

# what is BIBBOX ?

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# what is BIBBOX?

there is no Answer



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# what is BIBBOX?

there are 5 answers



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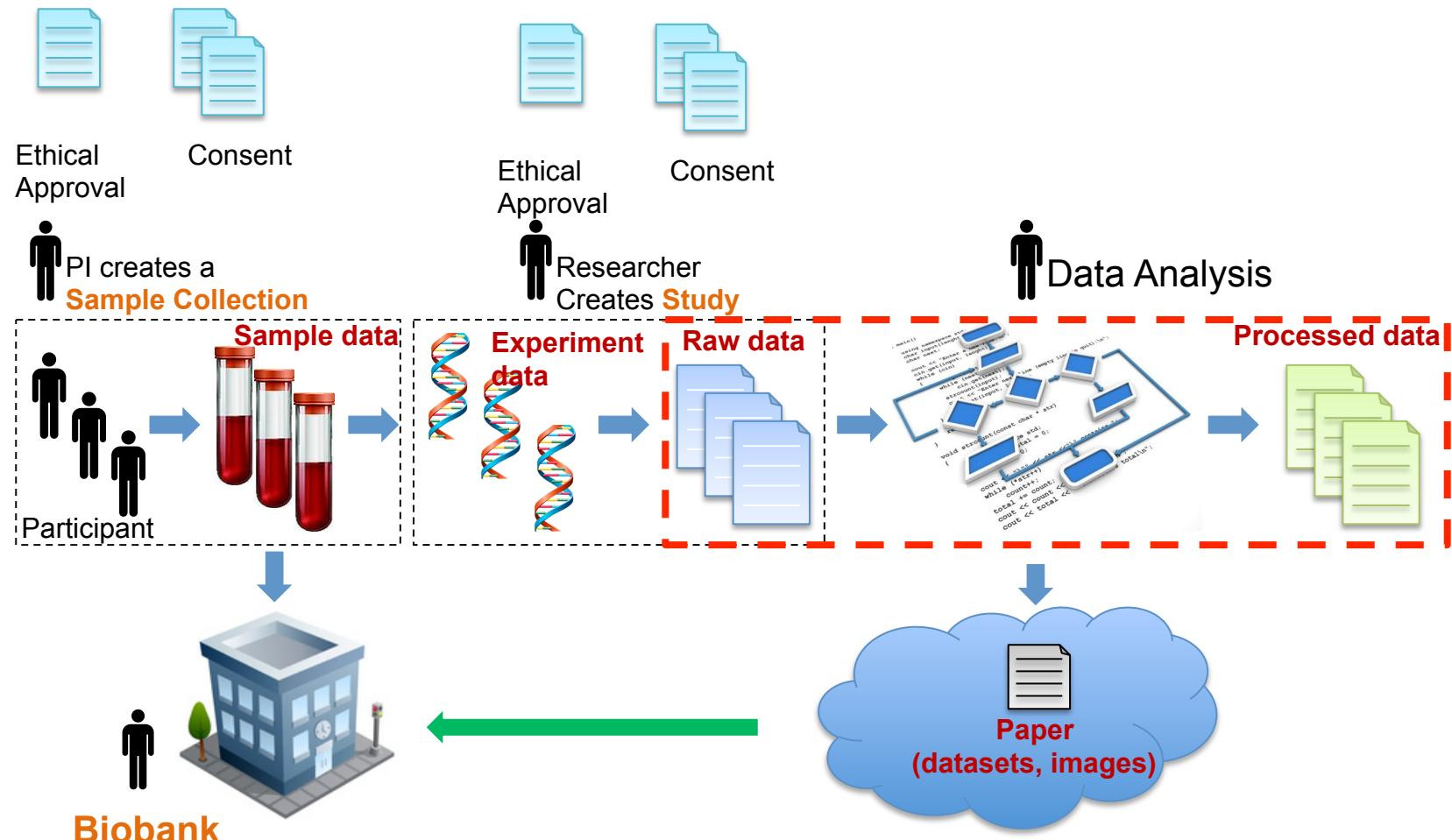
11/05/17 “3

# BIBBOX is ...

1. a VM running a PaaS based on a tomcat application server and bundled together with offline bioinformatics DBs.
2. A portal to install, configure, and backup biobanking and bioinformatics software tools available as orchestrated docker containers.
3. an out-of-the-box solution for biobank data management with MIABIS support.
4. a data integration, harmonization and metadata exchange toolkit according to the FAIR principles.
5. a set of useful software tools for my daily data management tasks in our biobank.



# Biomedical research process



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# BIBBOX Personas



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# B3Africa Personas



**Prof. Dr. Majmuna Sandu**

PI of the MAK Biobank

- Phd in Microbiologie
- 400+ publications
- Member of H2020 advisory board for rare diseases
- Head of ISBER working group on sample quality



**BIBBOX is a “out of the box solution” for biobank data management with MIABIS support.**

With bibbox my research group got a swiss knife for data management, preconfigured to our needs and directly connected to the BCnet catalogue



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# B3Africa Personas



**Alan Punter**

System Administrator @MAK Biobank

- hacker since he can think
- his motto: „127.0.0.1 sweet 127.0.0.1“
- speaks ruby, perl, python, and BASH shell fluently
- responsible for all software problems at the MAK biobank



**BIBBOX is a portal to install, configure, and backup  
biobanking and bioinformatics software tools available as  
orchestrated docker containers**



With **BIBBOX** my life get much more easy, as I can devote  
more time to my „127.0.0.1“.

# B3Africa Personas



**Roxana Rilling**

CTO @ the Makerere University IT department

- Has a ICT management position
- Expert in virtualization technologies in datacenters
- Counts Cores / Main Memory / Disk Capacity
- Responsible for all IT resources, especially server and networks



**BIBBOX is a virtual machine running a PaaS based on a tomcat application server and bundled together with offline bio-informatics databases**

I have to plan for more capacity in my datacenter, because lot of research groups will deploy a BIBBOX VM next year.



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# B3Africa Personas



**Santa Morello**

Curator @MAK Biobank

- Assistant of Prof. Sandu
- Currently working on her PhD in biomarker research
- Responsible for 2 international projects
- Doing the data stewardship for research cooperations



**BIBBOX a data integration, harmonization and metadata exchange toolkit according to the FAIR principles**

I can do all my data annotation and harmonization work with a simple interface, and I'm not relying on software developer for every simple task.



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# B3Africa Personas



**Carmen Rilling**

Operator / User of some BIBBOX apps @ MAK biobank

- 50/50 bewteen wetlab and data analysis
- Is the main operator for OpenSpecimen
- uses Phenotips fom time to time



**BIBBOX provides me a set of useful software tools for my daily data management tasks in our biobank.**

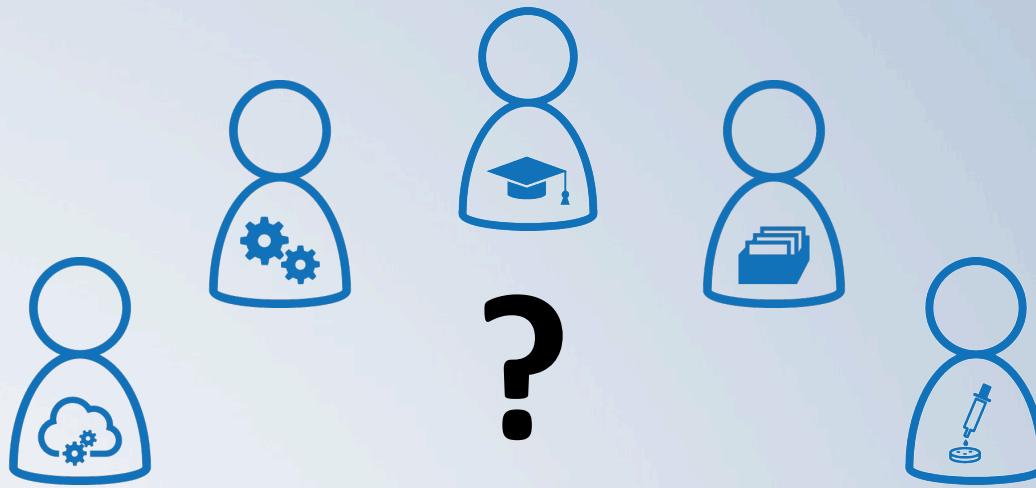
I met in the BIBBOX user group several OpenSpecimen users addressing the same challenges as we do at the MAK biobank.



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# Which is the closest persona to you?



Roxana



Alan



Maimuna



Santa



Carmen

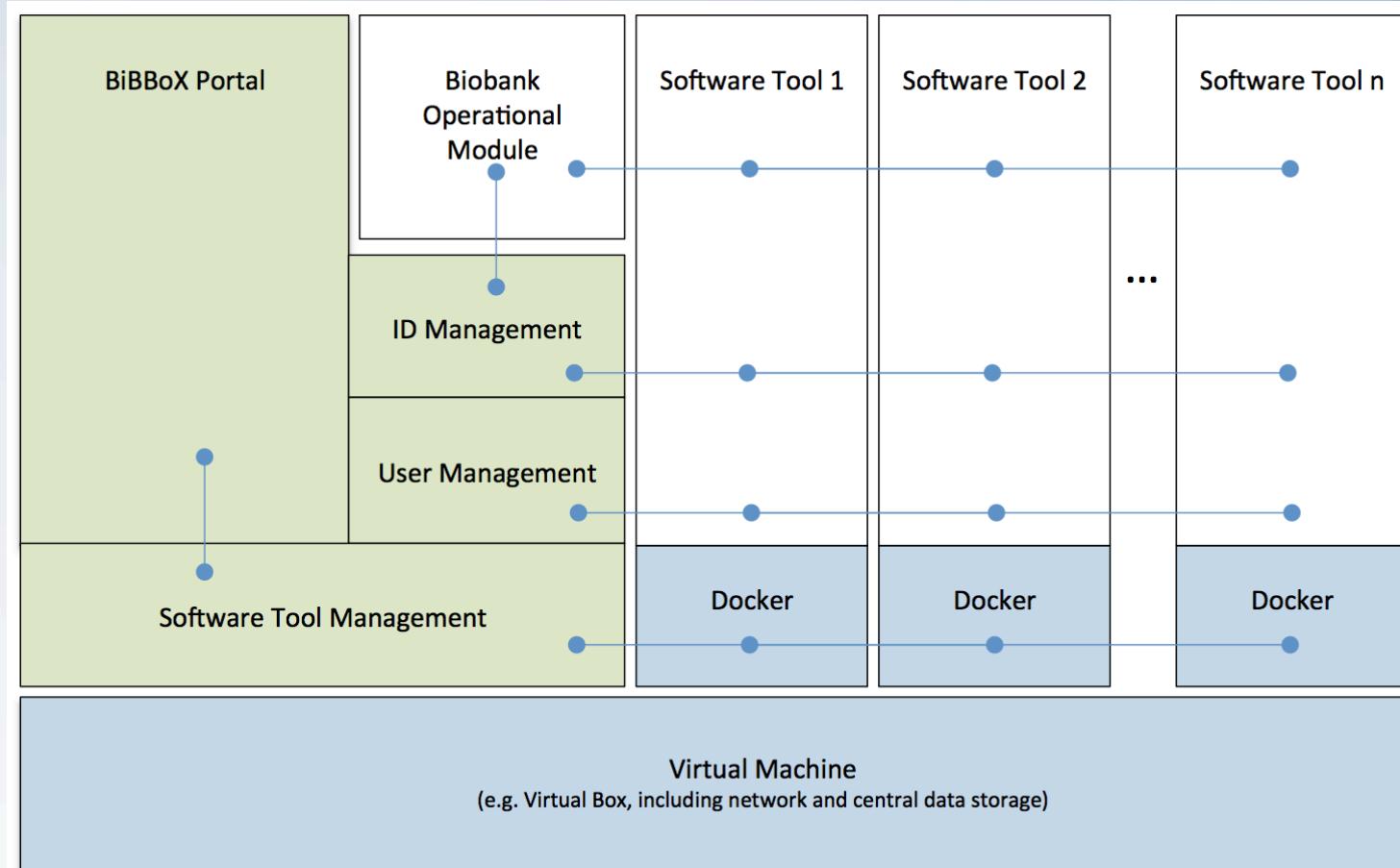


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# BIBBOX System Architecture



# BIBBOX in the Cloud

Dropbox concept:

- Connect instances of BIBBOX VMs
- Each BIBBOX “knows” apps running in others
- Implementation of FAIR principles
- Internet coverage: BIBBOX interoperability
- ID management for data discovery and sharing



# Biobank Application Store

<http://demo.bibbox.org/store> admin/graz2017

The screenshot shows a web-based application store interface for BIBBOX. The top navigation bar includes links for Welcome, Applications, Store (which is selected), Activities, and a user profile. On the left, there's a sidebar with a search bar and a 'Tags' section containing a large number of checkboxes for different application categories. The main content area is divided into sections: 'Biobank Applications' (BIKA.biobank, Open Specimen, Molgenis, PhenoTips, Jupyter Notebook, RDRF), 'Bioinformatics Applications' (Phenotips, Scaleus, STATegraEMS, RedCap, Galaxy), and 'Helper Applications' (represented by small icons). Each application item has a thumbnail, name, and a brief description.

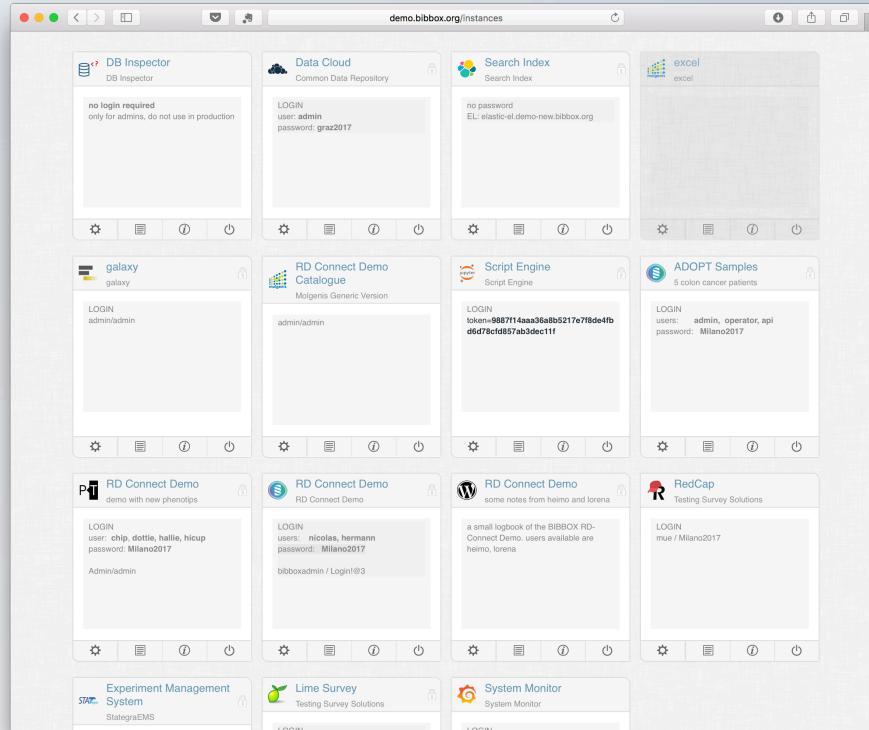


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# Biobank Admins Portal

<http://demo.bibox.org/instances> admin/graz2017



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# OpenSpecimen, Sample Management

<http://rdconnectdemo.demo.bibox.org/> hermann/Milano2017

The screenshot displays two windows of the OpenSpecimen software. The left window shows a detailed view of a sample visit (T0: Default Visit) with fields for Name, Visit Date, Clinical Diagnosis, Genotype, and a list of specimens. The right window shows a report titled 'Report of count of specimens by protocol, type a...' with a table of specimen counts categorized by protocol and type.

Title	Type	Blood	Not Specified	Skin, NOS	Total
<b>Grand Total</b>		4	8	3	15
<i>Cryopreserv...</i>		0	4	3	7
<i>Chromosom...</i>	<i>DNA</i>	3	0	0	3
	<i>Whole Blood</i>	1	1	0	2
<i>Rare Diseases...</i>	<i>DNA</i>	0	2	0	2
	<i>Whole Blood</i>	0	1	0	1



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# PhenoTips, Patient Management

<http://pt13rc1.demo.bibbox.org>

dottie/Milano2017

The left screenshot displays a family record for 'FAM0000007'. It includes an 'About' section with identifier 'Smurfette', a 'Members' section listing two individuals (9700 and 9701), and a 'Pedigree' diagram showing inheritance from two parents through several offspring. A 'Comments' section at the bottom indicates no comments have been added.

The right screenshot shows the 'Phenotype database' interface. It features a header with 'Administration', 'PHENOTIPS', and user information ('Chip Potts'). Below the header are sections for 'ACTIVE GROUPS' (listing 'RD Connect Demo' with 5 members and 0 cases), 'MY FAMILIES' (listing 'F00695' and 'Smurfette' with their respective details), and 'PATIENTS SHARED WITH ME' (listing various patients like 'Hiccup Dragon' and 'Dottle Peluche' with their report dates).



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# Jupyter, Scripting & Data Integration

<http://jupyter.demo.bibbox.org/>

token = 9887f14aaa36a8b5217e7f8de4fb6d78cf857ab3dec11f

The screenshot shows a Jupyter Notebook interface running on a Mac OS X desktop. The left panel displays a file tree with various Jupyter notebook files, including ones for connecting to MySQL, REST interfaces, and specific data integration tasks. The right panel shows a single notebook cell titled "Data Integration OpenSpecimen + PhenoTips to Molgenis Sample Catalogue". The cell contains Python code for reading sample information from OpenSpecimen and writing it to Molgenis. The code imports datetime, requests, urllib, json, and sys modules. It defines URLs for OpenSpecimen and Molgenis, sets headers for both APIs, and defines a function to flatten sample hierarchy. A note at the bottom indicates the code is for Rare Disease Biobank France and EBB Chromosomal Disorder Collection.

```
In [10]: # READ INFORMATION ABOUT ALL SAMPLES FROM OpenSpecimen and Phenotips
import datetime
import requests
import urllib
import json
import sys

cprIPerName = {}
parIPerName = {}

baseUrl = "http://rdconnectdemo.demo.bibbox.org/"
baseURLPT = "http://pt13rc1.demo.bibbox.org/rest/patients/"
baseUrlMolgenis = "http://generic-molgenis.demo.bibbox.org/api/v2/"

elasticBaseURL = "http://elastie-el.demo.bibbox.org"
bioportalURL = "http://data.biocontology.org/"

headersEL = {'Content-type': 'application/json', 'Accept': 'text/plain'}
headersBP = {'Content-type': 'application/json', 'Authorization': 'apikey token=e33a5239-ecc4-46'}
```

# 1 = Rare Disease Biobank France  
# 2 = EBB / Chromosomal Disorder Collection COLLECTION  
biobankIds = [1, 2]

```
def flattenSampleHierarchy(sampleDescription):
    sampleList = []
    aliquotDescription = []
    sampleDesc = {
        'specimenClass': sampleDescription['specimenClass'],
        'specimenType': sampleDescription['specimenType'],
        'label': sampleDescription['label'],
        'guid': 'SAMPLE#rdconnectdemo.demo.bibbox.org:' + str(sampleDescription['id']),
        'isPrimary': sampleDescription['isPrimary']
    }
    sampleList.append(sampleDesc)
    aliquotDescription.append(sampleDesc)
```



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# BIBBOX in Action

## Demo

<http://demo.bibox.org>

## Documentation

<http://bibbox.readthedocs.io/en/latest/>

## Developers Space

<https://github.com/bibox/bibox-documentation>

## Publication

Heimo Müller, Nicolas Malservet, Philip Quinlan, Robert Reihs, Matthieu Penicaud, Antoine Chami, Kurt Zatloukal, George Dagher

[From the evaluation of existing solutions to an all-inclusive package for biobanks](#)

Springer Health and Technology, DOI 10.1007/s12553-016-0175-x



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