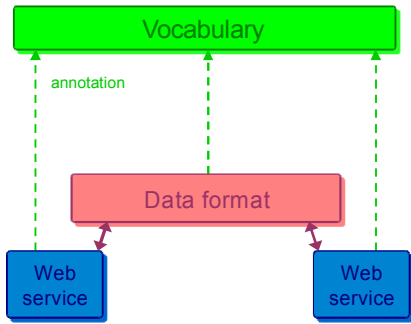


HOW TO PROVIDE INTEROPERABLE BIOINFORMATICS TOOLS



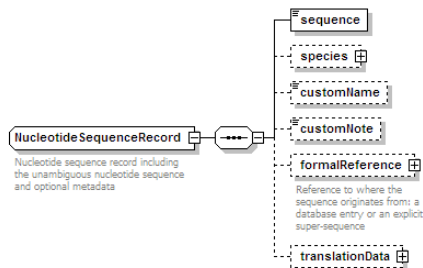
Matúš Kalaš
EMBRACE Course
CBS, Kgs. Lyngby
June 2nd, 2010



Part 1: DESIGN-CENTRIC DEVELOPMENT ACCORDING TO **EMBRACE**

```
<xsd:import
  namespace="http://..."
  schemaLocation="http://..."
/>
```

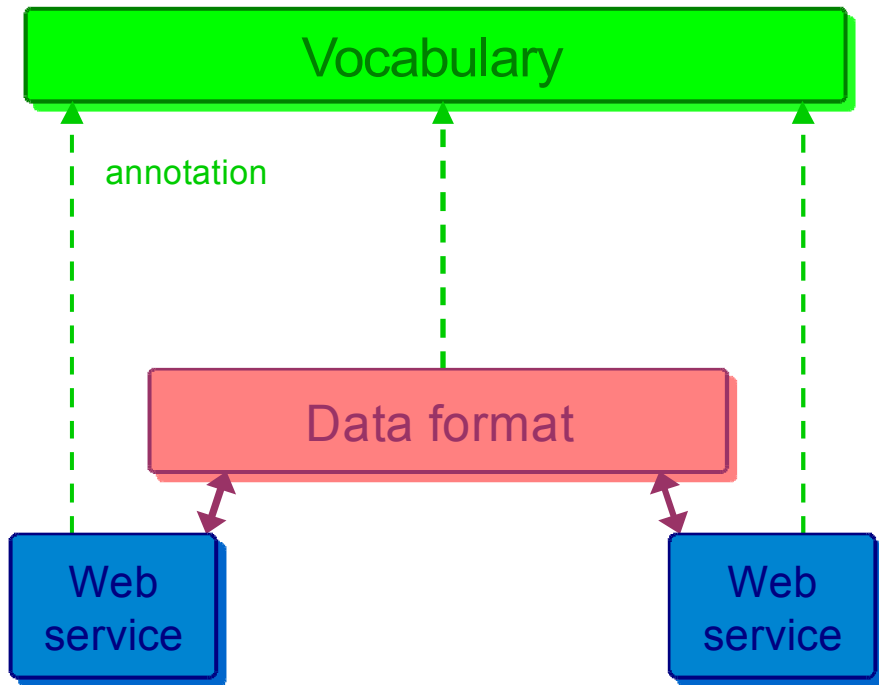
Part 2: USE OF EXTERNALLY DEFINED DATA TYPES



Part 3: INTRODUCTION TO **BioXSD**

Part 1:

DESIGN-CENTRIC DEVELOPMENT ACCORDING TO **EMBRACE**



What is your motivation for doing Web services?

What is your motivation for doing Web services?

**programmatic access
to remote
data & computing resources**

What is your motivation for standardisation?

What is your motivation for standardisation?

standardisation = interoperability

enables users to discover services

enables users to use services

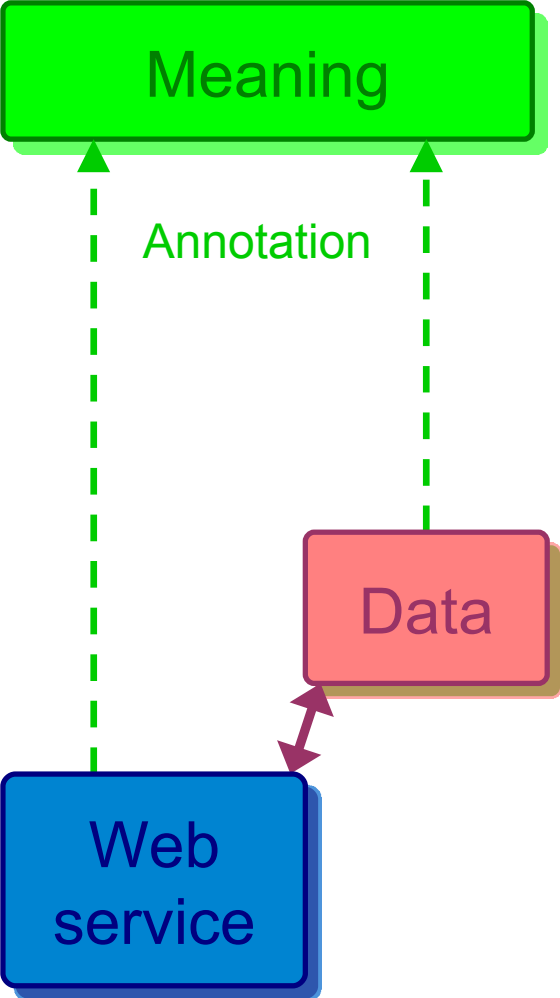
discover operations & parts of data

operate on standardised input/output formats

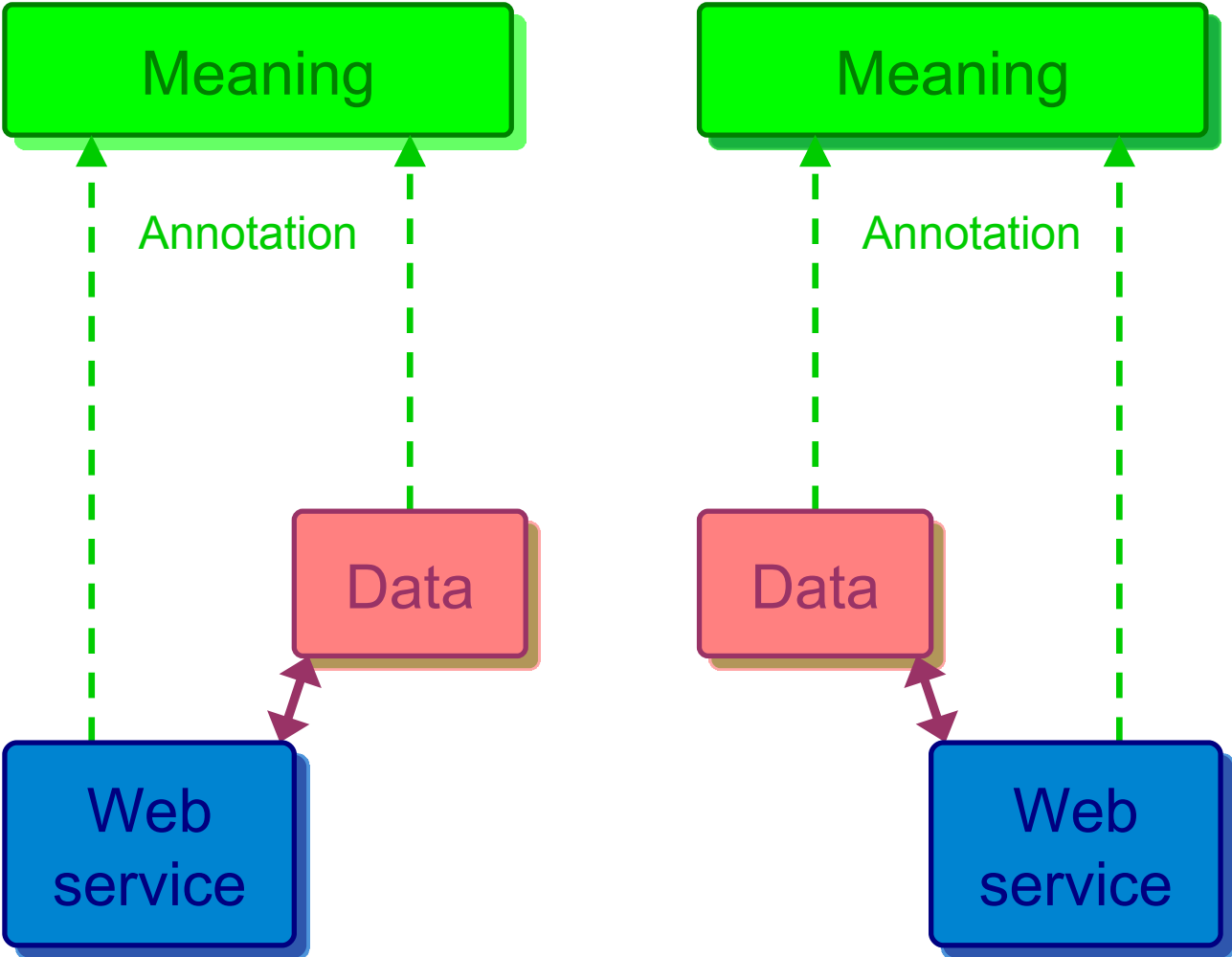
enables users to compose services

mix-and-match services smoothly into workflows/pipelines

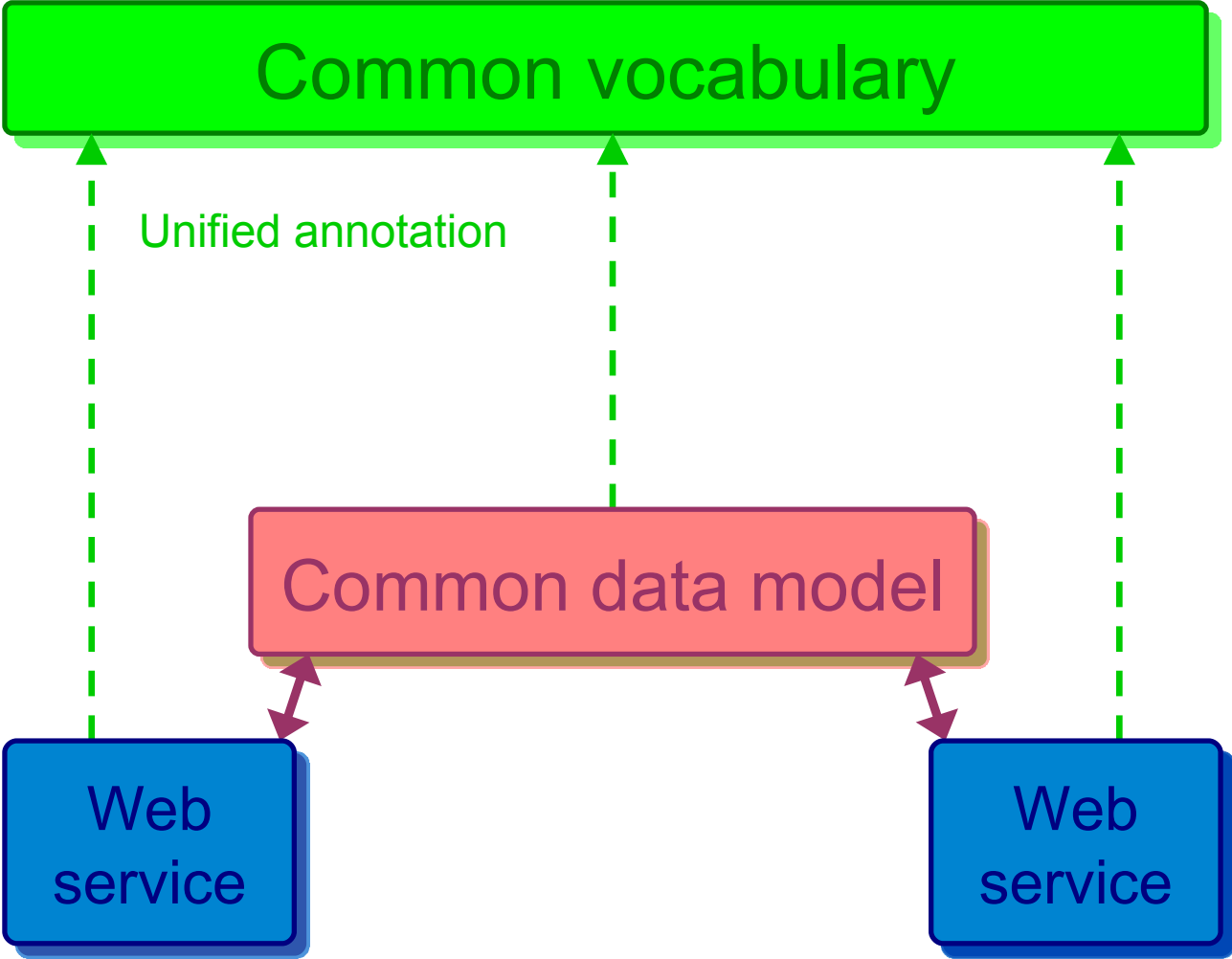
Content of tomorrow's hands-on:



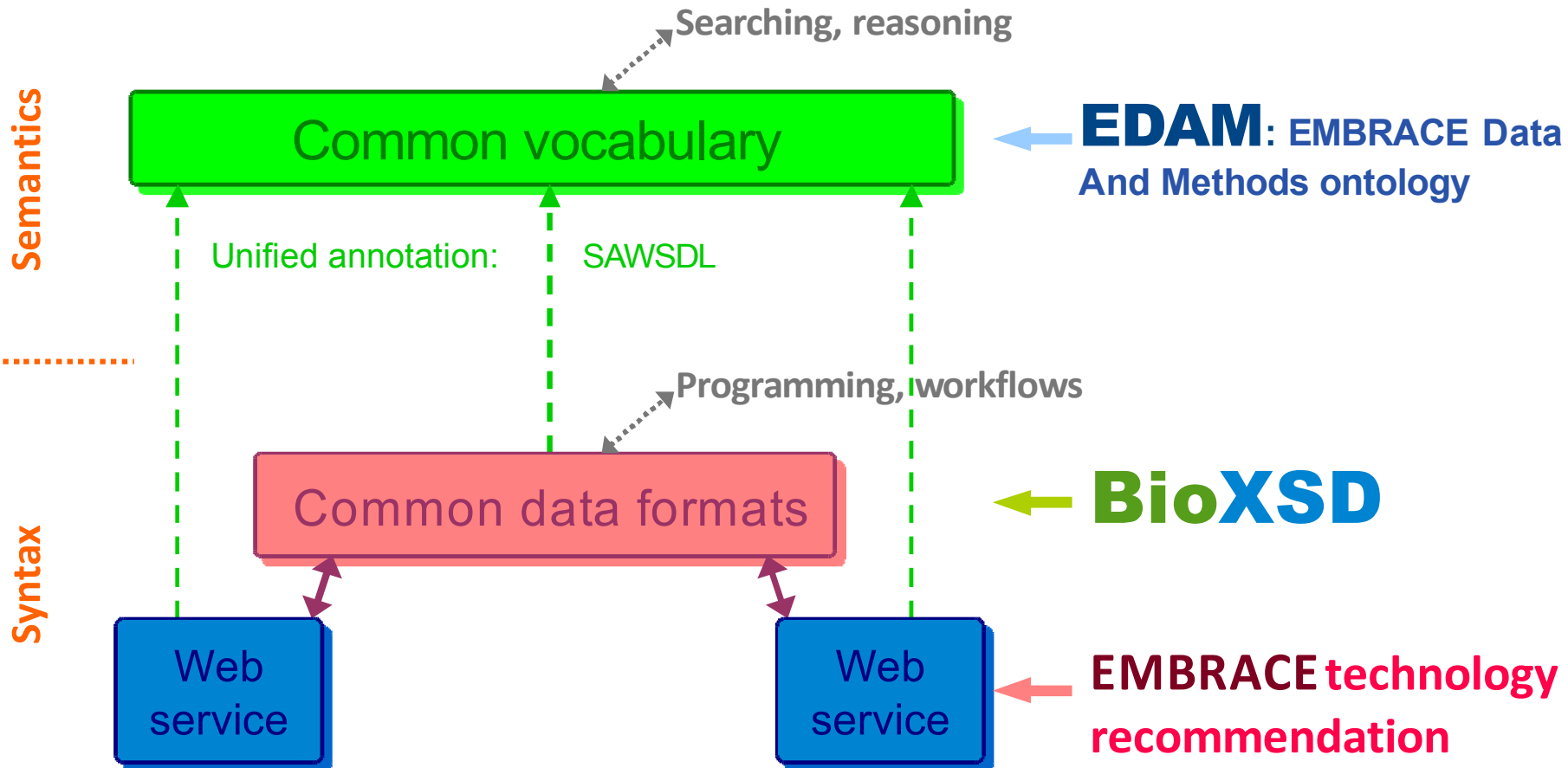
Keeping in mind the interoperability:



Keeping in mind the interoperability:



EMBRACE recommendation for providing interoperable bioinformatics tools & data sources



The recommended design-centric development:

- 1. write WSDL document**
- 2. use WS-I standard & doc-lit wrapped SOAP binding, design invocation pattern**
- 3. services and operations:**
 - name well
 - annotate by EDAM
- 4. structure the input and output data into XML**
 - write XSD complexTypes
 - name well
 - annotate by EDAM
 - use an external common data model when & where applicable (BioXSD complexTypes)
- 5. restrict values of atomic pieces of data**
 - restrict XSD simpleTypes
 - use an external common data model when & where applicable (BioXSD simpleTypes)
- 6. implement the Web service**
 - implement the request handler
 - connect to the tool function (via an API or calling an executable)
- 7. test the Web service & its interoperability**
 - example client programs

The content of tomorrow's hands-on:

1. **write WSDL document**
2. **use WS-I standard & doc-lit wrapped SOAP binding, design invocation pattern**
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7. **test the Web service & its interoperability**
 - example client programs

Part 2:

USE OF EXTERNALLY DEFINED DATA TYPES

```
<xsd:import  
    namespace="http://..."  
    schemaLocation="http://..."  
>
```

The pattern for using external data types in WSDL:

```
<wsdl:definitions
  name="MyService"
  targetNamespace="http://www.myOrg.org/myService"
  xmlns="http://www.myOrg.org/myService"
  xmlns:ext="http://www.externalOrg.org/externalSchema"
  xmlns:wSDL="http://schemas.xmlsoap.org/wsdl/"
  xmlns:xs="http://www.w3.org/2001/XMLSchema"
  .
  .
>

<wsdl:types>
  <xs:schema targetNamespace="http://www.myOrg.org/myService">

    <xs:import
      namespace="http://www.externalOrg.org/externalSchema"
      schemaLocation="http://www.externalOrg.org/someLocation/externalSchema.xsd"
    />

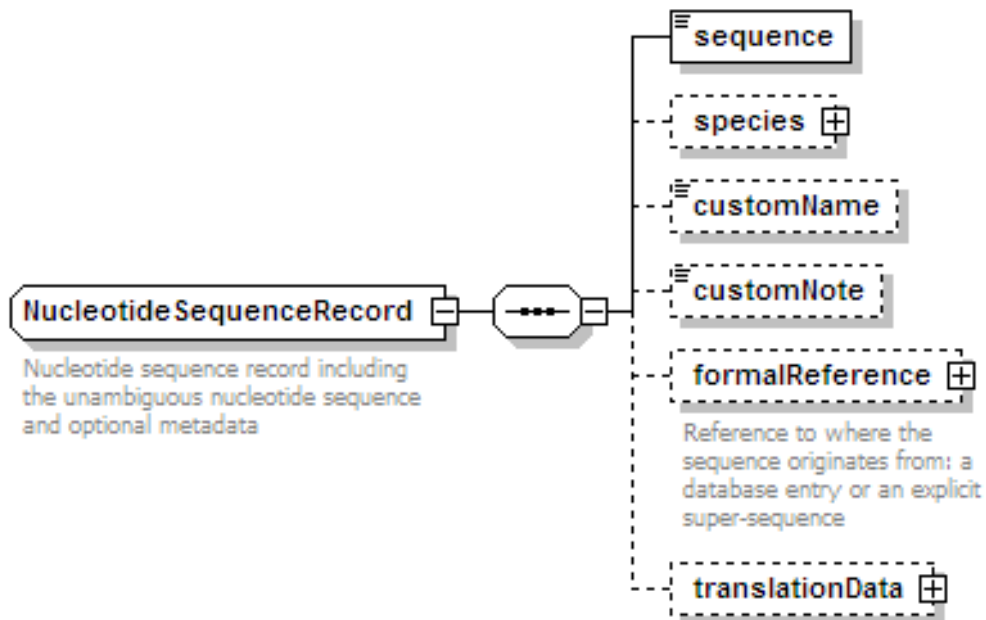
    <xs:element name="runMyService">
      <xs:complexType>
        <xs:sequence>
          <xs:element name="argument1" type="ext:ExternalType"/>
        </xs:sequence>
      </xs:complexType>
    </xs:element>

    .
    .
    .

  </xs:schema>
</wsdl:types>
```


Part 3:

INTRODUCTION TO BioXSD

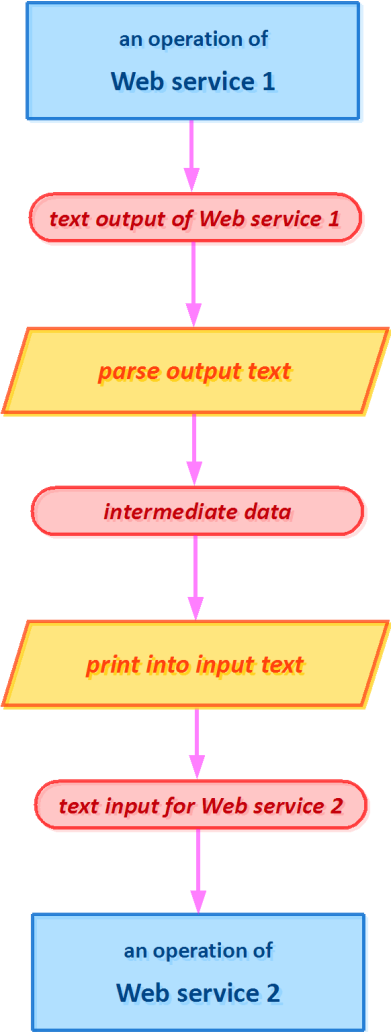


Motivation for users

What does **BioXSD** offer to service users?

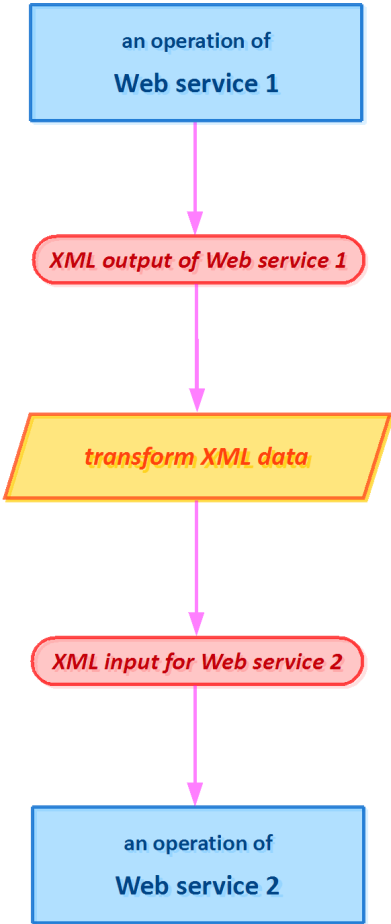
1.

plain-text data (or tabular or binary)



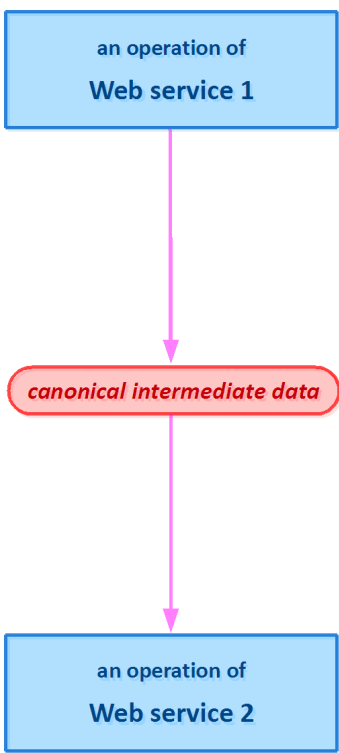
2.

proprietary XML data



3.

common XML Schema



Smooth orchestration!

Motivation for providers

What does **BioXSD** offer to service providers?

ready-made building blocks

Main **BioXSD** types:

SimpleTypes:

Accession(s)

NucleotideSequence

AminoacidSequence

GeneralNucleotideSequence

GeneralAminoacidSequence

Biosequence

helper types:

Name, FreeText

Uri

Integer(s), Decimal(s)

...a few more

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SimpleTypes:

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Biosequence

helper types:

Name, FreeText

Uri

Integer(s), Decimal(s)

...a few more

ComplexTypes:

NucleotideSequenceRecord

AminoacidSequenceRecord

GeneralNucleotideSequenceRecord

GeneralAminoacidSequenceRecord

BiosequenceRecord

..SequenceAlignment

AnnotatedSequence

DatabaseReference, EntryReference

OntologyReference, OntologyTerm

Species, SequenceReference, Method

helper types:

Score, SequencePosition(s)

...some more