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
- Comparision with equivalent constraints written as SPARQL queries
- Survey of the available libraries implementating 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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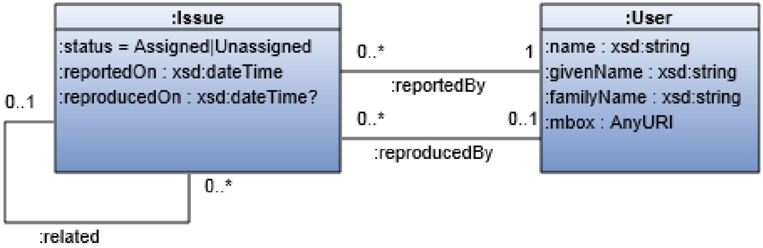
  - can have one mbox.

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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- 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
:reportedOn        xsd:date
```

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

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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 )?
```

- 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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( :reproducedBy @<UserShape>,
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The possible *cardinality constraints* are:

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```
( :reproducedBy @<UserShape>,
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```

- `*` for rules with cardinality at least 0, e.g.:

```
:related @<IssueShape> *
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- `*` for rules with cardinality at least 0, e.g.:

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  ```

- `+` for rules with cardinality at least 1, e.g.:

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- $\{m, n\}$ for rules with cardinality between m and n.

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

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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 (`.`)

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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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- Other uses: transforming RDF triplets into different formats, generating forms for user interfaces automatically, etc.

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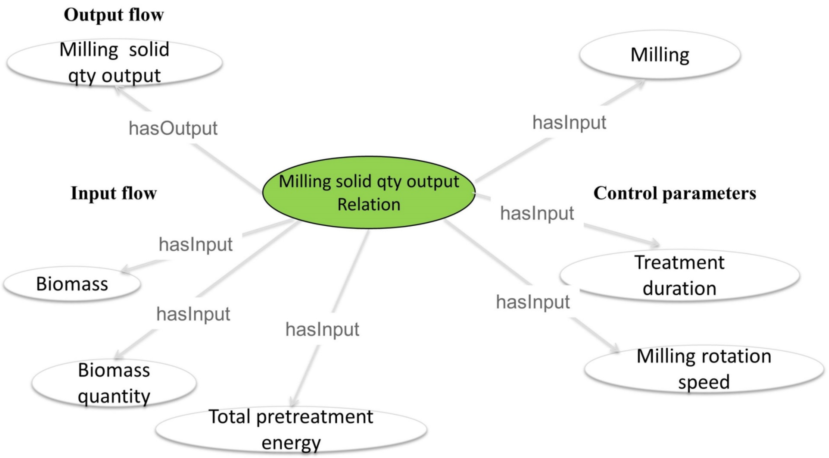
- Possible to express complex validation rules using.
- Multiple programming languages can be supported, depending on the implementation of shape expressions.
- Other uses: transforming RDF triplets into different formats, generating forms for user interfaces automatically, etc.

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.”

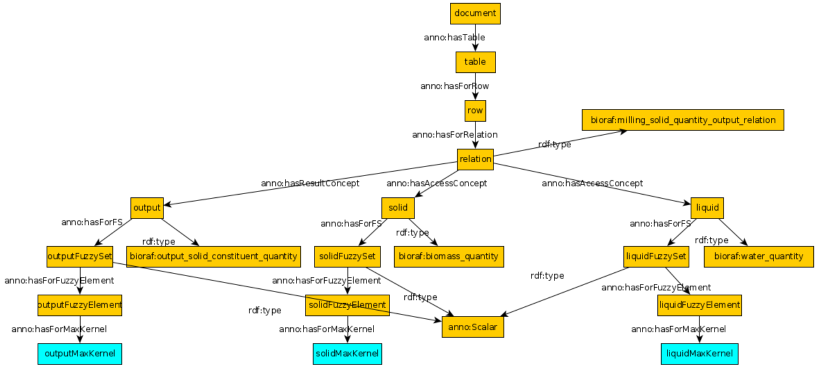
An integrity constraint

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> {
  rdf:type bioraf:milling_solid_quantity_output_relation,
  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) ”

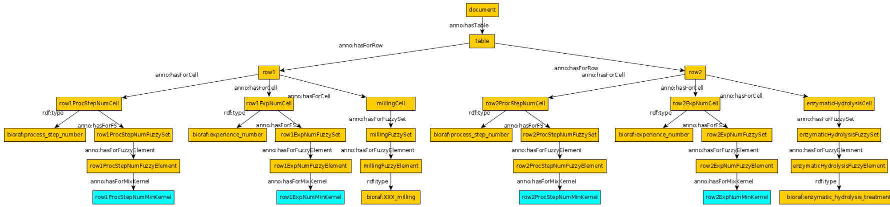
A classification constraint

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



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  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_mlling
                      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 @<ProcessStepeNumberCellShape>
}

<ExperienceNumberCellShape> {
  rdf:type bioraf:experience_number,
  anno:hasForFS @<FuzzySetShape>
}

<ProcessStepNumberCellShape> {
  rdf:type bioraf:experience_number,
  anno:hasForFS @<FuzzySetShape>
}

<FuzzySetShape> {
  rdf:type anno:Scalar,
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}

<FuzzyElementShape> {anno:hasForMinKernel xsd:string}
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- *FancyShExDemo*
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  - 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!