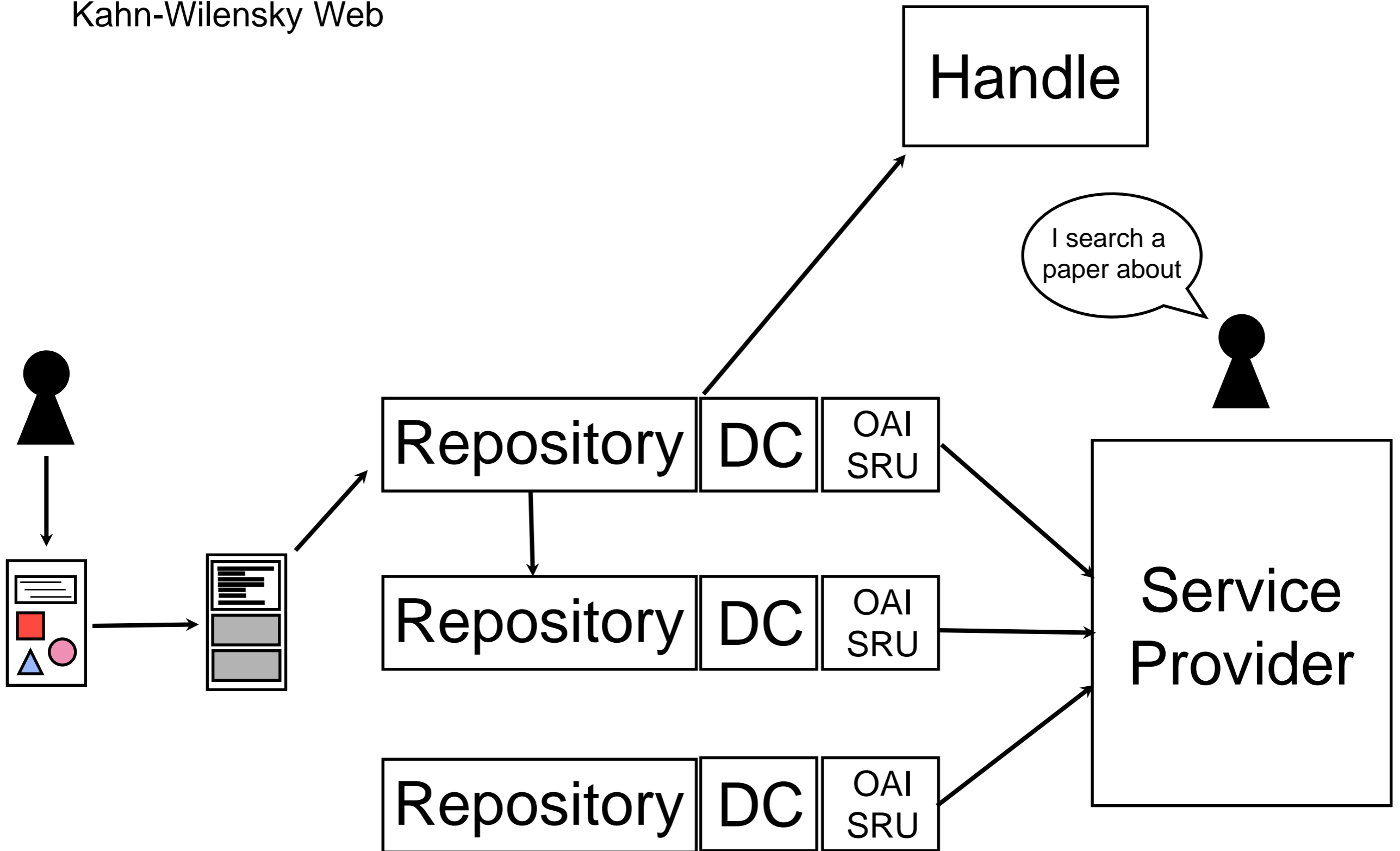


Kahn-Wilensky Web



Hypothesis 1: Network & Common

Schema

Hypothesis 2: Object Oriented Design

Hypothesis 3: The Resource is the Message

Hypothesis 1. Network & Common Schema

Project Database

Lund (3)

- PhD dissertations
- Institutional Repository
- Students Papers

Gent (3)

- Academic Bibliography
- Institutional Repository
- Archive Digitized Materials

Image
Database

Bielefeld (5)

Imaging Workflow

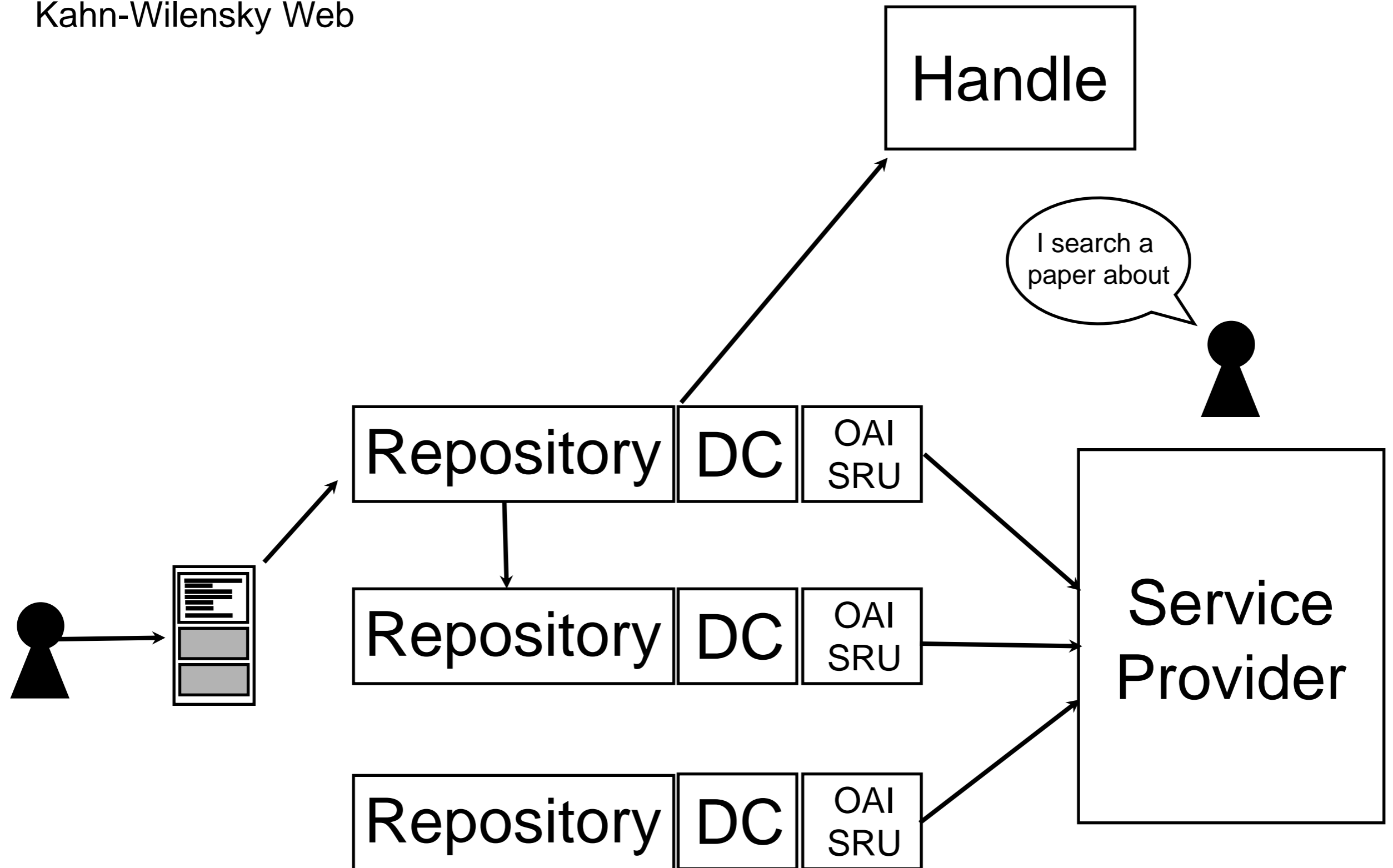
- Postprints
- Conference Proceedings
- Theses

Hypothesis 2: Object Oriented Design

- (Complex) Digital Objects
- Unique identifiers
- Key-Metadata + 1 or more data streams
- Metadata schemes invariant over repositories
- Specialized data types + service bindings on these types
- **Fragmented input**
- **Incomplete**
- **Metadata, Files, Metadata + Files**
- **Many schemas**
- **Simple data types (String, Array, Map)**
- **many native functions on these types**

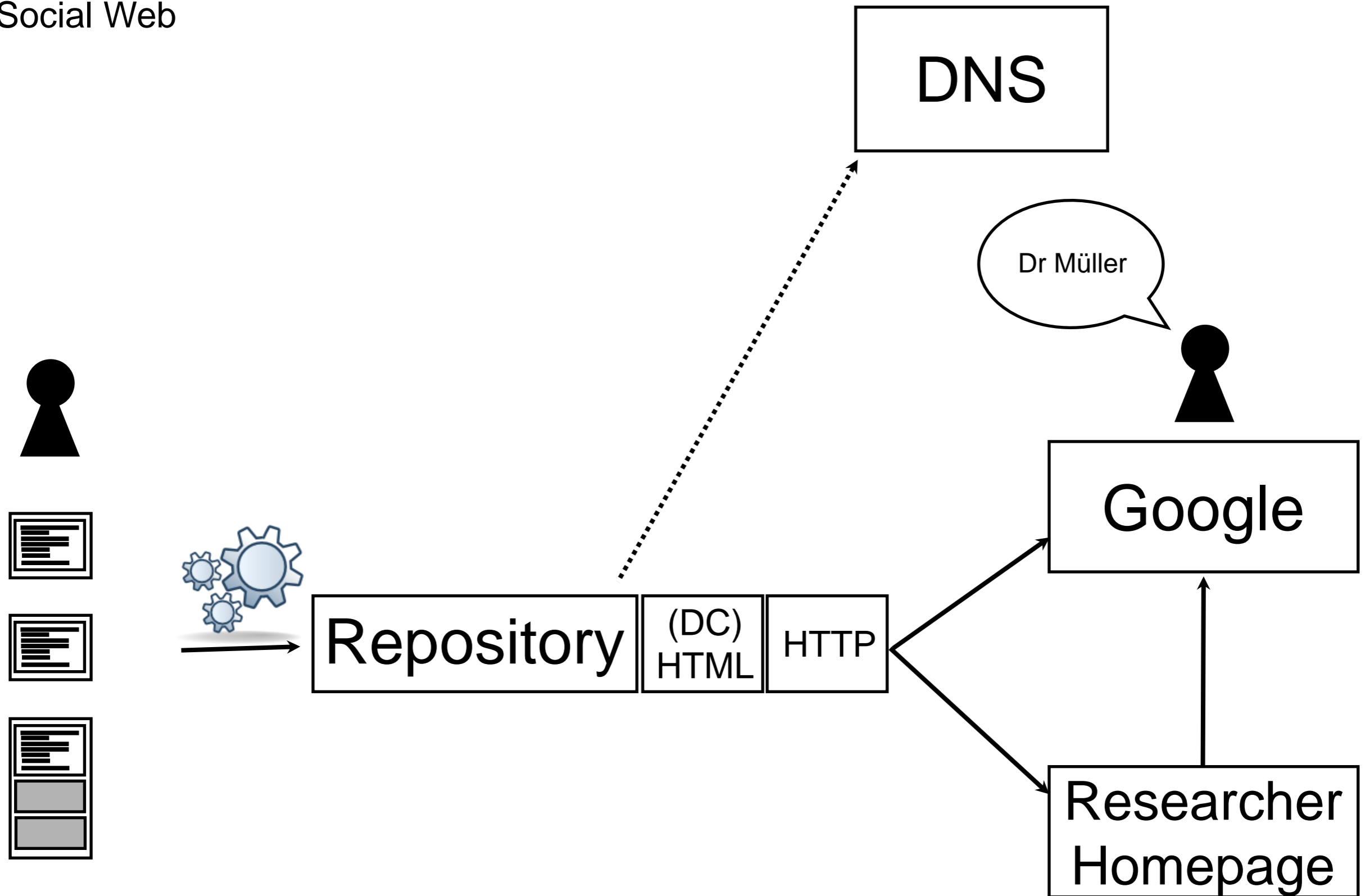
Hypothesis 3: The Resource is the Message

Kahn-Wilensky Web



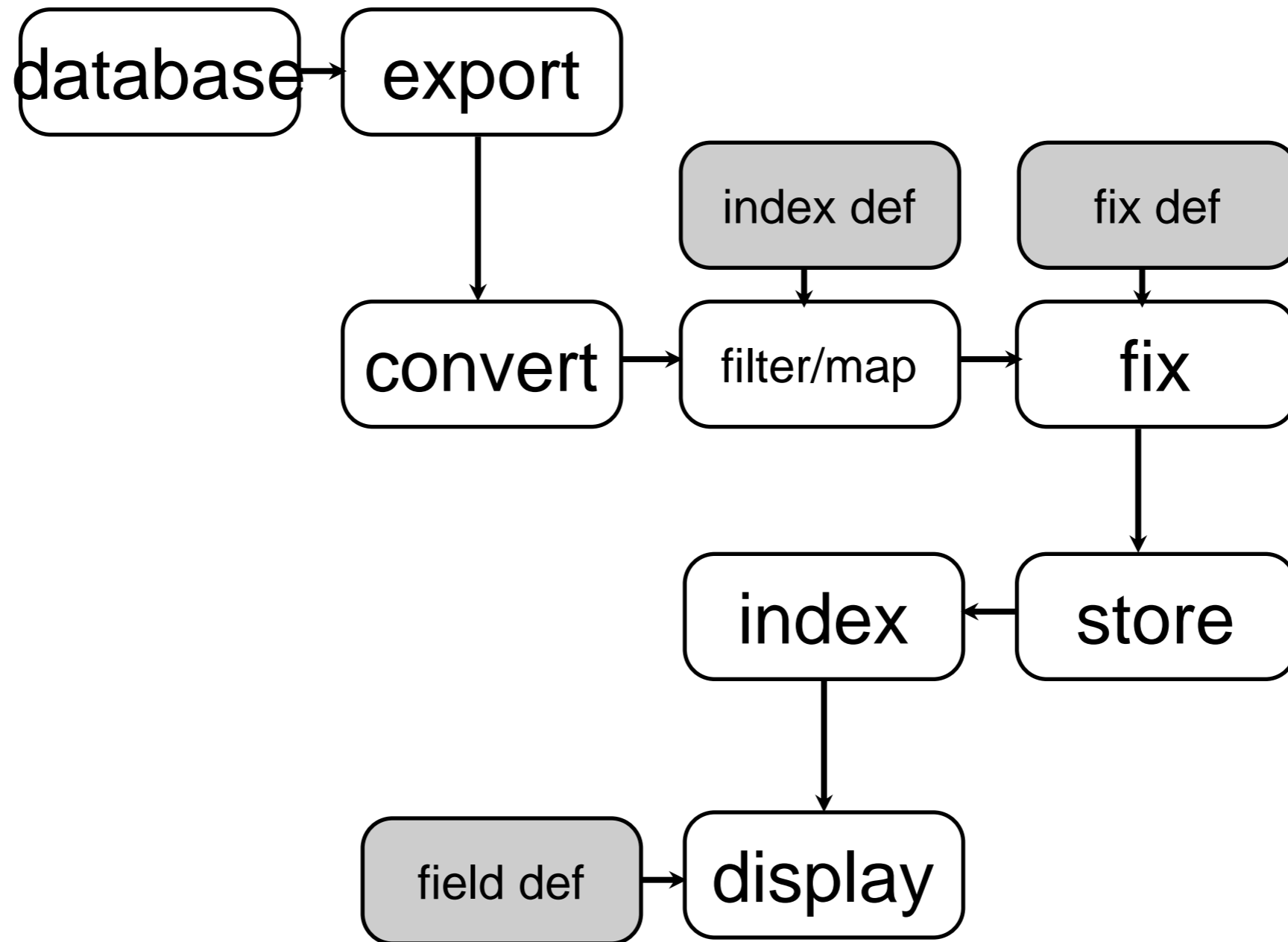
Hypothesis 3: The Researcher is the Message

Social Web



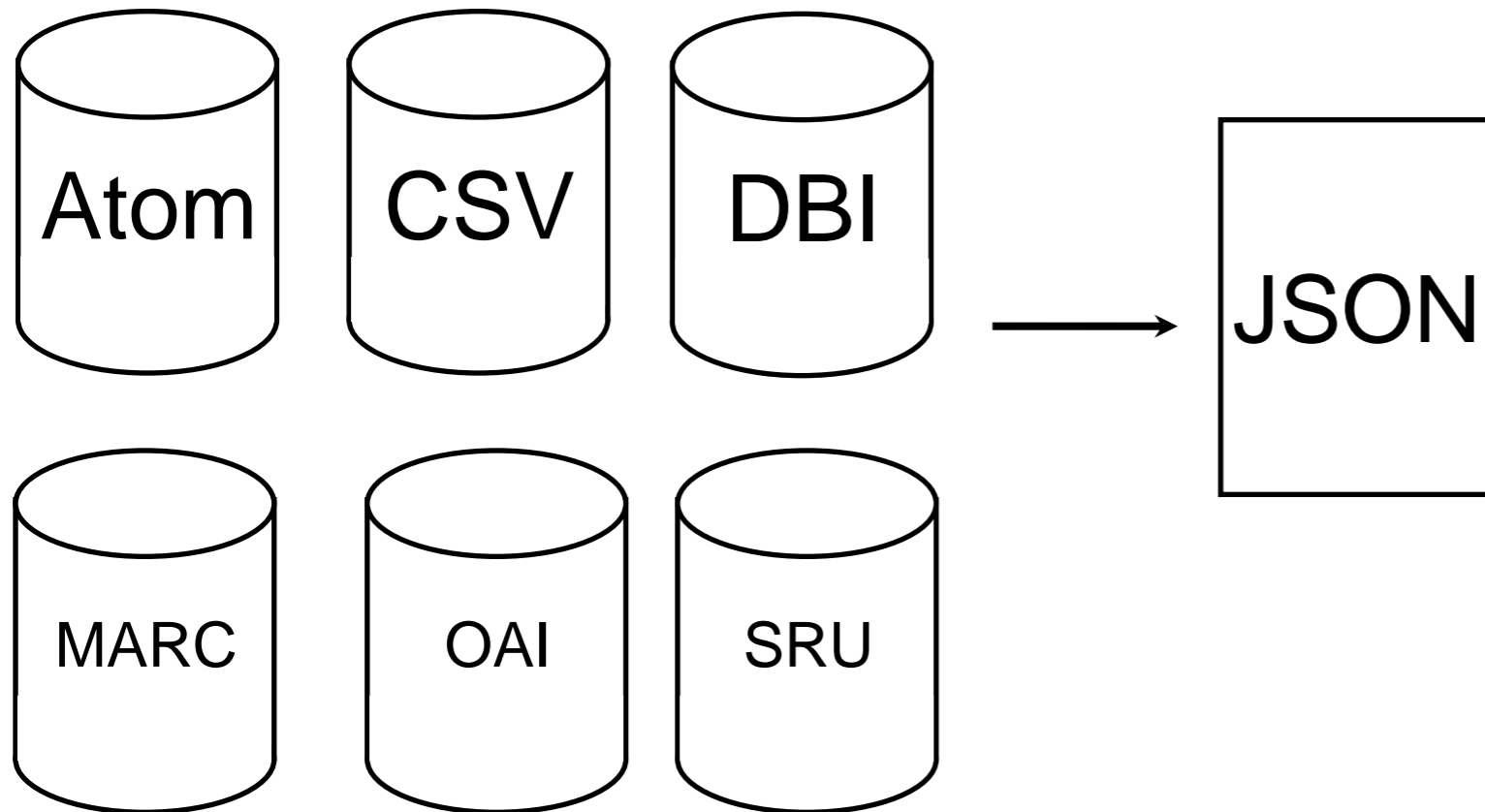
Project Catmandu

Anatomy of Search



Import

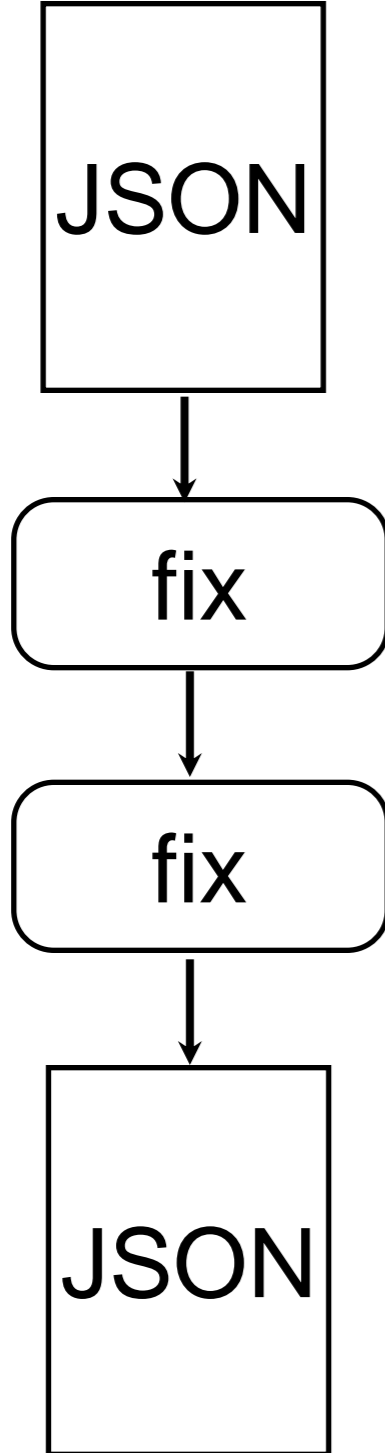
Import from many sources



importer

```
$obj->each({})  
$obj->first()  
$obj->rest()  
$obj->select({})  
$obj->any({})  
$obj->many({})
```

ETL



```
uppercase('job');
```

```
capitalize('first');
```

```
capitalize('last');
```

```
capitalize('my.deep.nested.0');
```

```
uppercase('my.deep.nested.0');
```

```
downcase('my.deep.nested.0');
```

```
substring('my.deep.nested.0', 0, 2);
```

```
add_field('test');
```

```
add_field('income', 0);
```

```
add_field('a.0.0.0', 1);
```

```
marc_map('100', 'my.authors.$append');
```

```
marc_map('710', 'my.authors.$append');
```

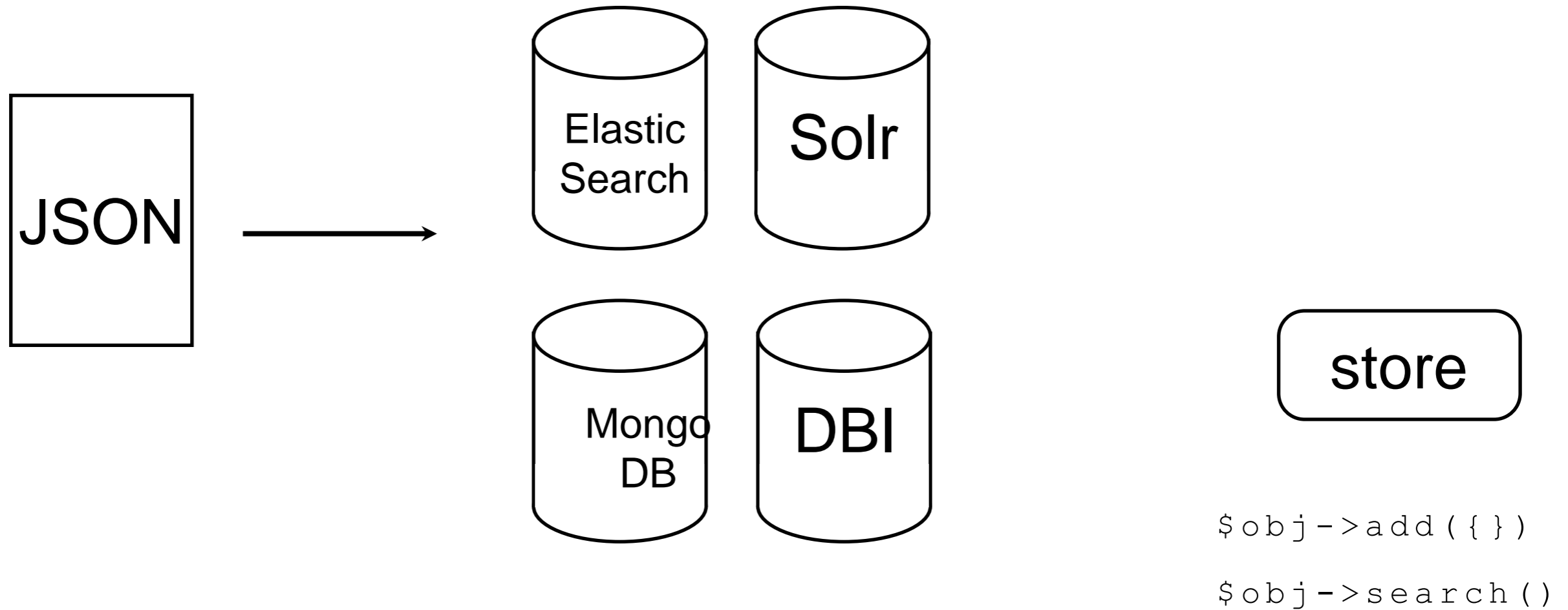
```
marc_map('600x', 'my.subjects.$append');
```

```
marc_map('008_/35-37', 'my.language');
```

```
join_field('colors.0', '/');
```

Store

Schemaless storage



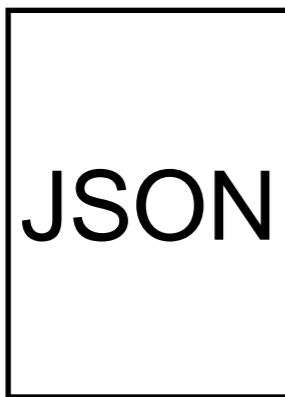
```
record.title:"rabbit" and record.author.firstName:"peter"
```

```
record.title any "rabbit" and record.author.firstName any "peter"
```

Favorite Epigram

"It is better to have 100 functions operate on one data structure than to have 10 functions operate on 10 data structures."

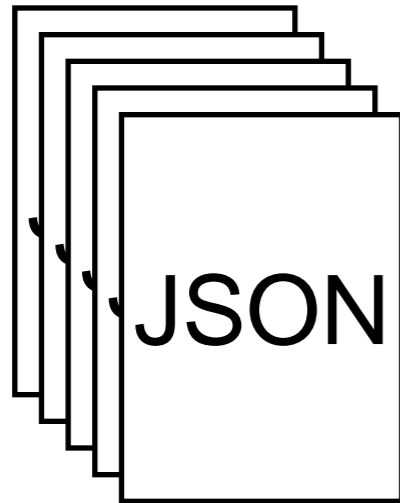
Alan J. Perlis



JSON



```
$hash  
$hash->{title}->[1]  
keys %$hash  
exists $hash->{isbn}
```



JSON



```
$it->count  
$it->each( sub { ... } )  
$it->any( sub { .. } )  
$it->map( sub { ... } )  
$it->reduce( sub { ... } )
```

MVC

Dancer

```
app/  
|--bin/  
|--public/  
|   |-- images/  
|   |-- css/  
|   \-- javascript/  
|--views/  
|   \-- hello.tt  
\--environments/
```

hello.tt

```
<html>  
<body>  
<h1>[% txt %]</ht>  
[% FOREACH obj IN res %]  
  <p>[% obj.title %]</p>  
[% END %]  
</body>  
</html>
```

```
get '/hello' => sub {  
  my $res = store->bag  
    ->search(query => ...)   
    ->reduce(...);  
  template 'hello', { res => $res, txt => "Hello, World!" };  
};
```

Project LibreCat



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Genome Research reference listings

Reference listing for Bernd Weisshaar. Note that publications with Bernd Weisshaar as co-author are listed, too.
(For a short cv check [here](#).)

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- **Publications**
 - CoGR-references
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 - additional data
- Positions / Jobs
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Elongation-related functions of LEAFY COTYLEDON1 during the development of Arabidopsis thaliana.
The Plant Journal Epub ahead of print.
[PUB](#) | [PubMed](#) | [UK PMC](#)
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Palaeohexaploid Ancestry for Caryophyllales Inferred from Extensive Gene-Based Physical and Genetic Mapping of the Sugar Beet Genome (Beta vulgaris).
The Plant Journal .
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Nucleic Acids Research 40(Database issue): D1211 - D1215.
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Epigenetic profiling of heterochromatic satellite DNA.
Chromosoma 120(4): 409 - 422.
[PUB](#) | [PubMed](#) | [UK PMC](#)
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

Rosso MG, Li Y, Strizhov N, Reiss B, Dekker K, Weisshaar B (2003)
Plant Molecular Biology 53(1): 247 - 259.

DOI: [10.1023/B:PLAN.0000009297.37235.4a](https://doi.org/10.1023/B:PLAN.0000009297.37235.4a)

Journal Article | *Published* | *English*

Authors: Rosso, MG ; Li, Y ; Strizhov, N ; Reiss, B ; Dekker, K ; Weisshaar, Bernd

Department: Centrum für Biotechnologie
 Fakultät für Biologie
 Genomforschung

Abstract:

The GABI-Kat population of T-DNA mutagenized *Arabidopsis thaliana* lines with sequence-characterized insertion sites is used extensively for efficient progress in plant functional genomics. Here we provide details about the establishment of the material, demonstrate the population's functionality and discuss results from quality control studies. T-DNA insertion mutants of the accession Columbia (Col-0) were created by *Agrobacterium tumefaciens*-mediated transformation. To allow selection of transformed plants under greenhouse conditions, a sulfadiazine resistance marker was employed. DNA from leaves of T1 plants was extracted and used as a template for PCR-based amplification of DNA fragments spanning insertion site borders. After sequencing, the data were placed in a flanking sequence tag (FST) database describing which mutant allele was present in which line. Analysis of the distribution of T-DNA insertions revealed a clear bias towards intergenic regions. Insertion sites appeared more frequent in regions in front of the ATG and after STOP codons of predicted genes. Segregation analysis for sulfadiazine resistance showed that 62% of the transformants contain an insertion at only one genetic locus. In quality control studies with gene-specific primers in combination with T-DNA primers, 76% of insertions could be confirmed. Finally, the functionality of the GABI-Kat population was demonstrated by exemplary confirmation of several new transparent testa alleles, as well as a number of other mutants, which were identified on the basis of the FST data.

Keywords: knock-out ; insertion mutagenesis ; FST ; gene function ; reverse genetics

ISSN: 0167-4412

PUB-ID: 1609190 | Link: <http://pub.uni-bielefeld.de/publication/1609190>

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Rosso MG, Li Y, Strizhov N, et al. An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics. *Plant Molecular Biology*. 2003;53(1):247 - 259.

Sources

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Supplements

 GenBank:

AY323492	AY333421	AY323491
AY300160	AY275835	AY271516
AY271515	AY271514	AY271513
AY268091	AY268090	AY268089
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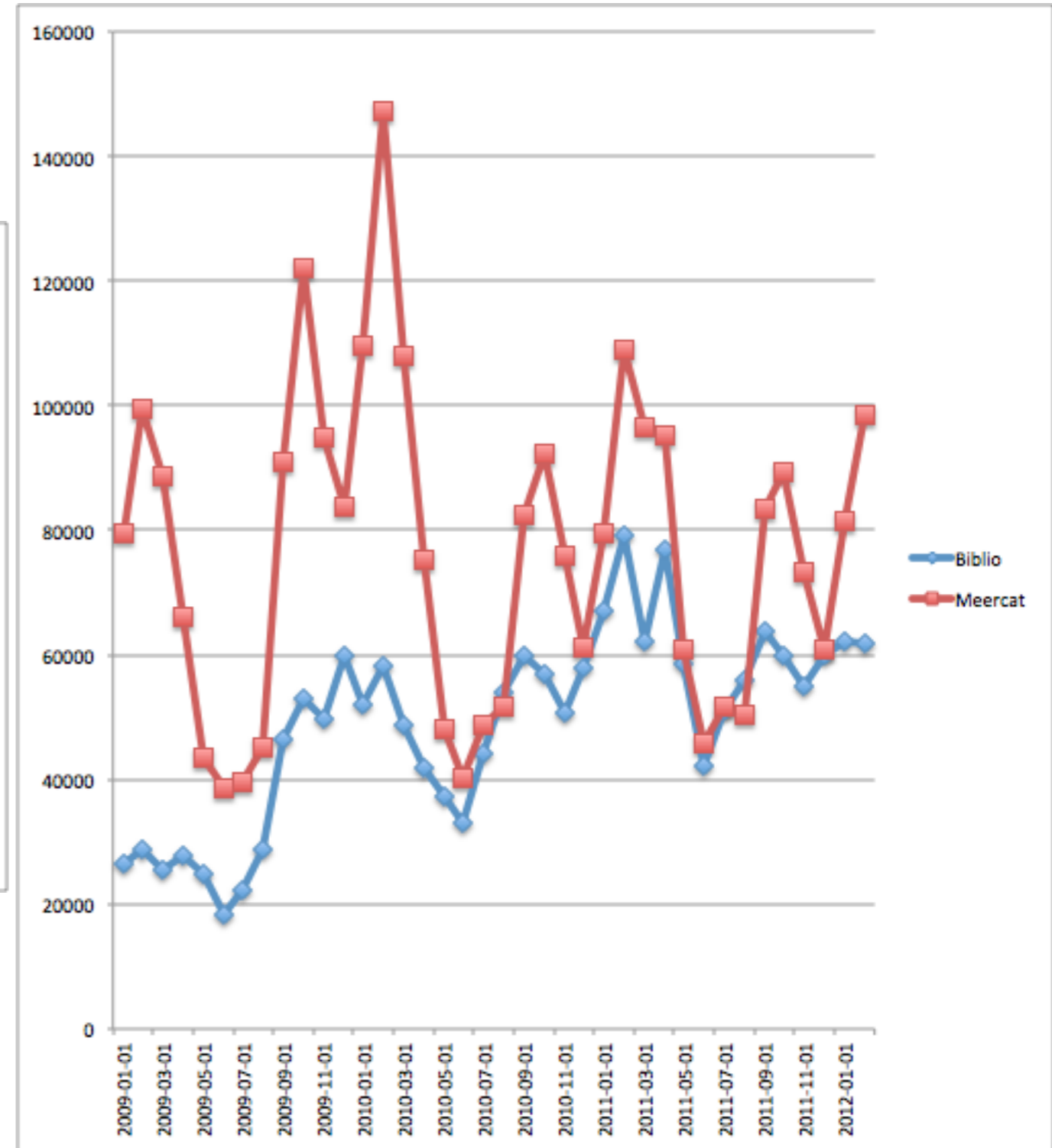
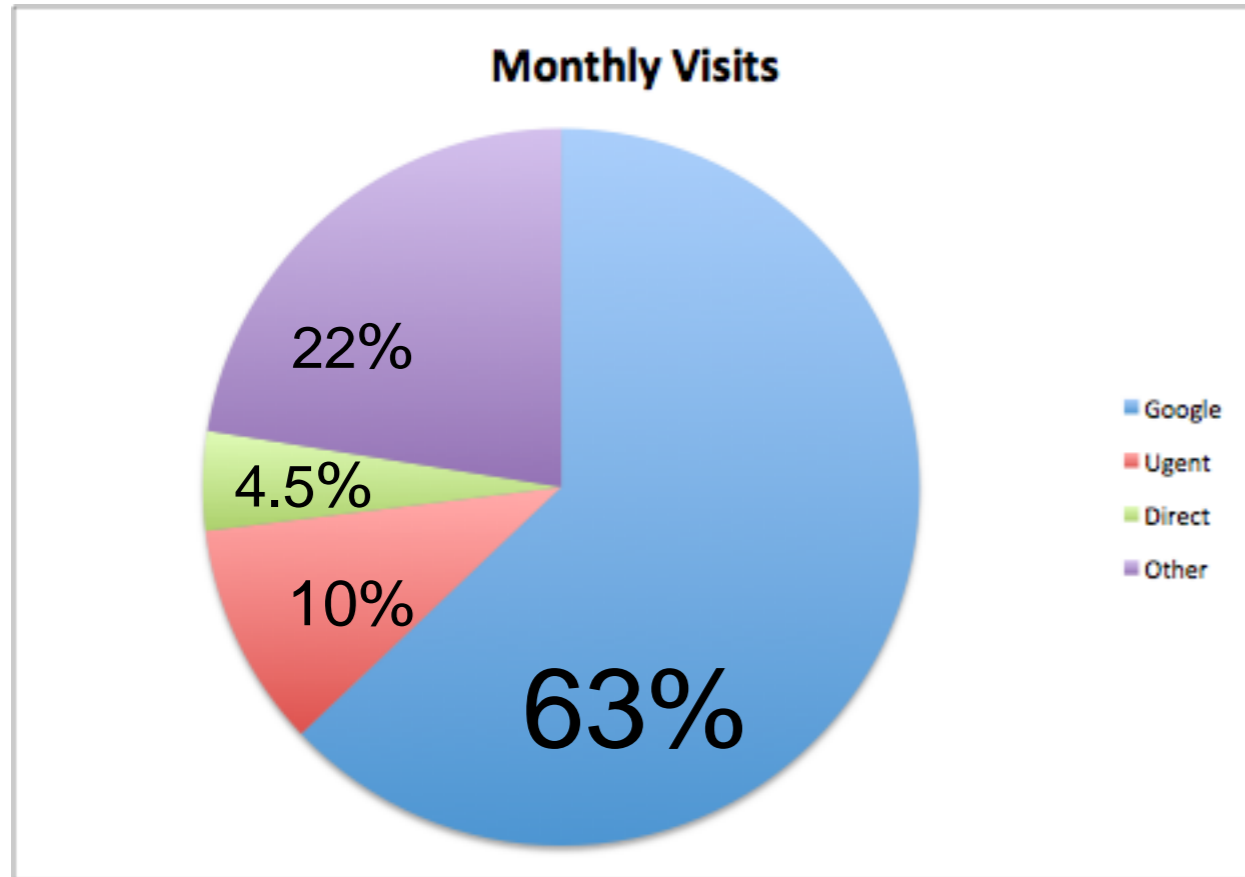
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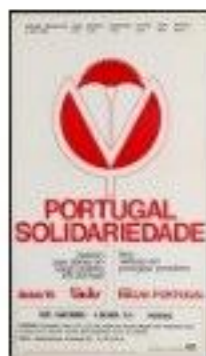
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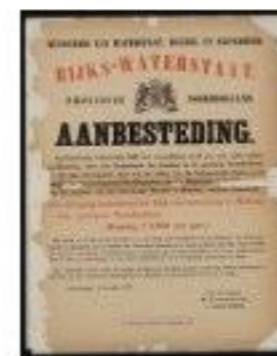
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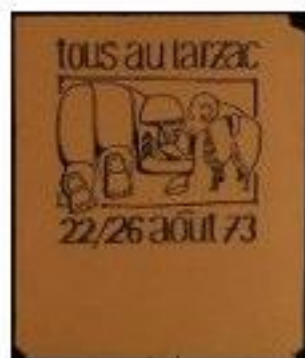
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Project Plan

- **Catmandu** : Open Source release of our toolkit
- **LibreCat** : Example programs we would like to share
 - **LibreCat-Search** : Facetted search engine
 - **LibreCat-Citation** : CSL-based citations
 - **LibreCat-Catalog** : Institutional Repository
 - **LibreCat-Grim** : IIPImage search engine
 - **LibreCat-Archive** : Front-End for Fedora
 - **LibreCat-Imaging** : Front-End MediaMosa

<http://librecat.org>

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