Opportunities and needs within the consortium

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Data integration to maximise the power of omics for grapevine improvement

Opportunities and needs within the consortium

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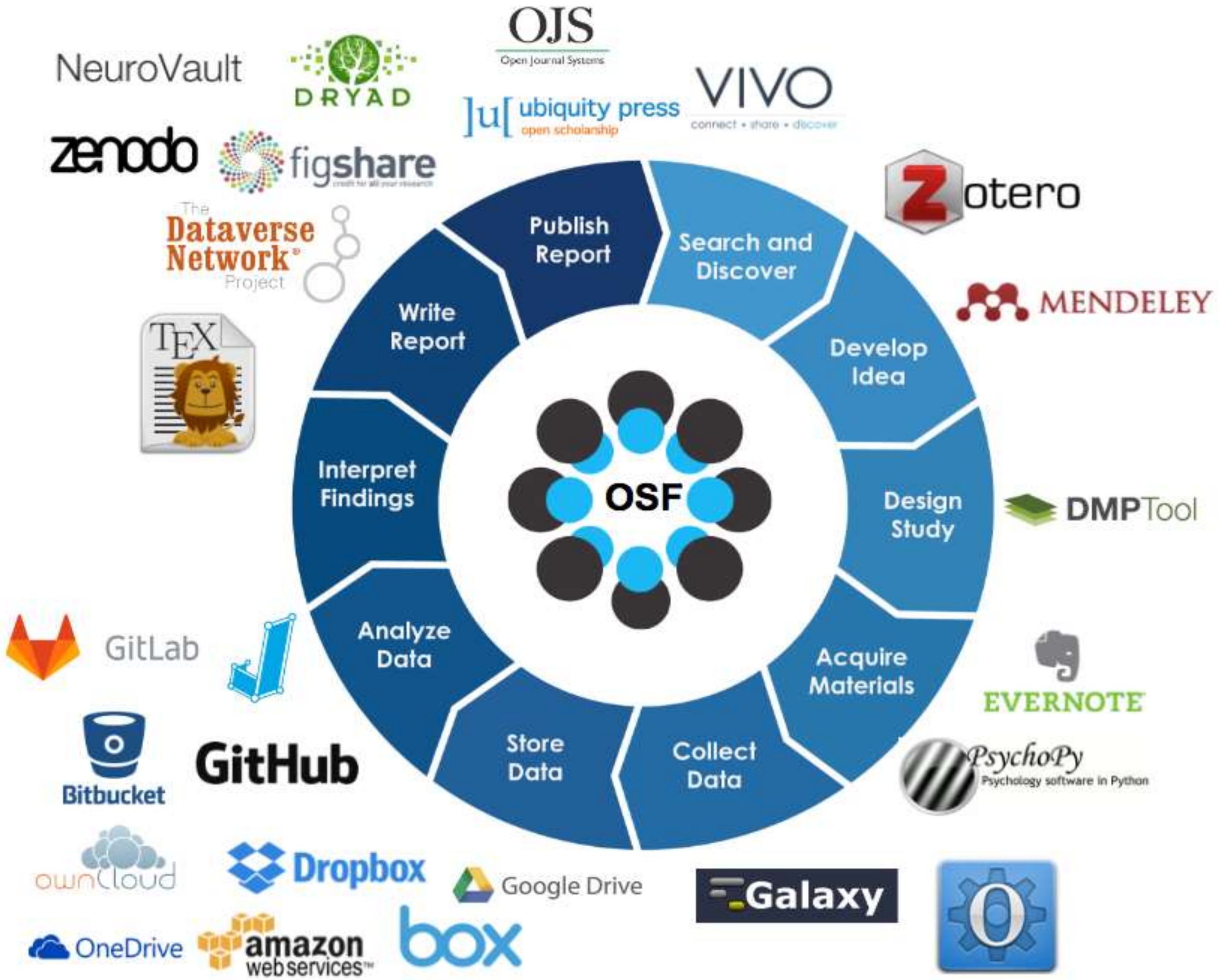
Europe has been continuously reinforcing its policy open access to FAIR research data

“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

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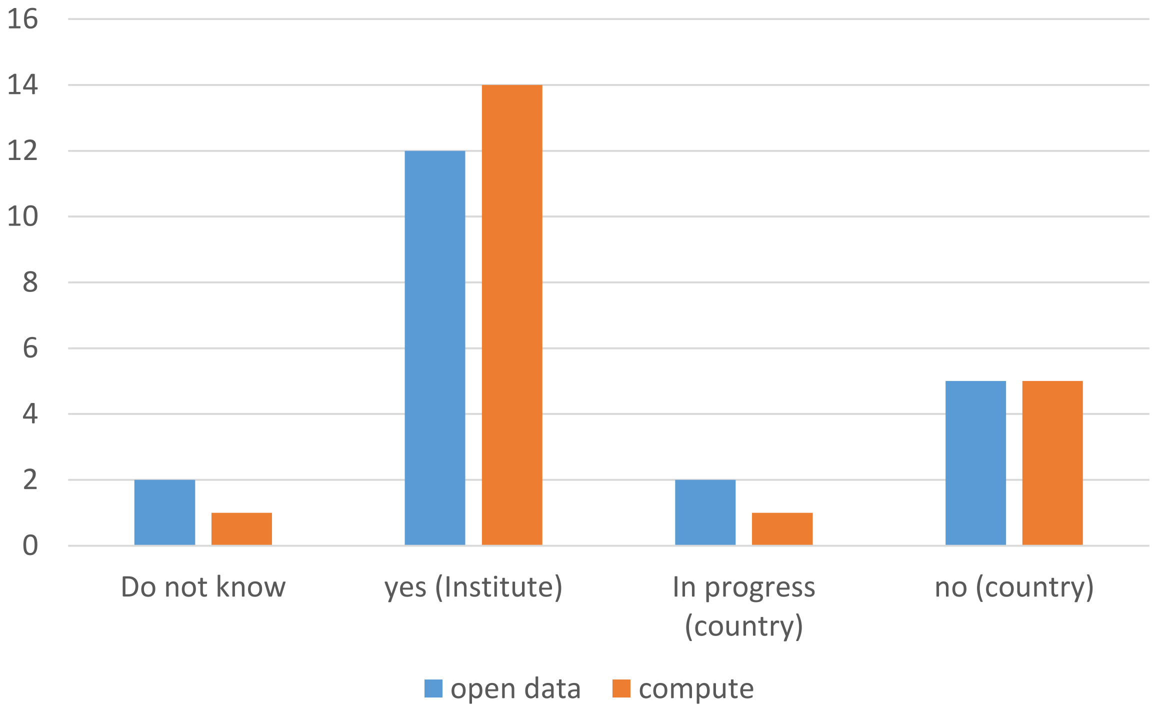
Short Survey sent to all the MC members

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

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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

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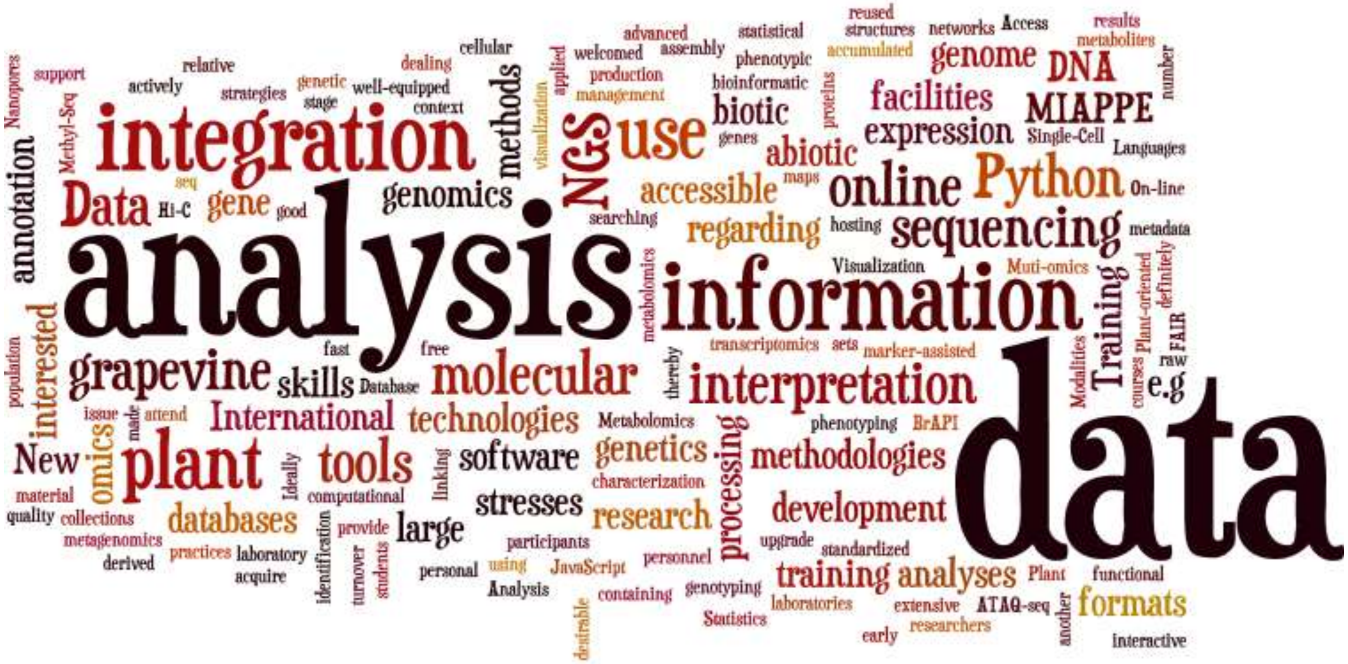
What would be the priority in terms of training?

- Genomic data analysis is the first need and to a lesser extent data standardization
- The target is mostly students but some mentioned also the management
- Online material, resources to allows students to attend courses are problematic for some respondents



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What would be the priority in terms of access to a bioinformatic infrastructure?

- Access to stable/reliable tools for omics data analysisis the most frequently cited need
- Storage capacity
- Help for the development of a policy and legislation compliant infrastructures
- National and transnational access (without the need to develop ad hoc collaborations) to powerful computing infrastructures

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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

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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, …

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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

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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

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