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Opportunities and needs within the consortium

Anne-Françoise Adam-Blondon, Mario Pezzotti, Holtgraewe Daniela, Paul Kersey

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Data integration to maximise
the power of omics
for grapevine
improvement

Opportunities and needs within the consortium

A-F Adam-Blondon (INRA, FR)
M. Pezzotti (U. Verona, IT)
D. Holtgraewe (U. Bielefeld, DE)
P. Kersey (Kew Garden, UK)

Europe has been continuously reinforcing its policy open access to FAIR research data

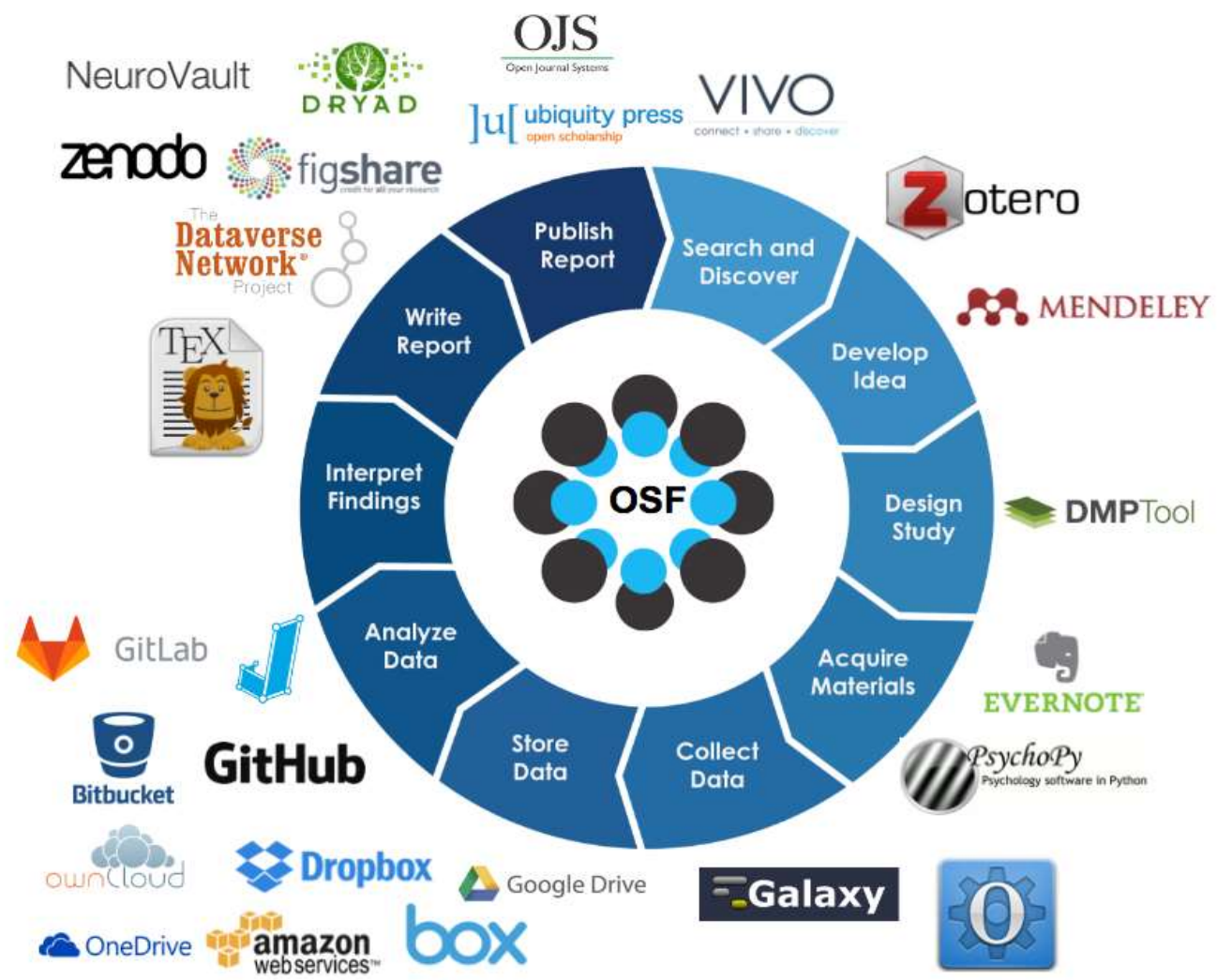


“Facilitating access to results encourages the re-use of research outputs and supports Open Science. This is essential for Europe's ability to enhance its economic performance and improve the capacity to compete through knowledge. [...] Results of publicly-funded research can therefore be disseminated more broadly and faster, to the benefit of researchers, innovative industry and citizens.



Recently funded projects were asked to add a WP supporting a FAIR compliant Data Management Plan

Integrape is about facilitating FAIR data management along all its life cycle



...which is still challenging!

From Rowan University, NJ, USA

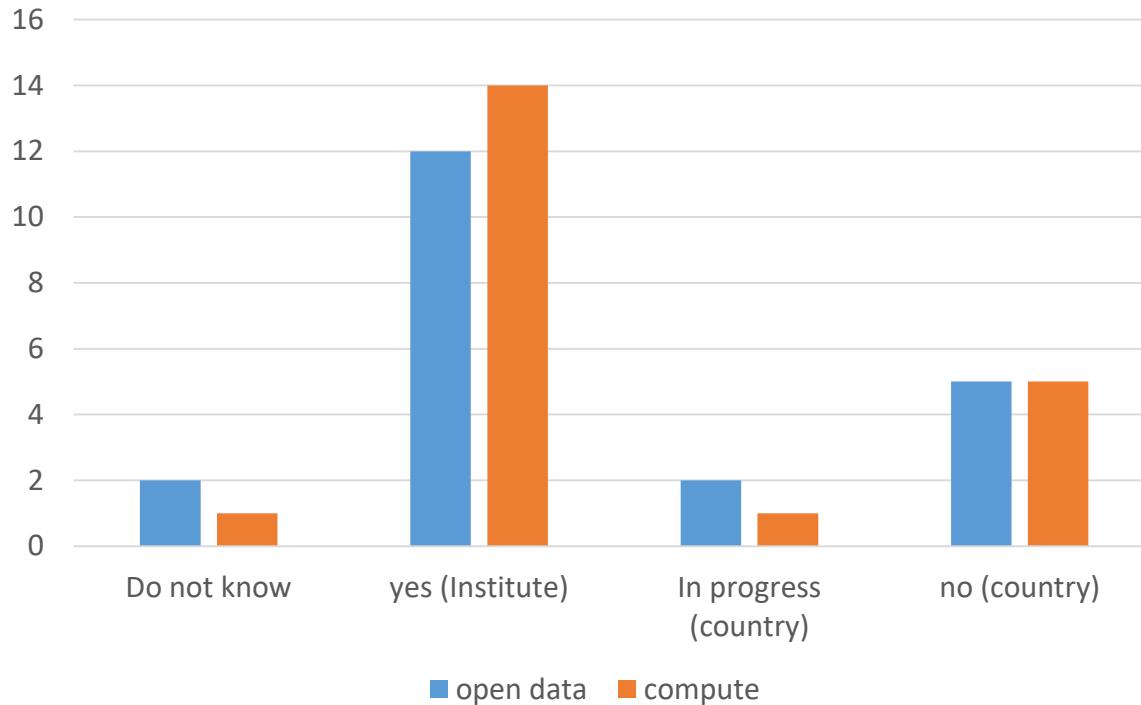
Short Survey sent to all the MC members

First part aimed at making an overview:

- National policies about open data in research
- Access to compute infrastructures
- Involvement in international infrastructure on bioinformatics or open data
- Use of database for the storage of data produced by the research units
- Needs in terms of training in bioinformatics
- Needs in terms of infrastructures

➔ Answers from 21 institutes of 16 countries

Country/Institute policies in terms of open data and of access to computing resources



10 institutes/countries involved in ELIXIR infrastructure, **2** in Life Watch +/- GBIF, **1** in DISSCO, **1** in PRACE, **1** in EMBL

What database/ computing infrastructure do you use?

Database

3 -> no use

15 -> local database maintained most of the time internally by its creator, sometimes with the help of IT central services

Commons -> international data repositories: VIVC, vitis-eu, INSDC archives (Genbank and co)

Computing infrastructure

11 -> no use

8 -> internally maintained servers

5 -> Access to (high performance) clusters maintained by the institute or at the national level

2 -> Access to national super computing facilities

1 -> commercial cloud



Short Survey sent to all the MC members

The second part aimed at digging a bit more into the data you produce and the way you manage it:

- What types/volumes of genomics-related data are you currently producing?
- How do you expect this to change over the next 5 years?
- How do you currently publish the data? Do you publish them at all?
- What are the obstacles to publishing the data?
- Are there data types you cannot publish?
- When you seek to use relevant published data, is it FAIR (Findable, Accessible, Interoperable, Re-usable)? If not, why?
- Are there existing norms in the area of data publishing that you adhere to?
- Are there candidate norms that you would like the community to adopt?
- Are there new norms that the community could usefully develop?
- Does the grape research community need its own dedicated Grape Information System, and if so, what would you like to be able to use or to contribute?

 Answers from 10 institutes

Type and volume of data produced, evolution in the next 5 years

- Metabolomics data/ a few hundreds of genotypes
- Whole genomes assemblies and annotations of *V. vinifera* and non-vinifera species; Annotations of specific gene families or genomic features (e.g. resistance genes, TE)
- Hundreds of RNAseq datasets every year
- Markers and genotyping data (SSR, SNP, SRAP, ...) from a large range of techniques; Maps, QTL,...
- Polymorphism, re sequencing data, RAD seq
- Phenotyping data
- Genetic resources
- Simulated data

Evolution

- Increase of the pace and volume of data
- New opportunities linked to technical changes but raising questions about references, standards, ...: pangenomics, single cell RNAseq, RiboSeq, ...

Practices in terms of data publication; possible bottlenecks

Most partners publish their data in international archives or file repositories

Bottlenecks

- **Mostly the peer review process of paper associated to the data**
- Lack of standards for some datatypes
- Workflow issue / Lack of dedicated and skilled persons
- Nagoya protocol

Can you effectively re-use already published data?

Many issues mentioned:

- Gene ID , identification of the plant material unclear or obsolete
- Incomplete metadata or in a challenging format for re-use
- Incomplete data (e.g. primer sequence) or low quality data

Whishes for the future

- **Open access to data, better published along with papers**
- Need for the development of non existing standards: e.g. in relation with pan genomics, API for metabolomics, ...
- A hub for grapevine research is definitely welcome