

From Bits to Bites: Software Development supporting Plant Genetics, Breeding and Genetic Resources

2nd April 2025 Marche Polytechnic University,
Ancona, Italy

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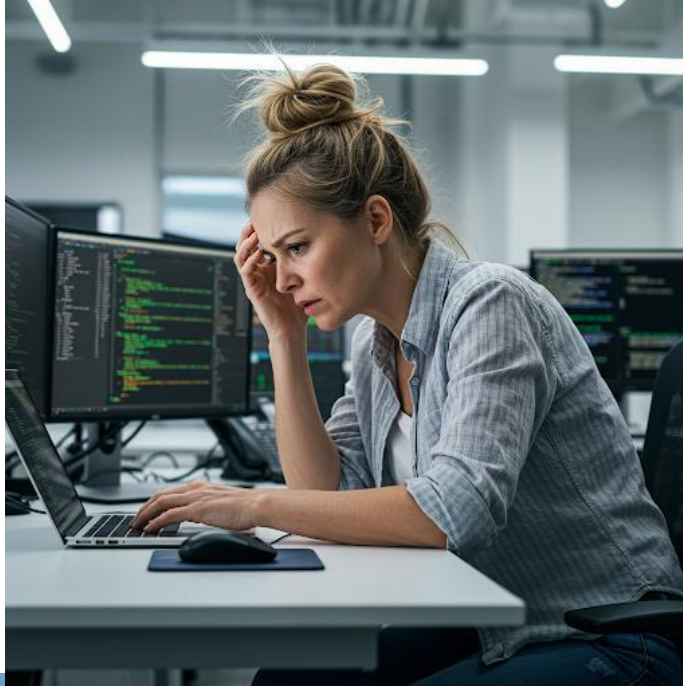


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Plant science produces a lot of data...

Google Gemini: 'Show me an image of a scientist working with data'



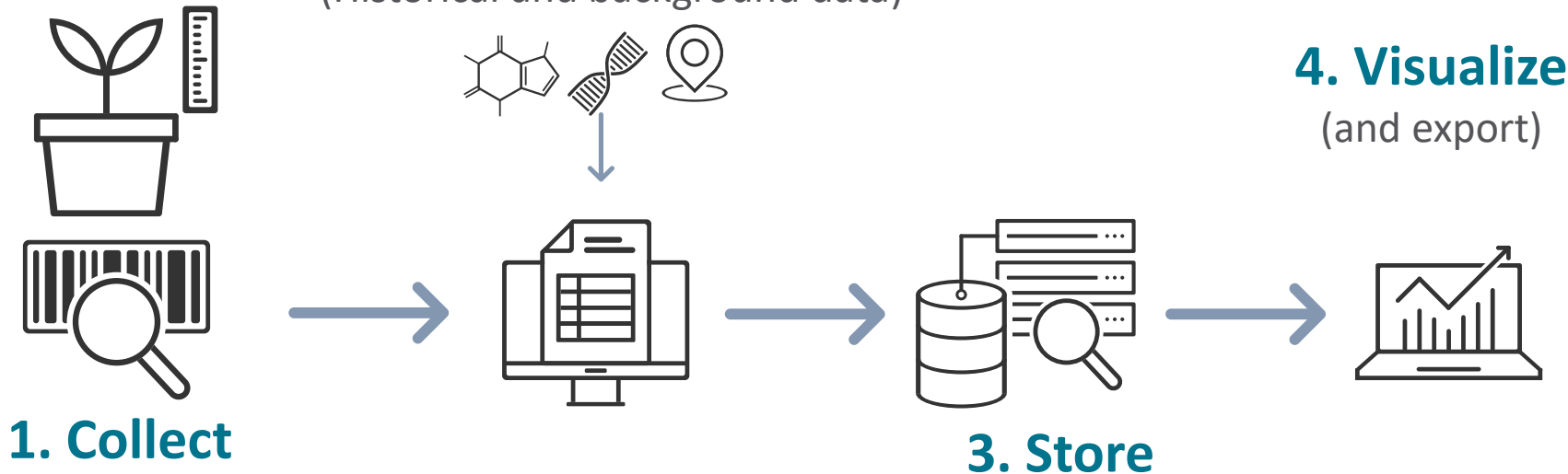
3* V's
Volume,
Variety,
Velocity,
Veracity and Value

But we really don't have any option...

Simplifying plant pre-breeding...

2. Merge and Wrangle

(Historical and background data)



Potential Solutions?



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Why?

- Size and complexity of data is challenging.
- Allowing people to collect, store, explore & interact with data.
- Aid understanding.
- Show relationships and patterns.
- Provide ***easy access*** in digestible chunks.
- Availability of information (FAIR etc.).
- Reduce errors.

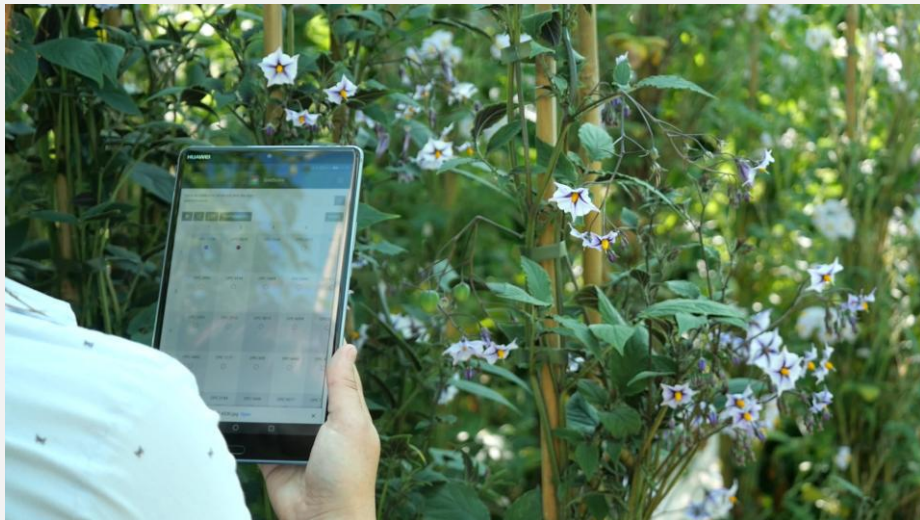
Making Diversity Available



GridScore

Mobile phenotypic data collection

gridscore.hutton.ac.uk



Raubach, S., Schreiber, M. & Shaw, P.D. GridScore: a tool for accurate, cross-platform phenotypic data collection and visualization. *BMC Bioinformatics* 23, 214 (2022).
<https://doi.org/10.1186/s12859-022-04755-2>



Common Errors and Mistakes



Number swaps

An easy mistake to make, e.g. 24 vs 42.
Trait limits and visualizations can help prevent and discover these errors.



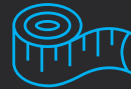
Decimal point issues

Decimal point in the wrong place.
Trait limits and visualizations can help prevent and discover these errors.



User differences

Different people may score the same trait differently.
Flower colour for example, "dark purple" vs "medium purple". Choose distinct categories and provide reference sheets.



Different units

Using different units to measure the same thing.
E.g. centimetres vs inches. Seems easy to avoid, but still happens. Provide trait descriptions including units.



Different categories between sites

The same trait might be scored differently between sites. "1, 3, 5, 7, 9" vs "very low, low, medium, high, very high". Share trait definitions with collaborators.



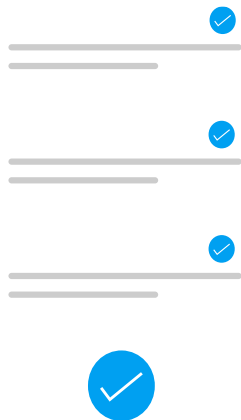
Plot mix-up

Scoring data for the wrong plot.
Use barcodes/QR-codes or guided walks to prevent this.

Stop Writing Stuff on Paper!

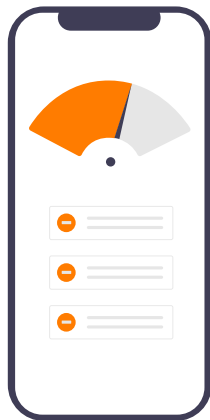
10%

Benefits



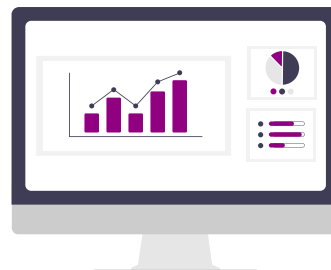
Data verification

Reduce errors by using automatic **data validation** coupled with interactive live visualizations of data.



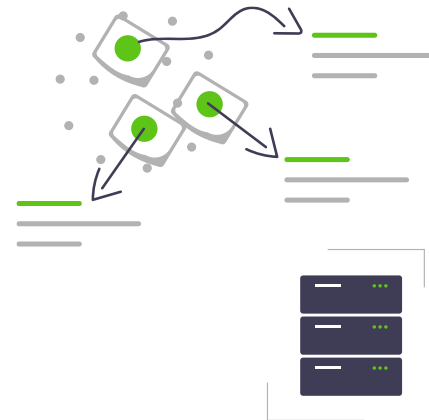
Better efficiency

Faster data collection, removal of hand-written notes, automatic **image tagging**, **GPS** tracking.



Data visualization

Spot outliers or interesting patterns in the data. These may **indicate errors** or **meaningful clustering** of data.



Data integration

Load germplasm and trait identifiers straight from central database. Everyone using the **same definitions**. Makes data **comparable/compatible**.

What happens if you don't collect high quality data?



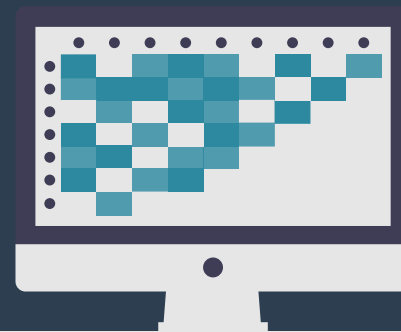
1. Inaccurate conclusions, false discoveries and skewed results
2. Wasted resources
3. Damage to scientific integrity and loss of trust
4. Delayed advancement
5. Difficulties in reproducibility

Science fictions: exposing fraud, bias, negligence and hype in science by Stuart J. Ritchie



Germinate

Plant genetic resources database
germinate.hutton.ac.uk



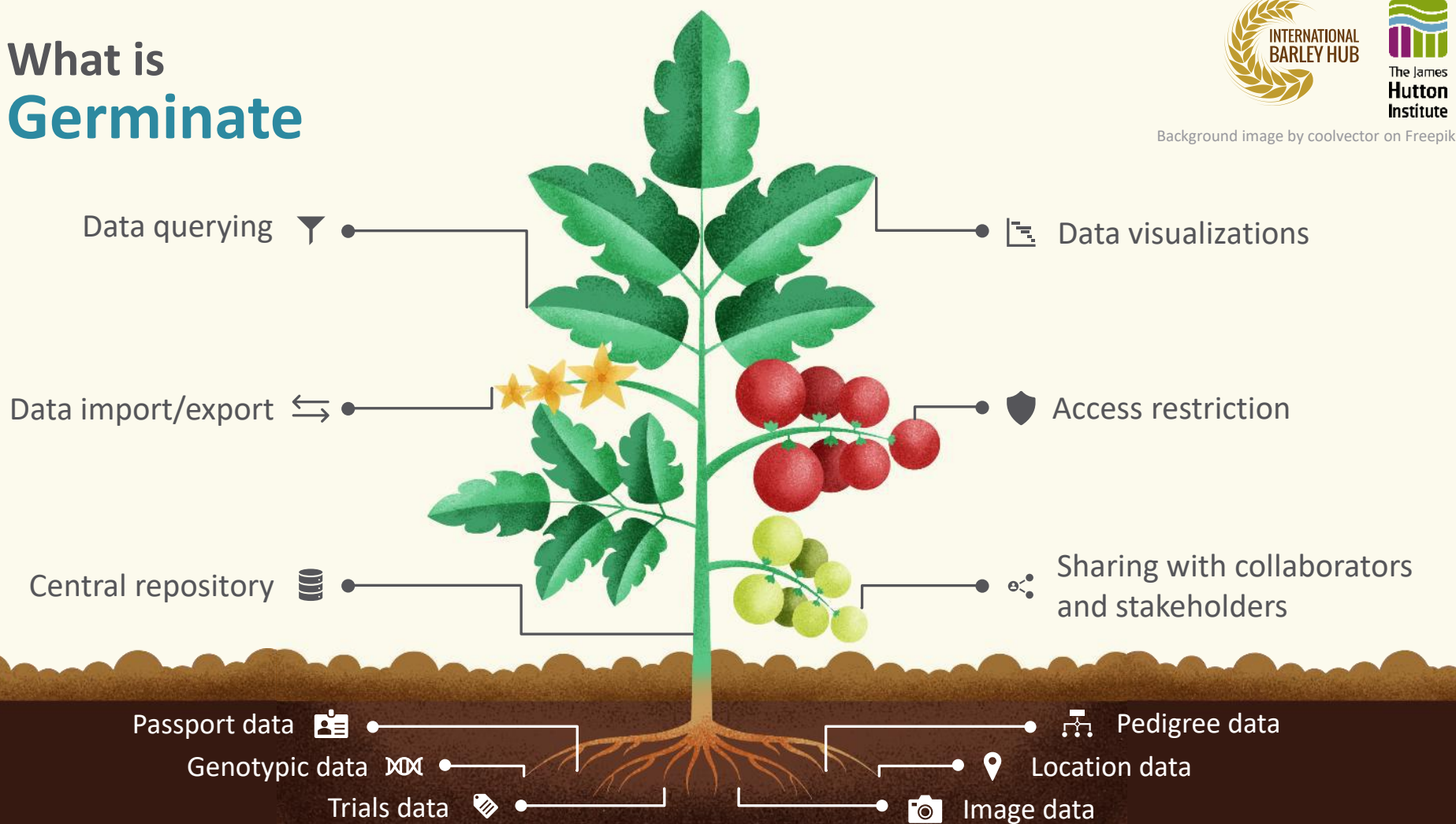
Raubach, S., Kilian, B., Dreher, K., Amri, A., Bassi, F. M., Boukar, O., Cook, D., Cruickshank, A., Fatokun, C., el Haddad, N., Humphries, A., Jordan, D., Kehel, Z., Kumar, S., Labarosa, S. J., Nguyen, L. H., Mace, E., McCouch, S., McNally, K., ... Shaw, P. D. (2021). From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. *Crop Science*, 61(3), 1538–1566.
<https://doi.org/10.1002/csc2.20248>

Shaw, Paul D., Sebastian Raubach, Sarah J. Hearne, Kate Dreher, Glenn Bryan, Gaynor McKenzie, Iain Milne, Gordon Stephen, and David F. Marshall. 2017. “Germinate 3: Development of a Common Platform to Support the Distribution of Experimental Data on Crop Wild Relatives.” *Crop Science* 57 (3): 1259–73.
<https://doi.org/10.2135/cropsci2016.09.0814>.

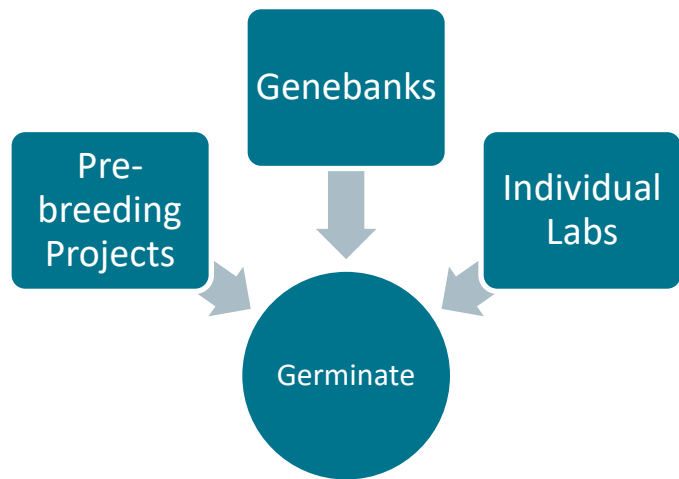
What is Germinate



Background image by coolvector on Freepik



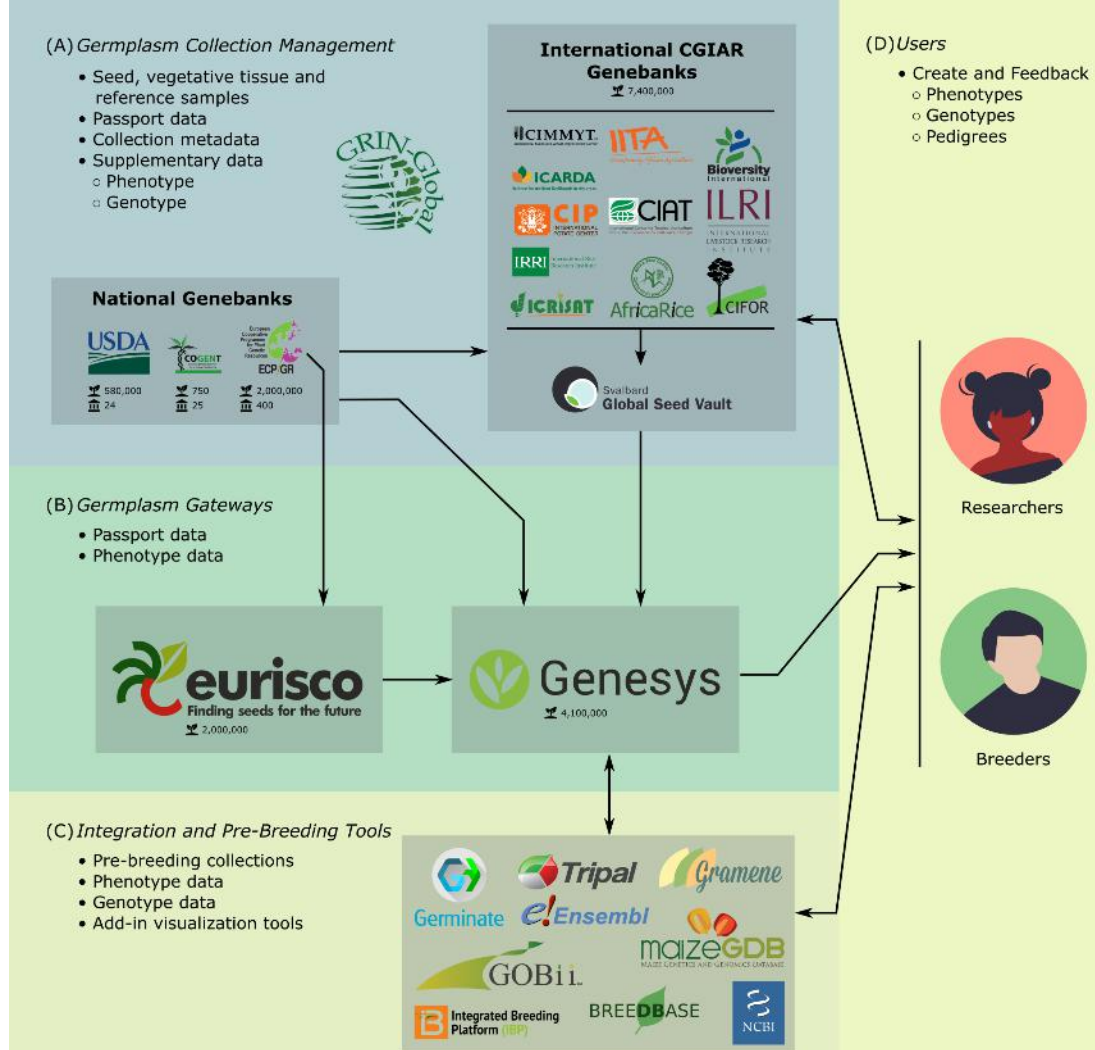
FAO GLIS Positioning



Shallow v Deep Data

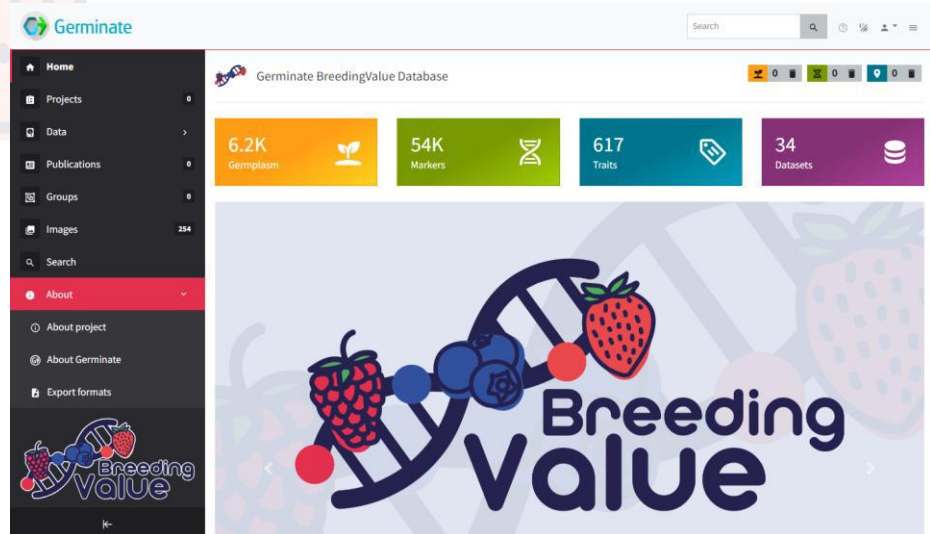
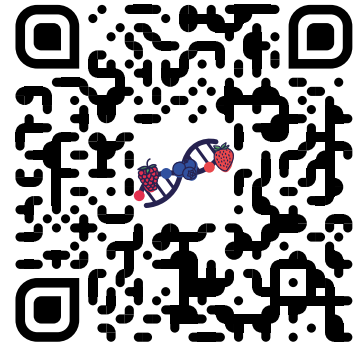
Wide and shallow – Narrow and deep

Shaw, Paul D., Stephan Weise, Matija Obreza, Sebastian Raubach, Susan McCouch, Benjamin Kilian, and Peter Werner. 2022. "Database Solutions for Genebanks and Germplasm Collections." In *Plant Genetic Resources for the 21st Century*, 285–309. New York: Apple Academic Press. <https://doi.org/10.1201/9781003302957-19>.



Where to find BreedingValue data?

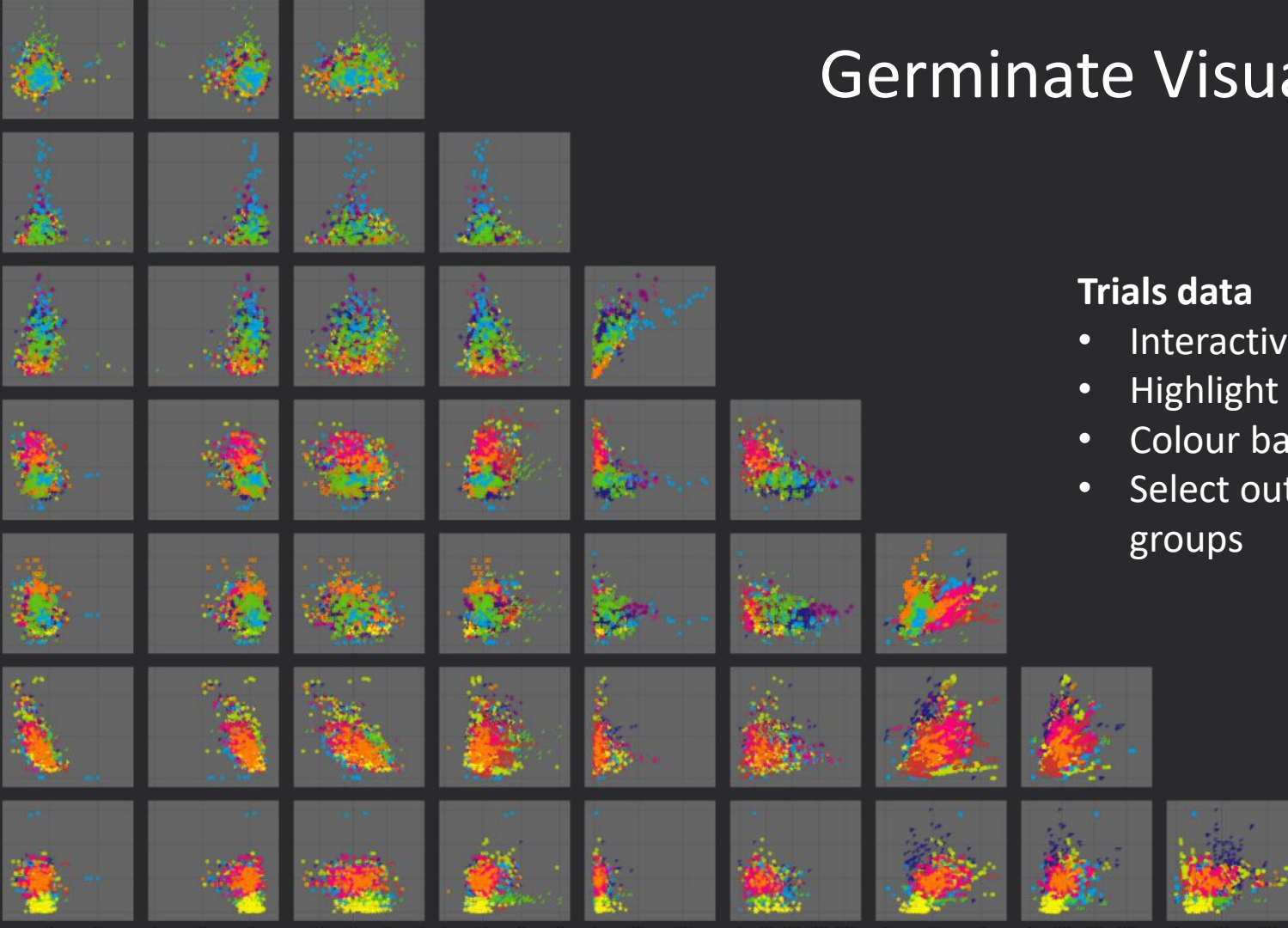
- BreedingValue data is available at:
<https://germinate.hutton.ac.uk/breedingvalue>
- Not all data public yet, but lots to explore
- No user account/registration required

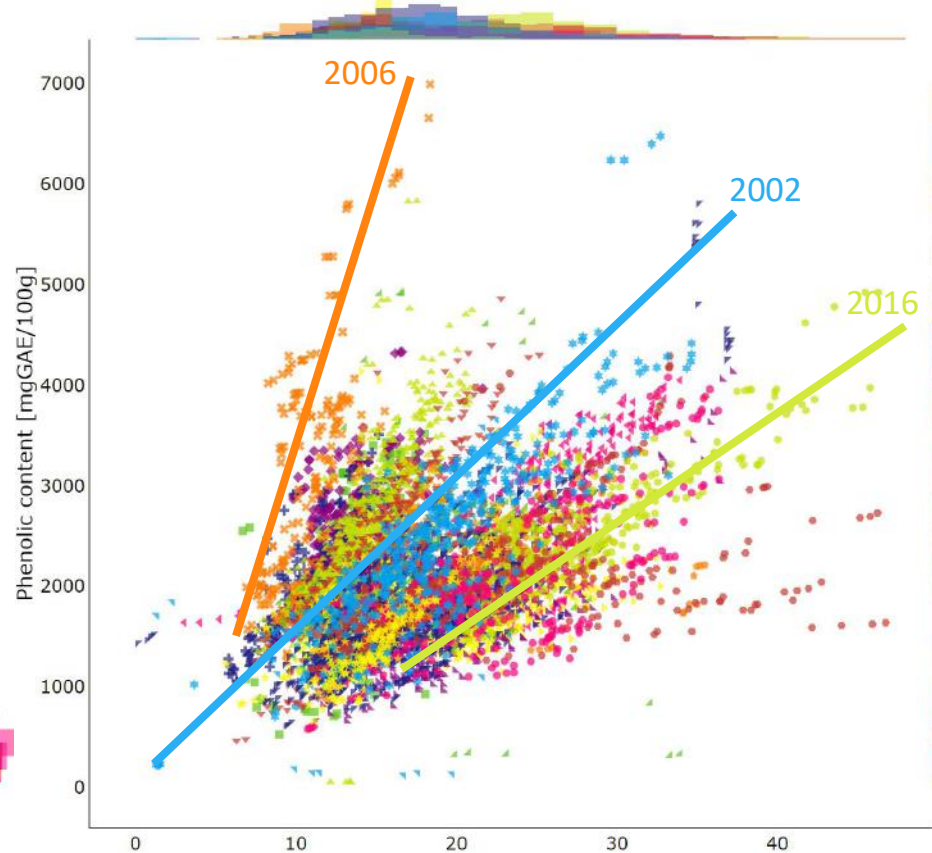
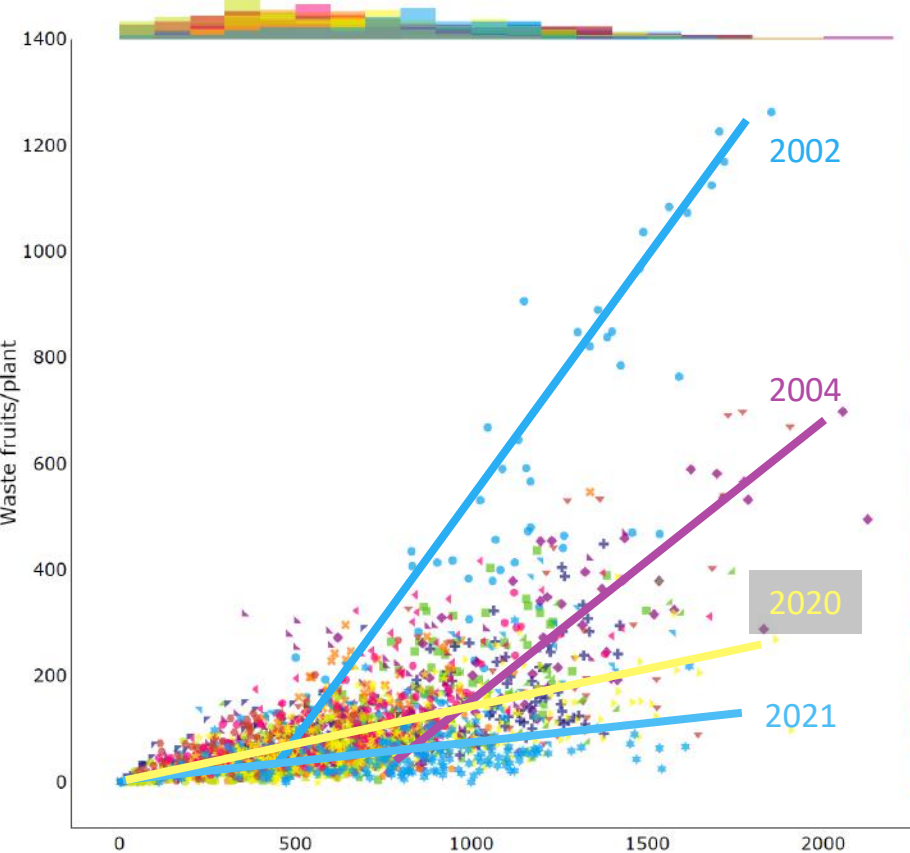


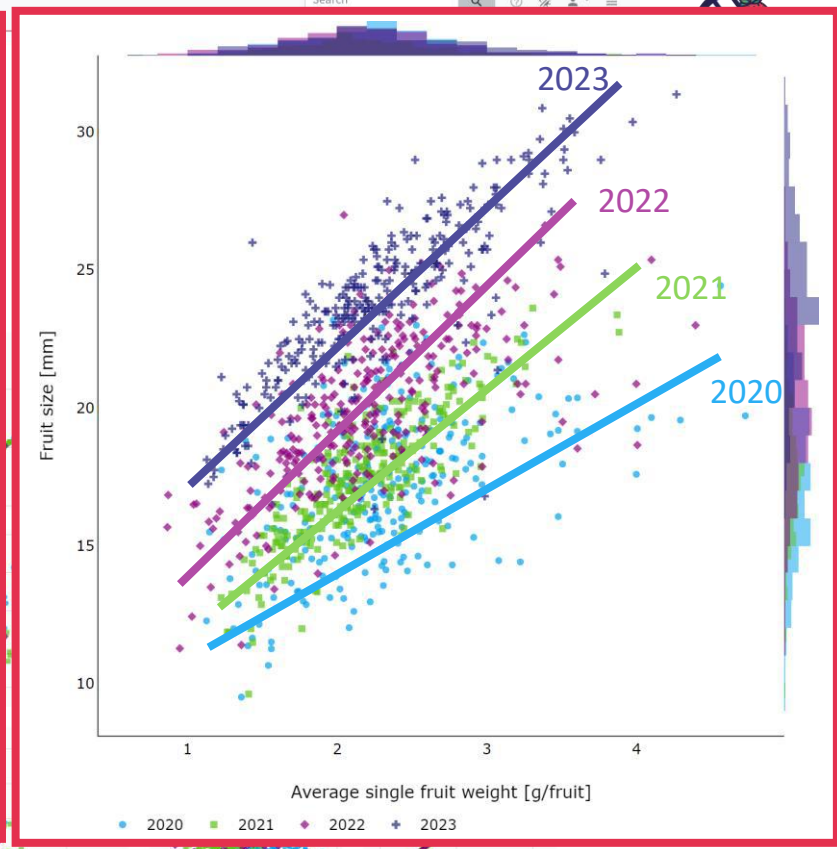
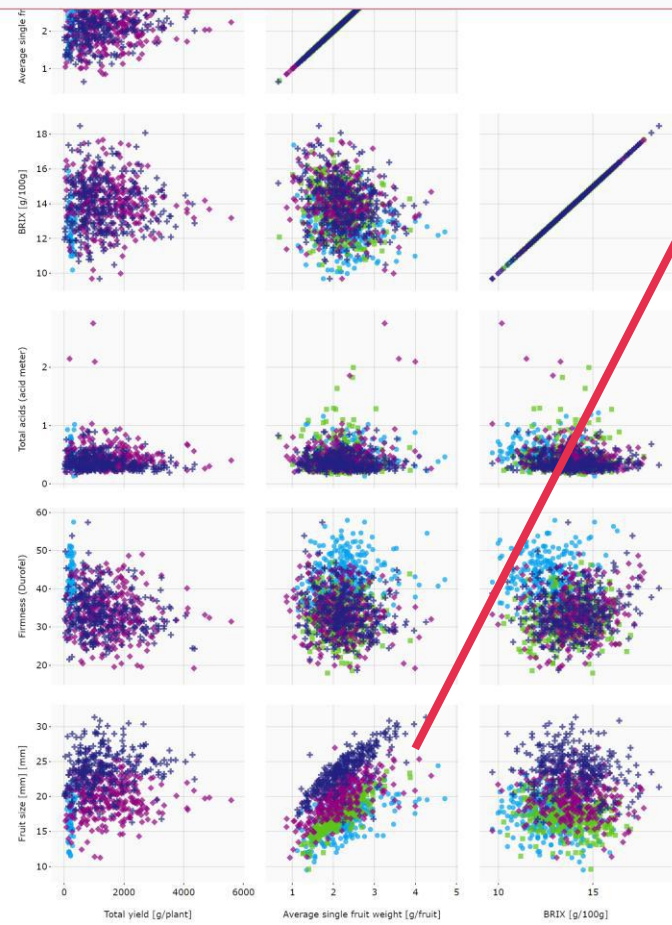
Germinate Visual Analytics

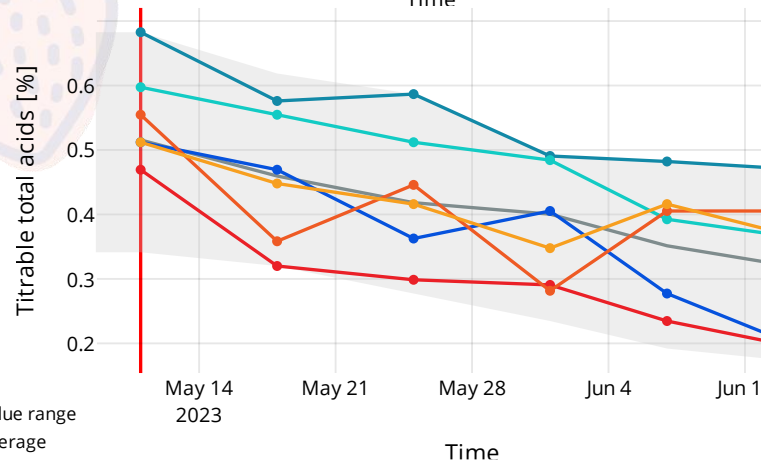
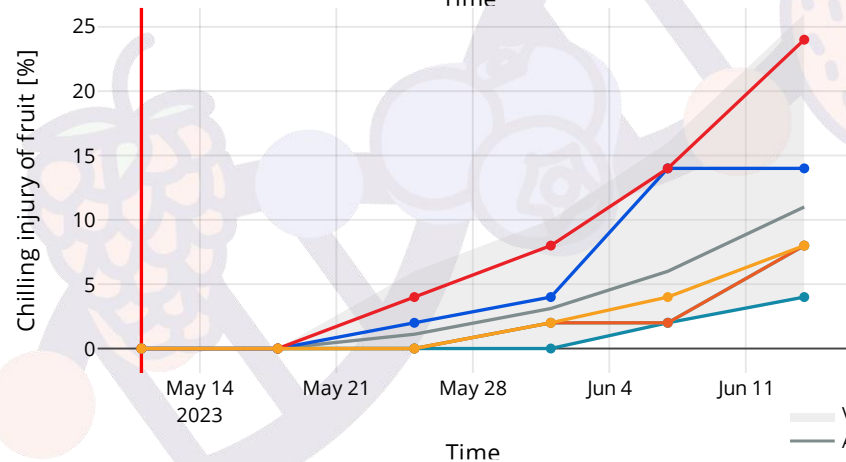
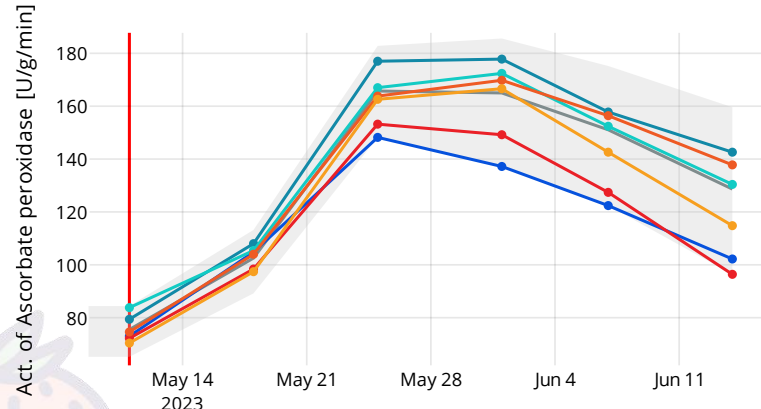
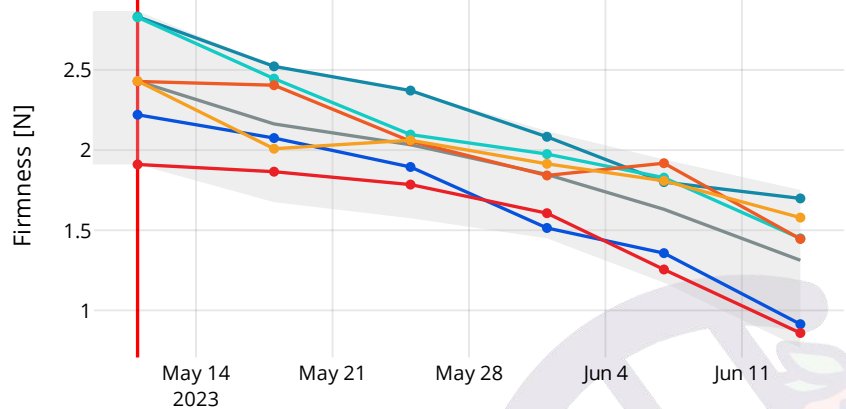
Trials data

- Interactive plots
- Highlight germplasm groups
- Colour based on *things*
- Select outliers and create new groups









- Value range
- Average
- Control-Biloxi:Vaccinium-1
- GABA-Biloxi:Vaccinium-1
- Hexanal-Biloxi:Vaccinium-1
- Control-Star:Vaccinium-1
- GABA-Star:Vaccinium-1
- Hexanal-Star:Vaccinium-1



Summary

- Think about your data and how you will collect, store and analyse it!
- **Go and use the data!**
- **Watch the seminar, have an explore, reach out to us!**
- We welcome contributions, feedback and ideas on how we can improve.
- Please just give us a shout if you want to try any of our tools with your own data or want an extended demo.
- **Don't write stuff down with pen and paper!**
- **Think about naming of samples!**

PGR Work @ Hutton

- Sebastian Raubach
- Elisa Senger
- Miriam Schreiber
- Micha Bayer
- Kelly Houston
- Susan McCallum
- Julie Graham
- Malcolm Macaulay
- Niki McCallum
- Mohamed Salama
- Gaynor McKenzie
- Joanne Russell
- Pauline Smith
- Luke Ramsay
- Robbie Waugh
- + barley, potato and soft fruit groups @Hutton

Acknowledgements



Scottish Government
Riaghaltas na h-Alba



European Commission



Department
for Environment
Food & Rural Affairs



Norway



NORWEGIAN MINISTRY
OF FOREIGN AFFAIRS



Scientific Services



Norad

RESAS

DIAGEO

syngenta



DIVSEEK
INTERNATIONAL
NETWORK INC.

SEFARI



SusCrop – ERA-NET
Cofund on Sustainable Crop Production
FACCEIPI



BBSRC



TEMPLETON WORLD
CHARITY FOUNDATION



Innovate
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Esmée
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FOUNDATION



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