

An introduction to Shape Expressions

And how they can be used to implement integrity and classification constraints within the **@Web** platform

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Outline of the presentation

- ▶ Introduction to Shape Expressions
- ▶ Examples of integrity and classification constraints for the **@Web** platform written as Shape Expressions
- ▶ Comparison with equivalent constraints written as SPARQL queries
- ▶ Survey of the available libraries implementing of Shape Expressions

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- ▶ Lets one decide whether a RDF graph satisfies all the required shapes.
- ▶ Also possible to deduce which triples conform to which shapes (useful for classification.)
- ▶ Roughly comparable to what the Data Definition Language (DDL) does for SQL databases, or what XML Schema does for XML documents.

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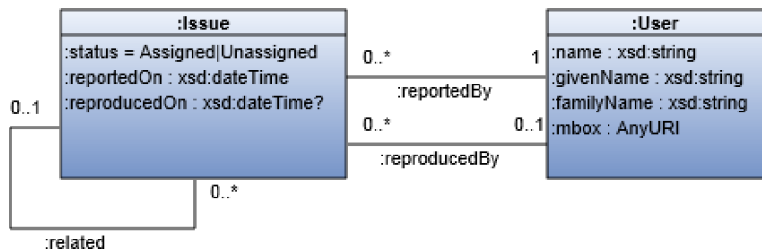
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 - ▶ can have one mbox.

Motivating example (II)



Example data (Turtle syntax)

Valid

```
:Issue1
  :status :unassigned ;
  :reportedBy :Bob ;
  :reportedOn "2013-01-23"^^xsd:date ;
  :reproducedBy :Thompson ;
  :reproducedOn "2013-01-23"^^xsd:date .

:Bob
  foaf:givenName "Bob" ;
  foaf:familyName "Smith" ;
  foaf:mbox <mail:bob@example.org> .

:Thompson
  foaf:givenName "Joe", "Joseph" ;
  foaf:familyName "Thompson" ;
  foaf:mbox <mail:joe@example.org> .
```

Invalid

```
:Issue2
  :status :checked ; # invalid :status.
  :reportedBy :Bob ;
  :reportedOn "2013-01-23"^^xsd:date ;
  :reproducedOn "2013-01-20"^^xsd:date ;
    # missing :reproducedBy.
    # :reproducedOn earlier than
    # :reportedOn.

:Anna
  foaf:givenName "Bob" ;
    # missing :familyName.
  foaf:mbox <mail:bob@example.org> .

:Pete
  foaf:name "Peter", "Pete" ;
    # multiple foaf:names.
```

Shape Expression: User

```
<UserShape> {  
  ( foaf:name xsd:string |  
    foaf:givenName xsd:string+ ,  
    foaf:familyName xsd:string  
  ),  
  foaf:mbox shex:IRI ?  
}
```

Shape Expression: Issue

```
<IssueShape> {  
  :status ( :unassigned  
            :assigned ),  
  :reportedBy @<UserShape>,  
  :reportedOn xsd:date,  
  ( :reproducedBy @<UserShape>,  
    :reproducedOn xsd:date  
  )?,  
  :related @<IssueShape>*  
}
```

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  ... pattern ...  
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- ▶ A schema is just a set of *shape expressions*.
- ▶ A shape expression is a labelled *pattern*, e.g.:

```
<label>: {  
  ... pattern ...  
}
```

- ▶ A pattern is a *conjunction* (denoted with a comma) of several *expressions*, e.g.:

```
<IssueShape>: {  
  :status ( :unassigned :assigned ), # an expression  
  :reportedBy @<UserShape>,          # another expression  
  :reportedOn xsd:date,               # yet another expression  
  ...  
}
```


The Shape Expressions language (II)

An expression can be:

- ▶ An *arc rule*, which is a *name definition* followed by a *value definition*, e.g.:

# name definition	# value definition
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```

- ▶ A *group rule* which groups several rules as a single rule (useful for cardinality constraints), e.g.:

```
( :reproducedBy @<EmployeeShape>,  
  :reproducedOn xsd:dateTime )?
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# name definition  # value definition
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( :reproducedBy @<EmployeeShape>,  
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```

- ▶ A list of *alternatives* such that the expression matches any of the alternatives in the list, e.g.:

```
( foaf:name xsd:string |  
  foaf:givenName xsd:string+, foaf:familyName xsd:string )
```

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 :reproducedOn xsd:dateTime)?
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 :related @<IssueShape> *
- ▶ + for rules with cardinality at least 1, e.g.:
 foaf:givenName xsd:string+
- ▶ $\{m, n\}$ for rules with cardinality between m and n .

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- ▶ an IRI, e.g. `foaf:name`
- ▶ an IRI prefix, e.g. `foaf:~`
- ▶ any predicate except some from a list, e.g. “ - `foaf:name`”
matches any predicate but `foaf:name`

The Shape Expressions language (IV)

A name definition matches predicate names. Can be either:

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- ▶ any predicate except some from a list, e.g. “ - `foaf:name`”
matches any predicate but `foaf:name`
- ▶ any predicate at all, denoted by the symbol dot (`.`)

The Shape Expressions language (V)

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- ▶ A *value type*, e.g. `xsd:date`
- ▶ A *value set* matching any nodes within a set, e.g. `(:assigned, :unassigned)`
- ▶ Any value except those in a particular set, e.g. “ – `:checked`”
- ▶ A node that has a particular shape, e.g. `@<UserShape>`

The Shape Expressions language (VI)

Shape inheritance can be achieved by using the ampersand symbol (&), e.g.:

```
<PersonShape> {  
  ( foaf:name xsd:string  
    | foaf:givenName xsd:string+,  
      foaf:familyName xsd:string  
    ),  
  foaf:mbox IRI  
}
```

```
<UserShape> {  
  & <PersonShape>  
}
```

```
<EmployeeShape> {  
  & <PersonShape>,  
  foaf:phone IRI+  
}
```

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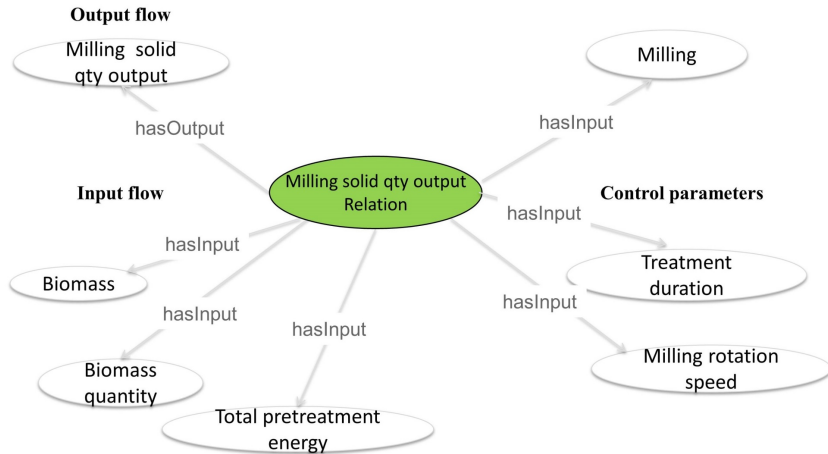
- ▶ Possible to express complex validation rules using.
- ▶ Multiple programming languages can be supported, depending on the implementation of shape expressions.
- ▶ Other uses: transforming RDF triplets into different formats, generating forms for user interfaces automatically, etc.

Example:

```
:reportedOn xsd:dateTime
  %js{ report = _.o; return true; %},
(:reproducedBy @<EmployeeShape>,
:reproducedOn xsd:dateTime
  %js{ return _.o.lex > report.lex; %}
  %sparql{ ?s :reportedOn ?rpt . FILTER (?o > ?rpt) %}
)
```

An integrity constraint

Milling solid quantity output relation



An integrity constraint

Guideline

“The output quantity of a step is equal to the sum of the quantity of water used and the quantity of biomass present in the step.”

An integrity constraint

SPARQL query

```
SELECT ?docid ?doctitle ?tableid ?tabletitle ?rownum  ?solid_qty ?liquid_qty ?output_qty
WHERE {
  ?doc anno:hasForID ?docid ;
        dc:title ?doctitle ;
        anno:hasTable ?table .

  ?table anno:hasForID ?tableid ;
        dc:title ?tabletitle ;
        anno:hasForRow ?row .

  ?row anno:hasForRowNumber ?rownum ;
        anno:hasForRelation [a bioraf:milling_solid_quantity_output_relation ;
                              core:hasAccessConcept ?solid ;
                              core:hasAccessConcept ?liquid ;
                              core:hasResultConcept ?output] .

  ?solid a bioraf:biomass_quantity ;
        anno:hasForFS [a anno:Scalar ;
                       anno:hasForFuzzyElement /
                       anno:hasForMaxKernel ?solid_qty] .

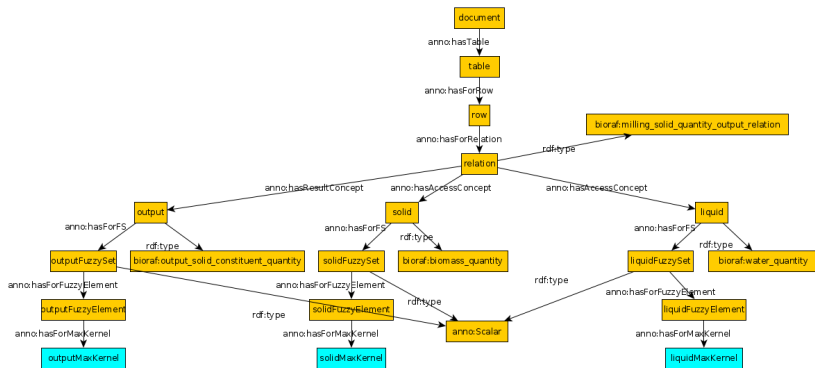
  ?liquid a bioraf:water_quantity ;
        anno:hasForFS [a anno:Scalar ;
                       anno:hasForFuzzyElement /
                       anno:hasForMaxKernel ?liquid_qty] .

  ?output a bioraf:output_solid_constituent_quantity ;
        anno:hasForFS [a anno:Scalar ;
                       anno:hasForFuzzyElement /
                       anno:hasForMaxKernel ?output_qty] .

  FILTER (xsd:float(?output_qty) != xsd:float(?solid_qty) + xsd:float(?liquid_qty))
}
```

An integrity constraint

Graph view of the SPARQL query



An integrity constraint

Shape Expression

```
<DocumentShape> { rdf:type anno:Document, anno:hasTable @<TableShape> }
<TableShape> { anno:hasForRow @<RowShape> }
<RowShape> { anno:hasForRelation @<MillingSolidQuantityOutputRelationShape> }

<MillingSolidQuantityOutputRelationShape> {
  core:hasAccessConcept @<SolidAccessConceptShape>,
  core:hasAccessConcept @<LiquidAccessConceptShape>,
  core:hasResultConcept @<OutputResultConceptShape>
}

<SolidAccessConceptShape> {
  rdf:type bioraf:biomass_quantity,
  anno:hasForFS @<FuzzySetShape>
}

<LiquidAccessConceptShape> {
  rdf:type bioraf:water_quantity,
  anno:hasForFS @<FuzzySetShape>
}

<OutputAccessConceptShape> {
  rdf:type bioraf:output_solid_constituent_quantity,
  anno:hasForFS @<FuzzySetShape>
}

<FuzzySetShape> {
  rdf:type anno:Scalar,
  anno:hasForFuzzyElement @<FuzzyElementShape>
}

<FuzzyElementShape> {
  anno:hasForMaxKernel xsd:string
}
```

A classification constraint

Guideline

“Topic Bioref-PM: it contains experiments with only one milling followed by the enzymatic hydrolysis (Pre-Milling). It does not include a physico-chemical step but it can include a washing and separation step. All control experiments should be indexed in this topic. (en) ”

A classification constraint

SPARQL query

```
SELECT ?docid ?doctitle ?tableid ?tabletitle
      ?rownum1 ?expnum1 ?stepnum1 ?milling
      ?rownum2 ?expnum2 ?stepnum2
WHERE {

  VALUES ?milling { bioraf:ball_milling
                     bioraf:wet_disk_milling
                     ... }

  ?doc anno:hasForID ?docid ;
       dc:title ?doctitle ;
       anno:hasTable [anno:hasForID ?tableid ;
                     dc:title ?tabletitle ;
                     anno:hasForRow ?row1, ?row2] .

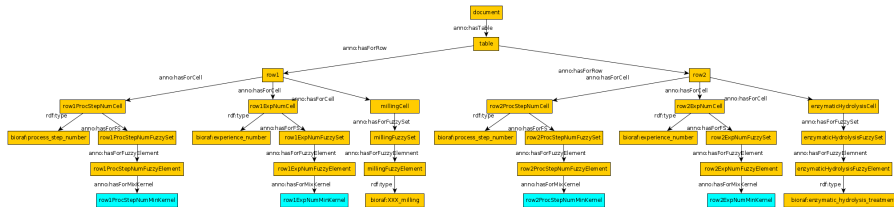
  ?row1 anno:hasForRowNumber ?rownum1 ;
        anno:hasForCell [a bioraf:experience_number ;
                        anno:hasForFS /
                        anno:hasForFuzzyElement /
                        anno:hasForMinKernel ?expnum1] ;
        anno:hasForCell [a bioraf:process_step_number ;
                        anno:hasForFS /
                        anno:hasForFuzzyElement /
                        anno:hasForMinKernel ?stepnum1] ;
        anno:hasForCell /
        anno:hasForFS /
        anno:hasForElement /
        a ?milling .

  ?row2 anno:hasForRowNumber ?rownum2 ;
        anno:hasForCell [a bioraf:experience_number ;
                        anno:hasForFS /
                        anno:hasForFuzzyElement /
                        anno:hasForMinKernel ?expnum2]
        anno:hasForCell [a bioraf:process_step_number ;
                        anno:hasForFS /
                        anno:hasForFuzzyElement /
                        anno:hasForMinKernel ?stepnum2]
        anno:hasForCell /
        anno:hasForFS /
        anno:hasForElement /
        a bioraf:enzymatic_hydrolysis_treatment .

  FILTER (?expnum1 = ?expnum2 &&
          xsd:float(?stepnum1) < xsd:float(?stepnum2))
```

A classification constraint

Graph view of the SPARQL query



A classification constraint

Shape Expression

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<DocumentShape> {  
  rdf:type anno:Document,  
  anno:hasTable @<TableShape>  
}  
  
<TableShape> {  
  anno:hasForRow @<PreMillingRowShape>,  
  anno:hasForRow @<EnzymaticHydrolysisRowShape>  
}  
  
<PreMillingRowShape> {  
  & <RowShape>,  
  anno:hasForCell @<PreMillingCellShape>  
}  
  
<PreMillingCellShape> {  
  & <RowShape>,  
  anno:hasForFS @<PreMillingFuzzySet>  
}  
  
<PreMillingFuzzySet> {  
  anno:hasForElement (bioraf:ball_milling  
                      bioraf:wet_disk_milling ...)  
}  
  
<EnzymaticHydrolysisRowShape> {  
  anno:hasForCell @<EnzymaticHydrolysisCellShape>  
}
```

```
<EnzymaticHydrolysisCellShape> {  
  anno:hasForFS @<EnzymaticHydrolysisFuzzySet>  
}  
  
<EnzymaticHydrolysisFuzzySet> {  
  anno:hasForElement bioraf:enzymatic_hydrolysis_treat  
}  
  
<RowShape> {  
  anno:hasForRowNumber xsd:integer,  
  anno:hasForCell @<ExperienceNumberCellShape>,  
  anno:hasForCell @<ProcessStepNumberCellShape>  
}  
  
<ExperienceNumberCellShape> {  
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- ▶ Prototype/proof-of-concept implementation of shape expressions

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- ▶ Implemented in the JavaScript programming language
- ▶ Prototype/proof-of-concept implementation of shape expressions
- ▶ Handles semantic actions
- ▶ Able to generate SPARQL queries

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Classification constraint (BIOREF-PM topic):

- ▶ Found **342** candidate experiments in **30** different documents.

Thanks!