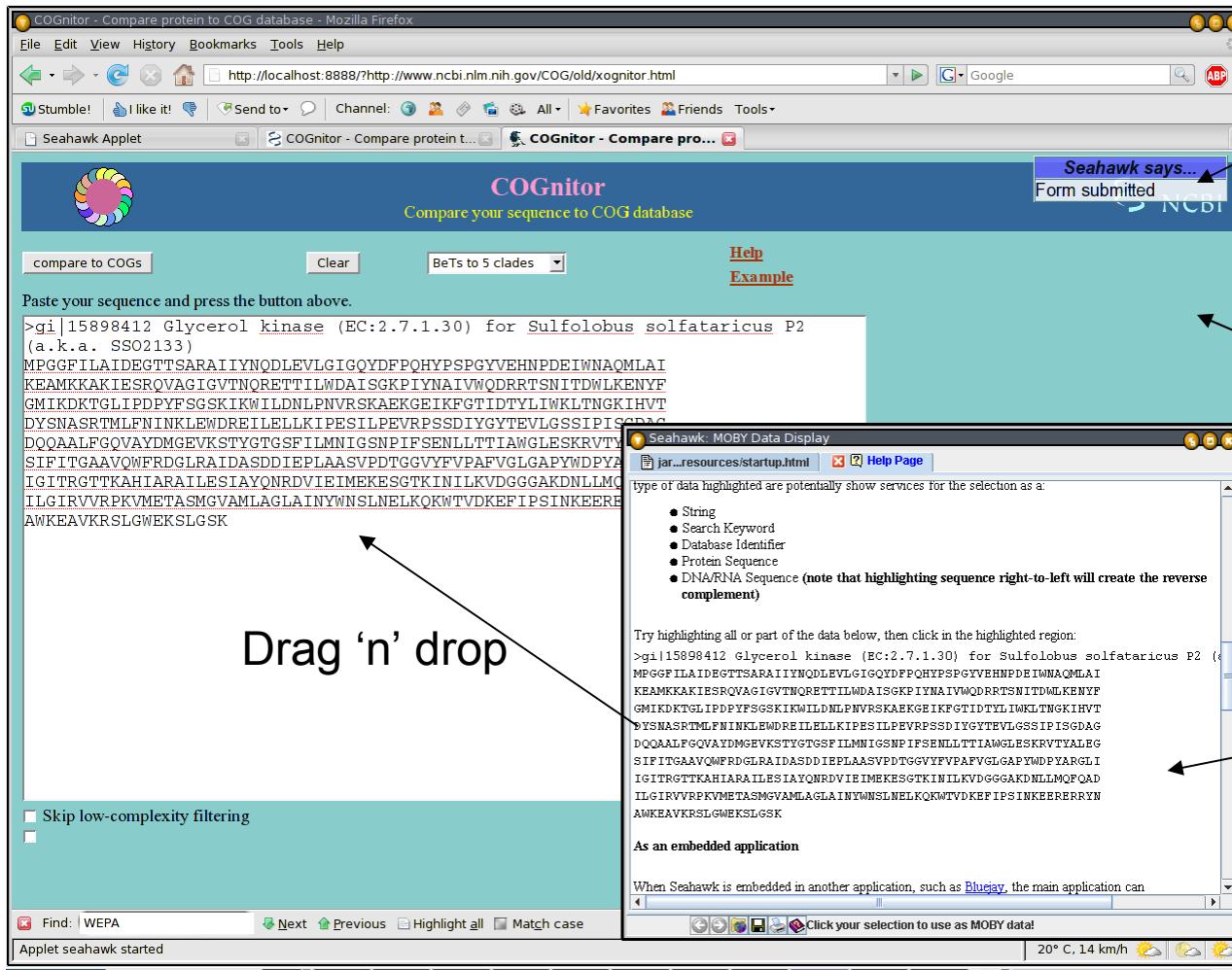
<meta name="moby:contact" content="gordonp@ucalgary.ca">

...
<form class="moby:CalcPCRPrimers:primers:Collection(DNASequence)" action="...
<textarea name="input" cols="61" rows="5" class="moby:inseq:DNASequence:fasta">
...<!-- existing selects, etc. -->
Na+ conc. (molar) <input type="text" size="7" name="salt_conc"
    value="0.05" class="moby::Float::[0,10]" alt="Na+ concentration (molar)"/>
PCR product: Minimum <input type="text" size="4" name="min_prod_len"
    value="200" class="moby:MinimumProductLength:Integer:100:[1,]" />
...
...
```

# Next: Client-Server Convergence

Legacy non-XML apps (by end-users!)

HTML = declarative “MOB” and “DEM” rules  
+ user drag ‘n’ drop in Seahawk



# Conclusions

- Semantics is enabling better “conversations” with the computer
- Distribute work amongst motivated participants
  - Ontology Building
  - Service Provision
  - Workflow Development
- Use a framework more general than you think you need, because you don’t actually know what you need

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