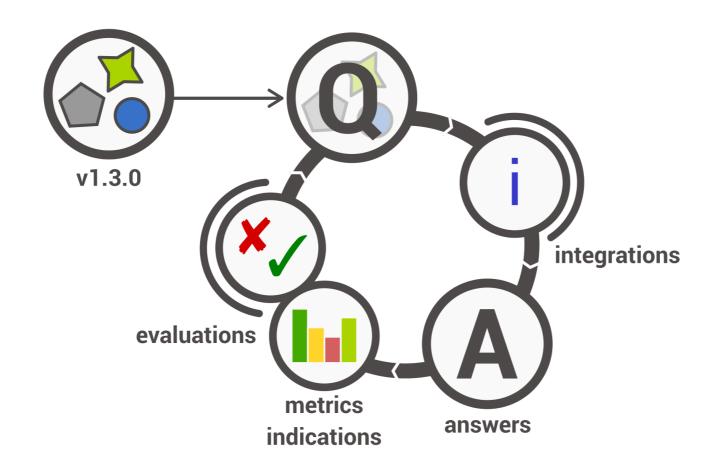


# **Data Steward Wizard**



Korbinian Bösl Data manager ELIXIR Norway 11 March 2020





## Developed by









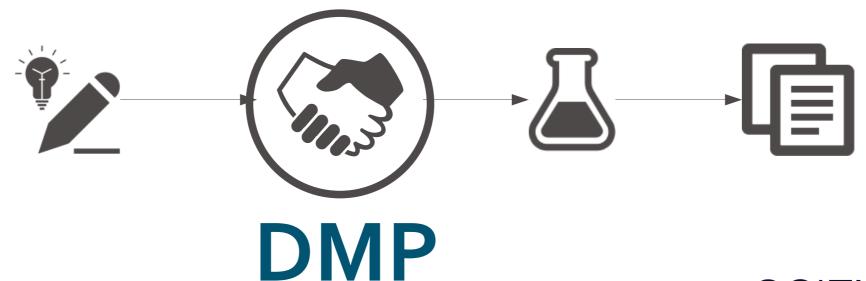




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ds-wizard.org github.com/ds-wizard

# Forskningsrådet









# Horizon 2020 → Horizon Europe

Open Research Data Pilot (ORD pilot)
Default since 2017 → mandatory 2021



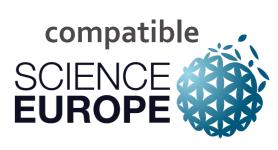




# Filled questionnaire $\rightarrow$ Template $\rightarrow$ DMP in various formats per funding body

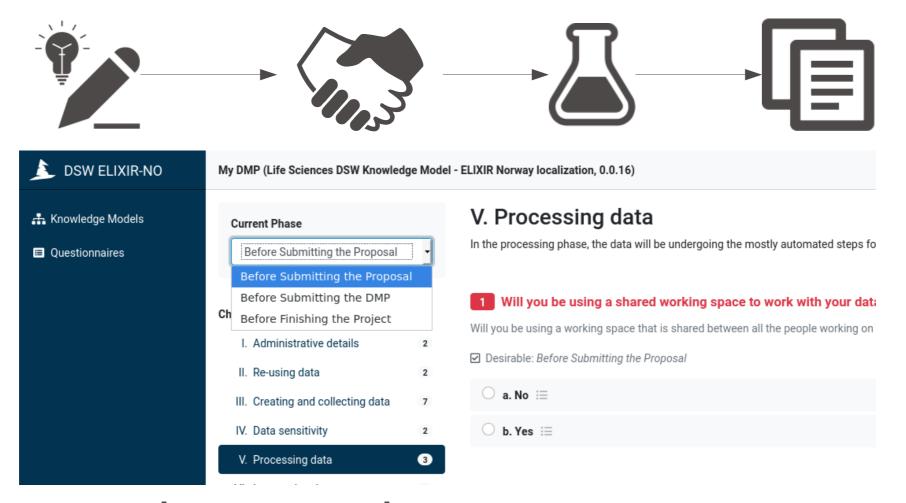
.docx, .tex, .html, .json





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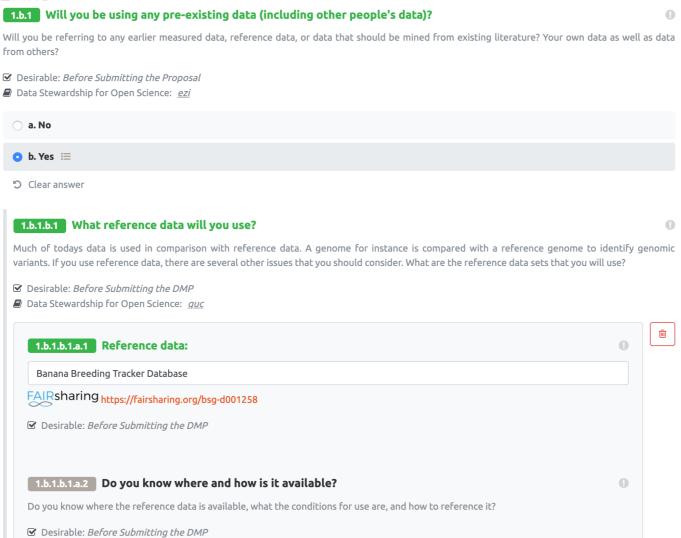




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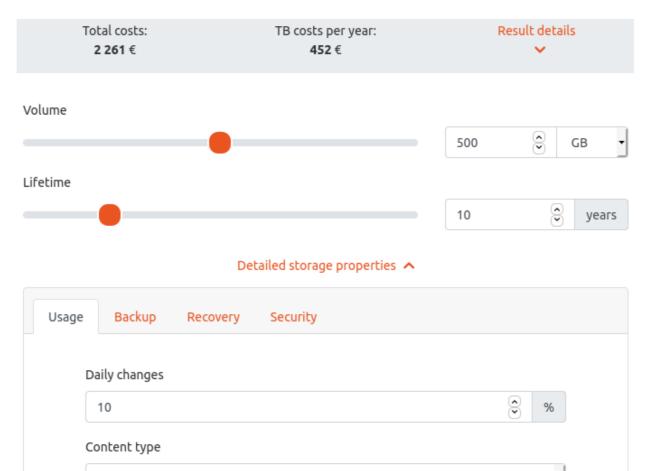
#### DATA STEWARDSHIP WIZARD



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Usage	Backup Recovery	Security	
Da	ily changes		
	10	<b>҈</b> %	
Co	ntent type		_
	Many small files		·
Ac	cess type		_
	One file on request		•
Dā	ily read volume		
	10	€ %	

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Go to App



Data Stewardship for Open Science: Chapter 2.5.1.2



## Can the original data be regenerated?

## What's up?

In some cases it might be cheaper (and acceptable) to regenerate data rather than storing them. Two examples: It may soon become cheaper to 're-sequence' a genome than to store it for 10 years. Also text mining the same massive corpus of text with the same tagger and the same thesaurus, should in principle give the exact same result when repeated at any time. However, in both examples, a number of assumptions would have to be made before a decision would be made to re-generate the data rather than storing the first version for extended period of time. First of all, the technology should not change; sequencers get more reliable by the day and therefore may give different results and the 'old sequencer' may not be in your possession anymore by the time you want to generate the results. Workflows are not necessarily stable but more importantly even 'stable' substrates (a genome of a living individual or a corpus of text) may not be as stable as you think. Changes to a text corpus may occur unbeknownst to you, but also, the somatic mutation rate in the genome of a living organism are not insignificant and therefore a new sample of cells to take DNA from may give different results and even if the DNA sample was stored in 'preserved state' there is no absolute guarantee that later re-sequencing of it will give exactly the same result. So in all cases, the decision to 'regenerate versus store' is a deep-scientific method discussion in the group and not a 'trivial decision'

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**Barend Mons** 

ds-wizard.org github.com/ds-wizard



### Information and insight



Metric	Measure	Findability
Findability	0.70	Openness Accessibility
Accessibility	0.22	
Reusability	1.00	
Good DMP Practice	0.67	Good DMP Practice Reusability
Openness	0.69	

### **Metrics Explanation**

#### F - Findability

The Findability metric describes how easily data can be located. The score associated with an answer will be higher if it makes it easier for humans or for computers to locate your data set, e.g. if it ends up in an index or has a unique resolvable identifier.

#### A - Accessibility

The Accessibility metric describes how well the access to the database is described and how easy it is to implement. The score associated with an answer will be higher if it makes it easier for humans and computers to get to the data. This is determined by e.g. the protocol for accessing the data or for authenticating users, and also by the guaranteed longevity of the repository. Note that this is different from the Openness metric!

elixir-no.ds-wizard.org



# elixir-norway.org digitallifenorway.org



contact@bioinfo.no



@elixirnorway @DigitaltLiv













The Research **Council of Norway** 





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UiO University of Oslo



Norwegian University of Science and Technology



Norwegian University of Life Sciences

Data Steward Wizard development











