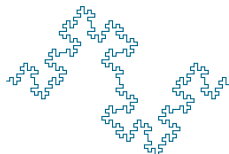


# BioBanks Catalog

Hocine Bendou

*South African National Bioinformatics Institute*



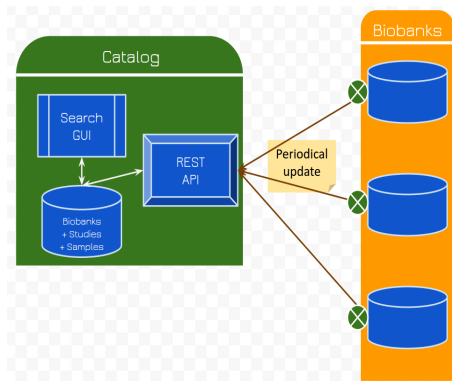
August 17, 2015

# PROBLEMATIC

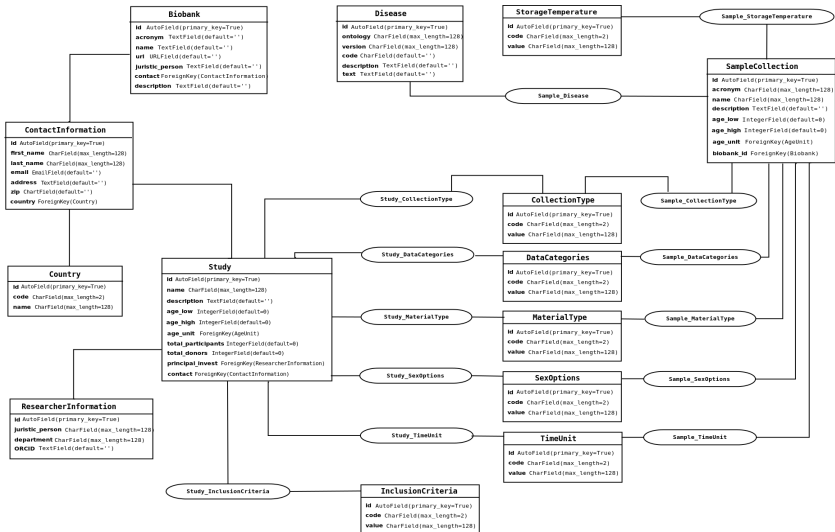
- ▶ Three biorepositories in three different Africa countries
- ▶ Biorepositories: specialised stores for biospecimens
- ▶ Different Laboratory Information Management System (LIMS)
- ▶ Access to LIMS is restricted from outside
- ▶ Multiple queries/multiple access to search the biorepositories

# SOLUTION PROPOSED

- ▶ Provide a unified platform for scientists
- ▶ Implement a custom database to house LIMS data

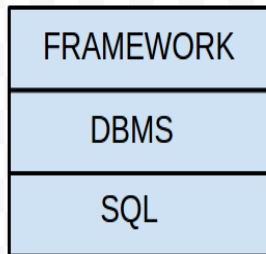


# ER DIAGRAM



# ER TO DATABASE

- ▶ Database management system: SQLite, MySQL, etc.
- ▶ Structured query language
- ▶ Framework tools: Django, Flask, Pyramid, etc.



# DJANGO

- ▶ Free and open source web application framework, written in Python
- ▶ Develop dynamic websites faster and easier
- ▶ Support many different database servers, SQLite, PostgreSQL, etc.

```
bbc/  
  manage.py  
  bbc/  
    __init__.py  
    settings.py  
    ...  
  source/  
    __init__.py  
    migrations/  
    models.py  
    ...
```

# SETTINGS.PY

```
# Database
# https://docs.djangoproject.com/en/1.8/ref/settings/#databases

DATABASES = {
    'default': {
        'ENGINE': 'django.db.backends.sqlite3',
        'NAME': os.path.join(BASE_DIR, '../database/db.sqlite3'),
    }
}
```

# MODELS.PY

```
class Biobank(models.Model):
    acronym = models.TextField(default='')
    name = models.TextField(default='')
    url = models.URLField(default='')
    juristic_person = models.TextField(default='')
    country = models.CharField(max_length=2,
                               choices=COUNTRIES,
                               default='')
    contact = models.ForeignKey(ContactInformation, default=None)
    description = models.TextField(default='')

    def __str__(self):
        return self.name
```

Biobank	
<b>id</b>	AutoField(primary_key=True)
<b>acronym</b>	TextField(default='')
<b>name</b>	TextField(default='')
<b>url</b>	URLField(default='')
<b>juristic_person</b>	TextField(default='')
<b>contact</b>	ForeignKey(ContactInformation)
<b>description</b>	TextField(default='')



# DATABASE GENERATION

```

hocine@hocine:~/dataIntegProj/bbc/source
/bbc/source $ ../virtualenv/bin/python manage.py makemigrations

```

```

hocine@hocine:~/dataIntegProj/bbc/source
/bbc/source $ ../virtualenv/bin/python manage.py migrate

```

```

class Migration(migrations.Migration):

    operations = [
        migrations.CreateModel(
            name='Biobank',
            fields=[
                ('id', models.AutoField(verbose_name='ID', primary_key=True,
                                         auto_created=True)),
                ('name', models.TextField(default='')),
                ...
            ]
        )
    ]

```

# ADD DATA

```
b2 = Biobank.objects.create(  
    acronym="IBRH3AU",  
    name="Integrated Biorepository H3Africa Uganda",  
    url="http://www.ibru.mak.ac.ug",  
    juristic_person="Makerere University",  
    country="UG",  
    contact=cb2,  
    description="BRH3AU is an intergrated biorespository under the H3Africa Biorespository "  
    "Initiative located at Makerere University College of Health Sciences (MakCHS)."
```

# QUERY DATA

```
def querying(self, entity=''):
    """
    Query studies
    """
    result = None
    attrs, b_attrs, d_attrs, c_attrs, m_attrs, s_attrs, i_attrs, \
        t_attrs = self.query_attributes(entity)
    result = Study.objects.all().filter(**attrs)
    if b_attrs:
        result = result.filter(reduce(operator.or_, b_attrs))
    if d_attrs:
        result = result.filter(reduce(operator.or_, d_attrs))
    if c_attrs:
        result = result.filter(reduce(operator.or_, c_attrs))
    if m_attrs:
        result = result.filter(reduce(operator.or_, m_attrs))
    if s_attrs:
        result = result.filter(reduce(operator.or_, s_attrs))
    if i_attrs:
        result = result.filter(reduce(operator.or_, i_attrs))
    if t_attrs:
        result = result.filter(reduce(operator.or_, t_attrs))
    return result
```

## Result of your search



- Lupus

## Advanced Search

Study

Sample Collection

## Study Name

Lupus

## Select Biobank(s)

- ☒ Institute for Human Virology Nigeria
- ☐ Integrated Biorepository H3Africa Uganda
- ☐ Clinical Laboratory Services

## Principal Investigator

Larry

## Study Design

Case-control, Cohort ▾

## Material Type

Nothing selected ▾

## Total Participants

From To

## Age

From

## Total Donors

From To

To

## Data Categories

Nothing selected ▾

## Sex

Male ▾

## Inclusion Criteria

Nothing selected ▾

Nothing selected ▾

Search »

## ► Pros: Easy, less coding, faster(objects in RAM)

```
$sql = "SELECT * FROM ( "
. "SELECT C.course_title, COUNT(DISTINCT T.personnel_code) AS 'teach_num', "
. "COUNT(DISTINCT Q.personnel_code) as 'train num', P.timepoint_name, "
. "IF(T.funding_code LIKE '%FB0016%', 'Yes', 'No') AS h3a_funded, "
. "CONCAT(C.course_location, ' (' ,L.country_name,')') AS location "
. "FROM teaching_dyn AS T "
. "LEFT OUTER JOIN (SELECT M.personnel_code, M.course_code, M.timepoint "
. "FROM training_dyn AS M WHERE M.uname = :user_name) AS Q "
. "ON (T.course_code = Q.course_code AND T.timepoint = Q.timepoint) "
. "LEFT JOIN courses_core C ON C.course_code = T.course_code "
. "LEFT JOIN time_reference_table P ON P.timepoint = T.timepoint "
. "LEFT JOIN country_list L ON C.country = L.country_code "
. "WHERE T.uname = :user_name AND T.timepoint IN (".implode(',', $report_periods).") "
. "GROUP BY T.course_code "
. "UNION "
. "SELECT C.course_title, COUNT(DISTINCT Q.personnel_code) AS 'teach_num', "
. "COUNT(DISTINCT T.personnel_code) AS 'train num', P.timepoint_name, "
. "IF(T.funding_code LIKE '%FB0016%', 'Yes', 'No') AS h3a_funded, "
. "CONCAT(C.course_location, ' (' ,L.country_name,')') AS location "
. "FROM training_dyn AS T "
. "LEFT OUTER JOIN (SELECT M.personnel_code, M.course_code, M.timepoint "
. "FROM teaching_dyn AS M WHERE M.uname = :user_name) AS Q "
. "ON (T.course_code = Q.course_code and T.timepoint = Q.timepoint) "
. "LEFT JOIN courses_core C ON C.course_code = T.course_code "
. "LEFT JOIN time_reference_table P ON P.timepoint = T.timepoint "
. "LEFT JOIN country_list L ON C.country = L.country_code "
. "WHERE T.uname = :user_name AND T.timepoint IN (".implode(',', $report_periods).") "
. "GROUP BY T.course_code) AS R ORDER BY R.timepoint_name DESC";
```

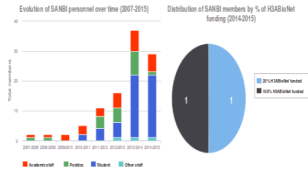
## ► Cons: Many queries → many objects → less RAM

# CONCLUSION



## H3ABioNet

Pan African Bioinformatics Network for H3Africa  
H3ABioNet Annual SANBI August 2014 to July 2015 Report



### Narrative:

- Describe successes and challenges in retaining or recruiting node members?
- Describe how H3ABioNet has contributed to your success/challenges in retaining/recruiting node members?

### III.2 Graduating Students (current Reporting Period + 2 years upstream):

Student	Preparing	Supervisor	H3ABioNet Funded	Start Date	End Date	Graduated
Carlington Moppe	PhD	Dr-Nicole Tiffin	No	2013-01-07	2015-10-10	Not yet
Evelyn Munungu	Postdoc	Prof Alan G Christofidis	No	2013-02-04	2013-12-20	Yes