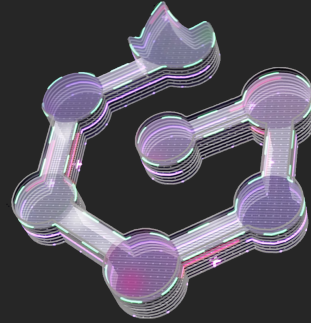


Integrating genetics, omics, and literature-based data for grapevine improvement:



I2SysBio



José Tomás Matus

Transcriptional Orchestration of Plant Secondary Metabolism (TOMS lab)
Institute for Integrative Systems Biology (I2SysBio, UV-CSIC), Spain

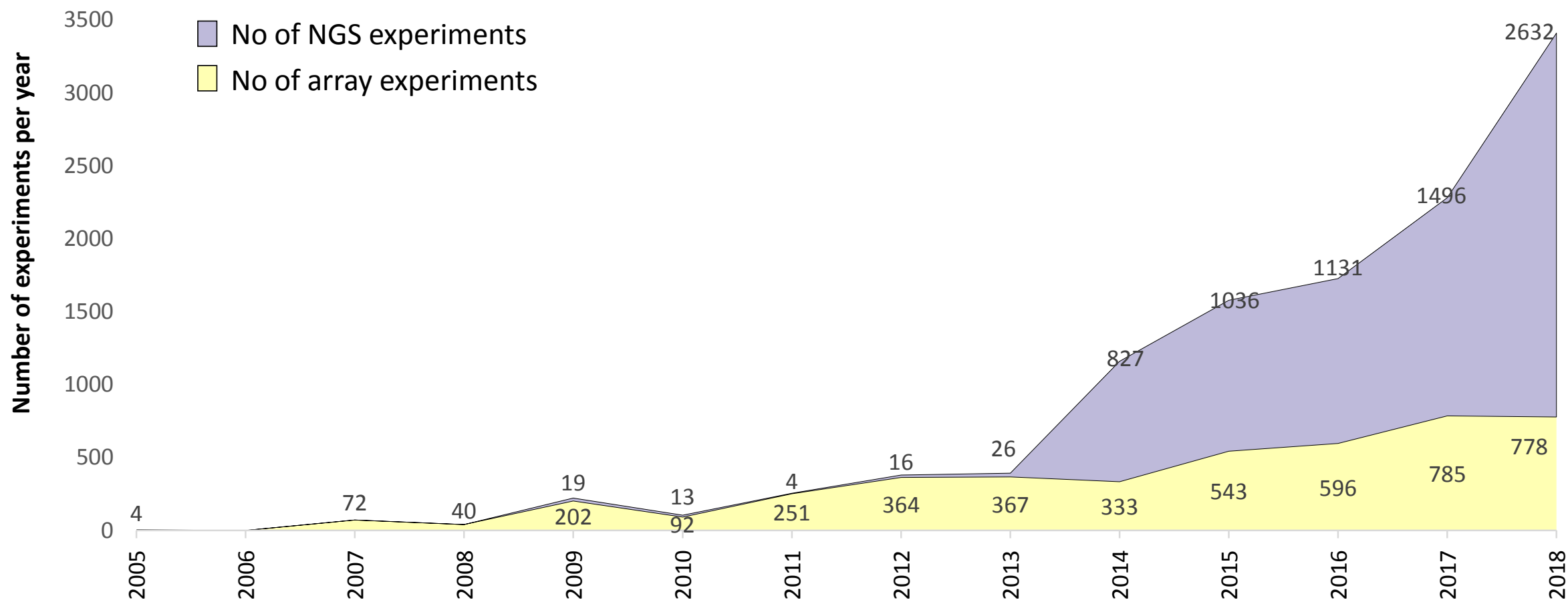


Justin Lashbrooke

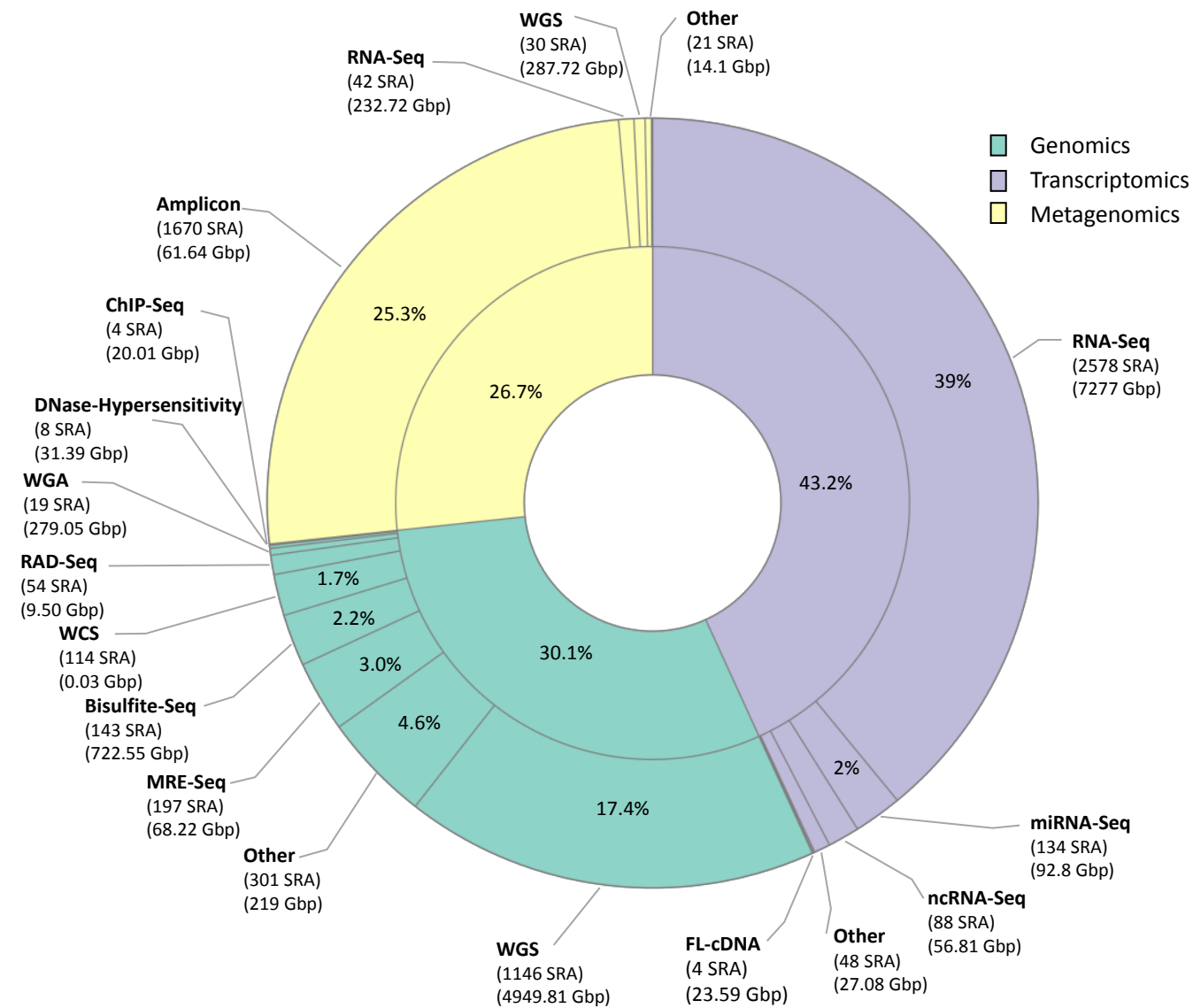
Department of Genetics
Stellenbosch University, South Africa.



We are in the Era of Big Data & Databases



Matus et al. Prospects of Systems Biology in Grapevine. In: The Grape Genome. Cantu, Walker, Eds.



Matus et al. Prospects of Systems Biology in Grapevine. In: The Grape Genome. Cantu, Walker, Eds.



<i>Vitis vinifera</i> ssp. <i>vinifera</i>	Black Corinth
<i>Vitis vinifera</i> ssp. <i>sylvestris</i>	Cabernet Franc
<i>Vitis acerifolia</i>	Cabernet Sauvignon
<i>Vitis arizonica</i>	Carménère
<i>Vitis aestivalis</i>	Chardonnay
<i>Vitis berlanderi</i>	Merlot
<i>Vitis girdiana</i>	Nebbiolo
<i>Vitis monticola</i>	Pinot Noir
<i>Vitis mustangensis</i>	Pixie
<i>Vitis riparia</i>	Riesling
<i>Vitis rupestris</i>	Sauvignon Blanc
<i>Vitis 101-14 Mgt</i>	Semillon
<i>Vitis 110R</i>	Zinfandel
<i>Vitis Kober5BB</i>	PN40024 [External]
<i>Muscadinia rotundifolia</i>	

omics.com

Hosted by Cantu Lab @ UC Davis



Current tools available for the grape community

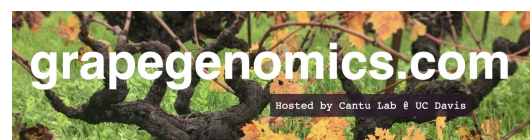
Genome
browsers

Transcriptome
explorers

Cultivar
collections

Metabolite
repository

Gene
Networks



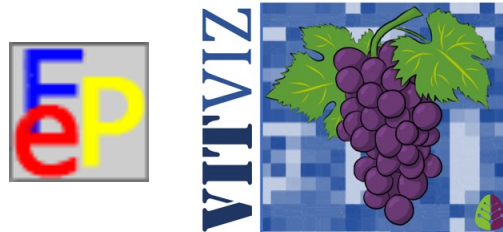
vespucci



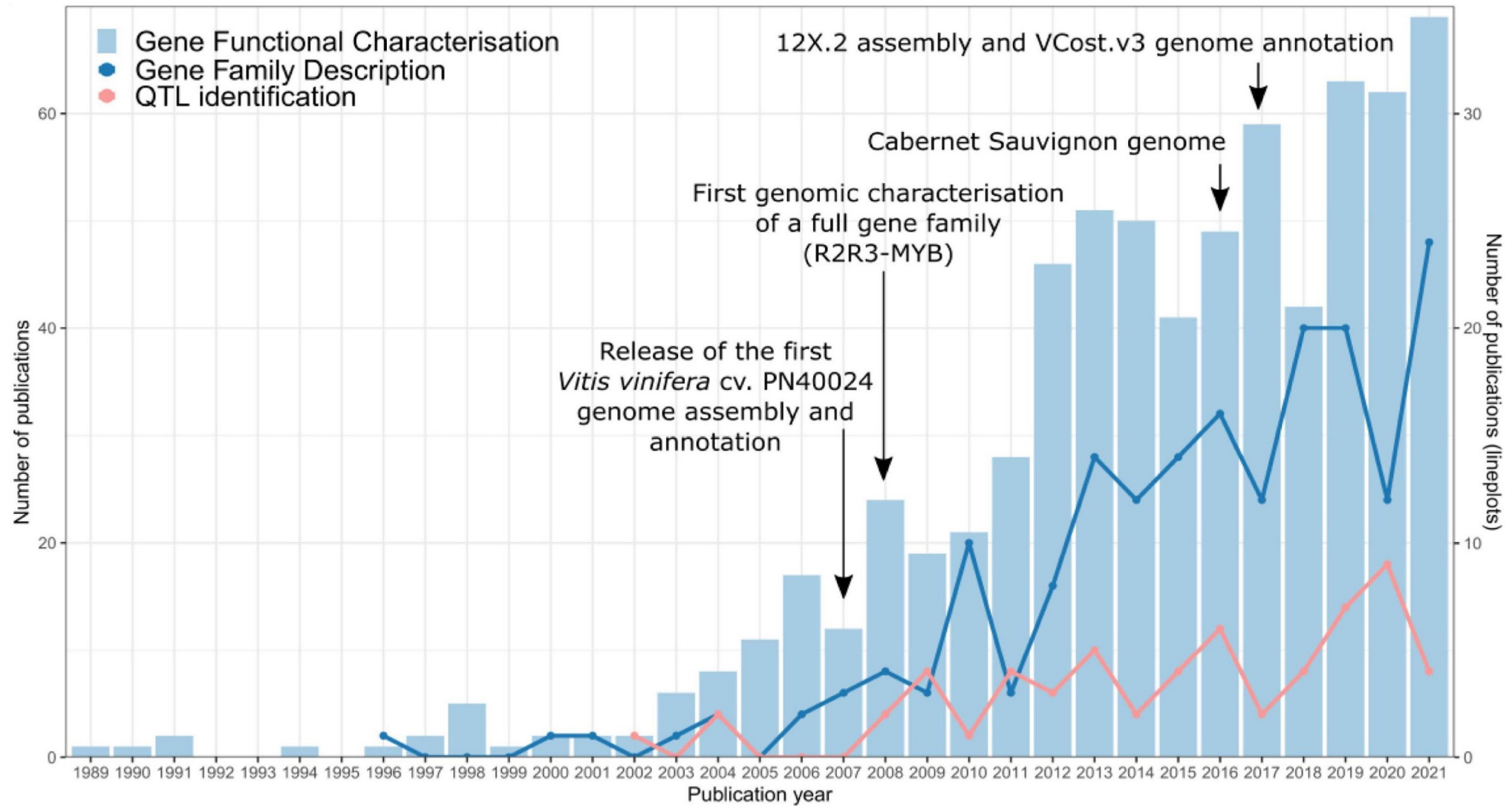
Others
(mostly private)

GREAT

Vitis International Variety Catalogue VIVC






Literature data?



Navarro-Payá et al. 2022. The Grape Gene Reference Catalogue as a resource for gene selection and Genetic Improvement

Developed tools: Gene Cards

Catalogue Gene Cards Gene Cards Catalogue Table



Search:

[Download Catalogue file](#) [Help](#)

Navarro-Payá, D., Santiago, A., Orduña, L., Zhang, C., Amato, A., D'Inca, E., Fattorini, C., Pezzotti, M., Tornielli, G. B., Zenoni, S., Rustenholz, C., & Matus, J. T. (2022). **The Grape Gene Reference Catalogue as a Standard Resource for Gene Selection and Genetic Improvement.** *Frontiers in Plant Science*, 12, 803977. <https://doi.org/10.3389/fpls.2021.803977>.

Gene Card Vitvi01g00457

Gene Vitvi01g00457 is not present in the Reference Catalogue, add it here.

12X.v2 VCOST.v3: Vitvi01g00457

12Xv1 VIT code: VIT_01s0011g05390

Gene description: Invertase/pectin methylesterase inhibitor

Expression across SRA experiments (Updated to 28 April 2021)

Dots correspond to single SRA Runs selected according to their metadata and found in the link below (manually curated when needed)

[Download Metadata file](#)

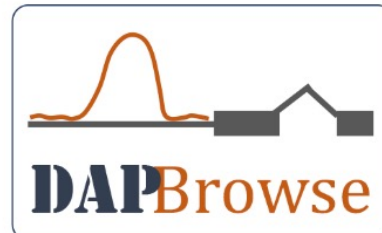
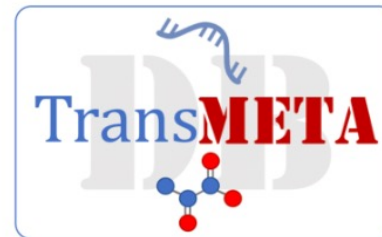


Developed tools: PlantViz platform

<http://vitviz.tomsbiolab.com/>



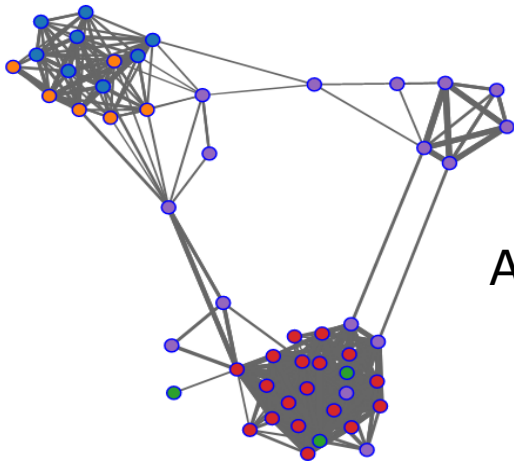
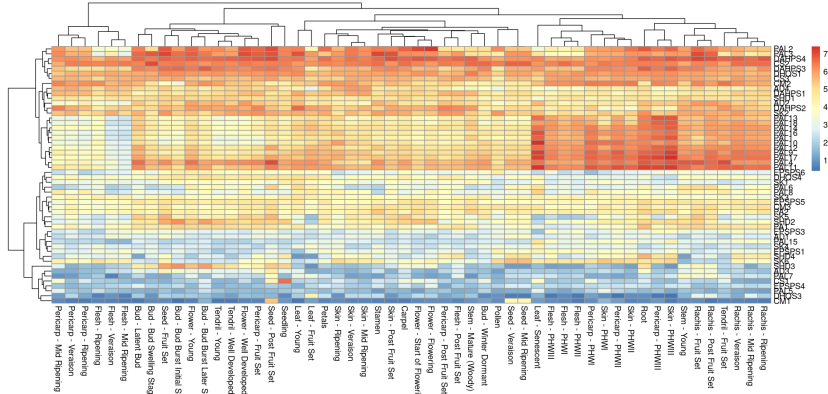
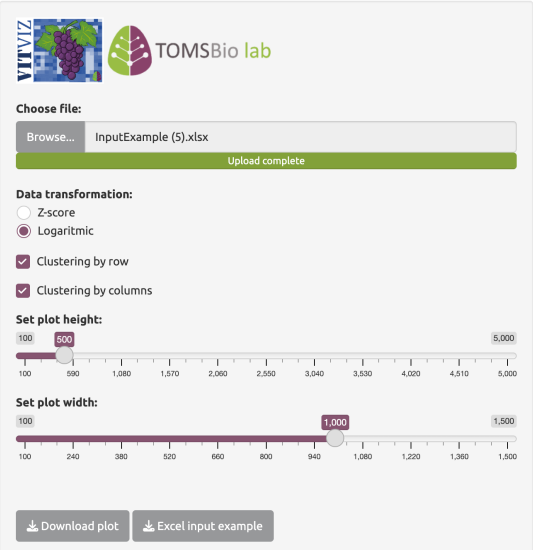
Web-based platform with several tools to visualize gene expression data in the form of expression heatmaps of a desired list of genes, and gene- or list-centered coexpression networks. A Browser with DAP-seq data published in our lab is also offered. The tool also includes a search engine for looking correspondencies between all PN40024 genome annotations and the Grape Reference Catalogue.



Developed tools: PlantViz platform

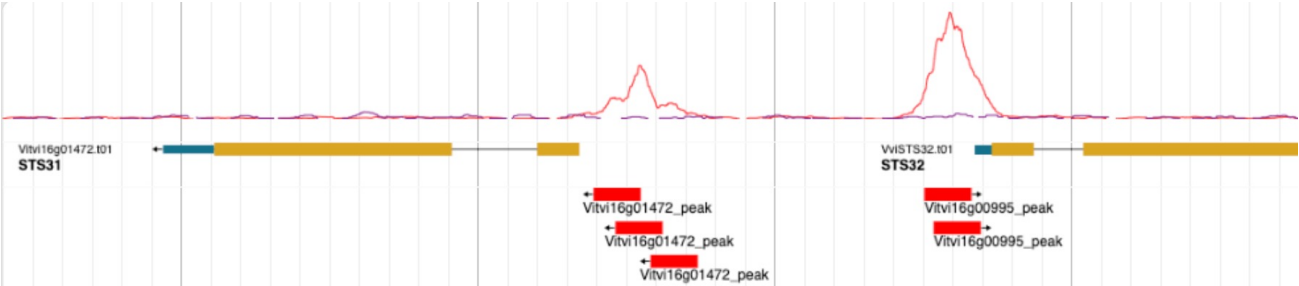


EX-ATLAS



AggGCNs

DAPBrowse



TransMETA

0.049 (0.8)	0.06 (0.8)	-0.007 (0.8)	-0.23 (0.1)	-0.3 (0.1)	-0.21 (0.1)	0.22 (0.1)	0.27 (0.8)	0.064 (0.7)	0.29 (0.8)	0.31 (0.3)	0.33 (0.1)	0.34 (0.3)	0.24 (0.1)	0.33 (0.3)	0.002 (0.9)	-0.18 (0.5)	0.087 (0.6)	0.21 (0.4)	-0.14 (0.4)	-0.35 (0.3)	-0.12 (0.4)	0.13 (0.4)
0.11 (0.7)	0.22 (0.4)	-0.33 (0.2)	-0.27 (0.07)	0.13 (0.4)	-0.44 (0.03)	-0.27 (0.06)	-0.26 (0.07)	-0.27 (0.07)	0.26 (0.08)	0.11 (0.4)	0.28 (0.05)	0.4 (0.4)	0.087 (0.6)	0.22 (0.1)	0.16 (0.3)	-0.38 (0.1)	-0.25 (0.08)	0.25 (0.3)	0.11 (0.5)	0.061 (0.7)	0.054 (0.7)	0.033 (0.8)
-0.34 (0.2)	-0.52 (0.03)	-0.21 (0.4)	-0.24 (0.1)	0.07 (0.4)	-0.41 (0.03)	-0.75 (0.03)	-0.7 (0.03)	-0.52 (0.04)	0.56 (0.05)	0.41 (0.04)	0.57 (0.05)	0.67 (0.07)	0.47 (0.04)	0.49 (0.04)	0.47 (0.04)	0.2 (0.4)	-0.57 (0.03)	-0.51 (0.03)	-0.24 (0.1)	-0.1 (0.5)	-0.32 (0.03)	-0.35 (0.01)
alcohol dehydrogenase	lipoxygenase	lipoxygenase	alpha-tubulin	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase	glucanase

visit <http://tomsbiolab.com>



Funding sources



Institut
d'Estudis
Catalans

TABLE GRAPE CONFERENCE, CAPE TOWN. 2023

Current tools available for the grape community

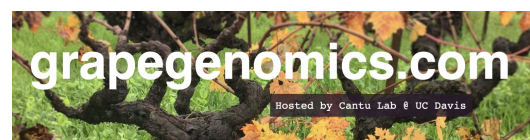
Genome
browsers

Transcriptome
explorers

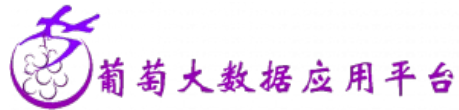
Cultivar
collections

Metabolite
repository

Gene
Networks



vespucci



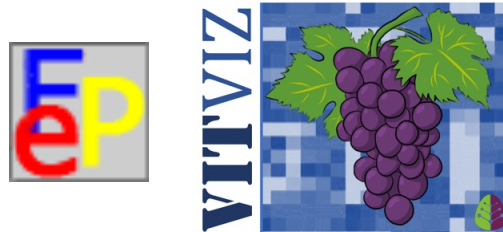
Vitis International Variety Catalogue VIVC



Others
(mostly private)

GREAT

Literature data





Available tools

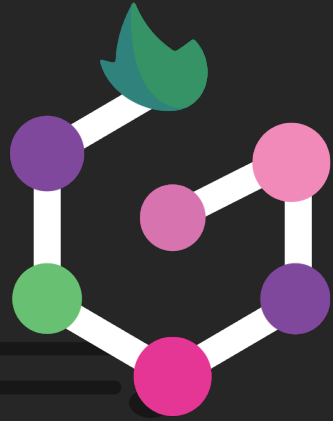
Not yet F.A.I.R.

Not yet available

Phenotypes

QTL

Climate data

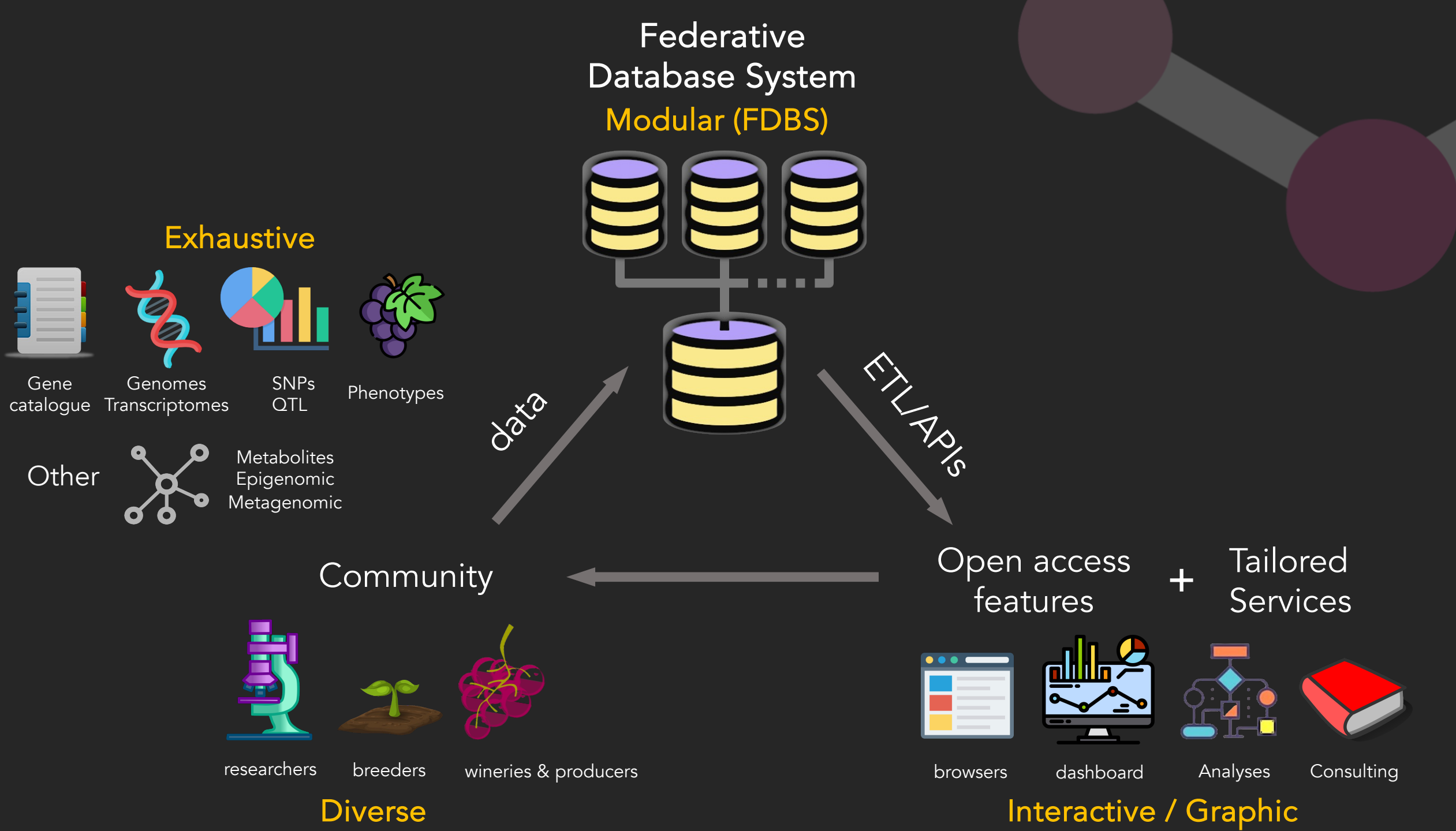


Grapedia

The Grapevine Genomics Encyclopedia

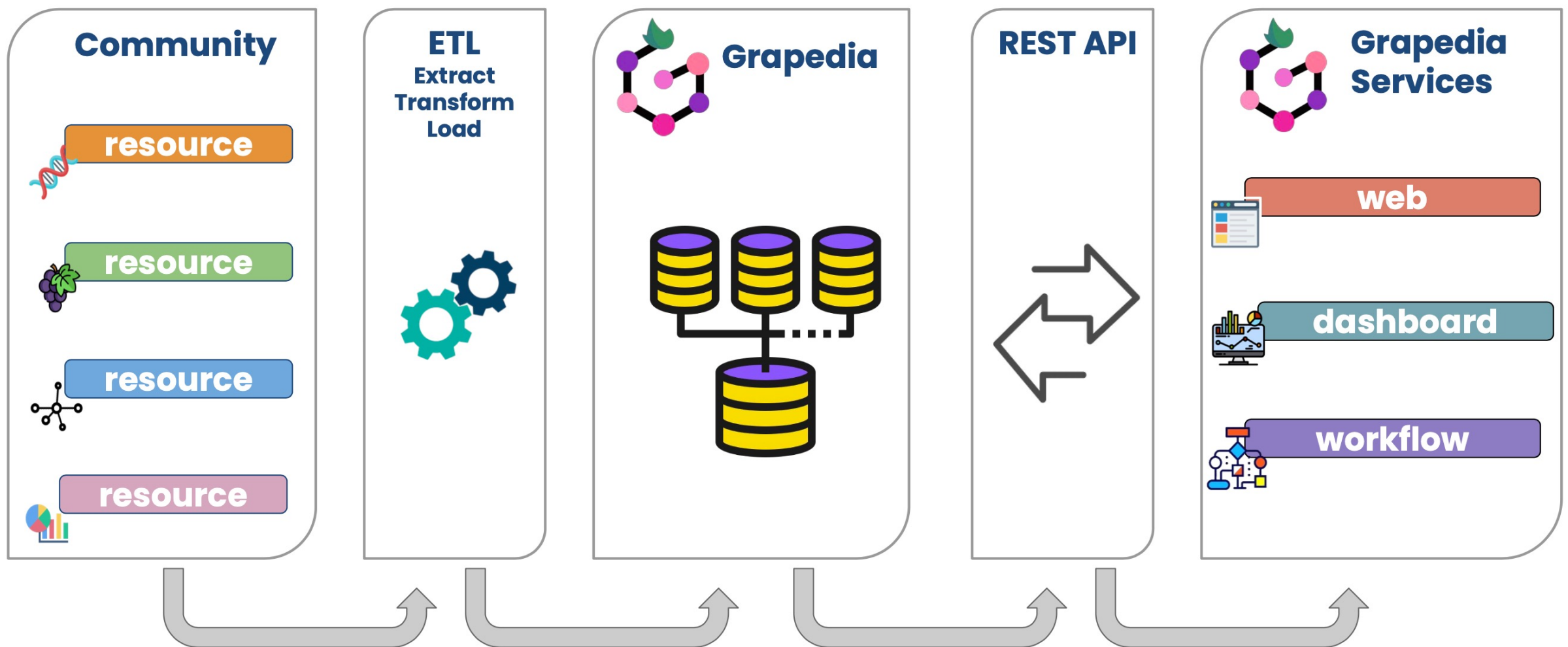
an innovative portal that integrates biological knowledge,
genetic and genomic resources and customized services
for the grape scientific community and industry

visit <http://grapedia.org>



BACKEND

FRONTEND

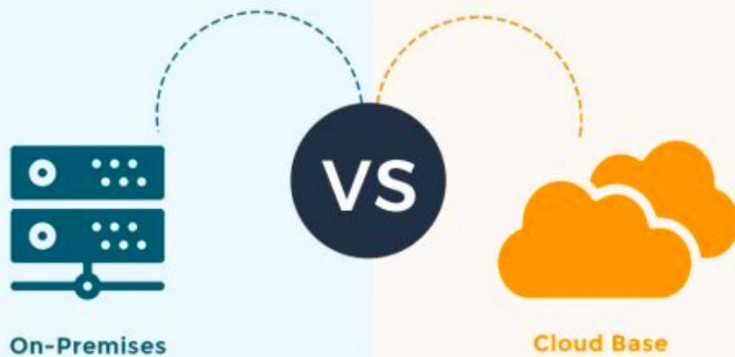


Infrastructure

Scalability
Flexibility
Reproducibility



On-Premises VS Cloud Base



On-Premises

Pros

- » Full Data Control
- » Full Hard- and Software Control
- » Full Access Reliability
- » No Operating Software Cost
- » Performance
- » Customizations

Cons

- » Maintenance and Acquisition Costs
- » Internal Knowledge
- » Full Responsibility
- » Long-term Reliability



Cloud-Base

Pros

- » Easy Set-up
- » Low Acquisition and Maintenance Costs
- » Flexibility and Scalability
- » Accessibility and Integration
- » Updates and Security
- » Back-up and Data Restore
- » Disaster Recovery

Cons

- » On-going Software Costs
- » Performance Limitations
- » Internet Access



Single Gene Dashboard

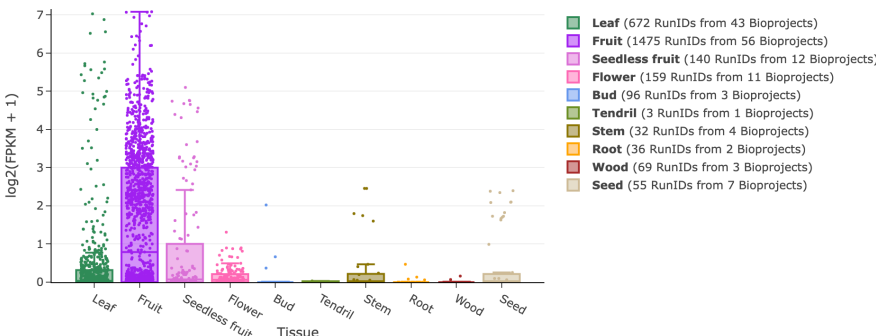
This dashboard is meant to explore a single gene in different contexts. From genome browser to its expression level across different tissues, as well as gene co-expression networks

► Catalogue & Gene Cards Explorator

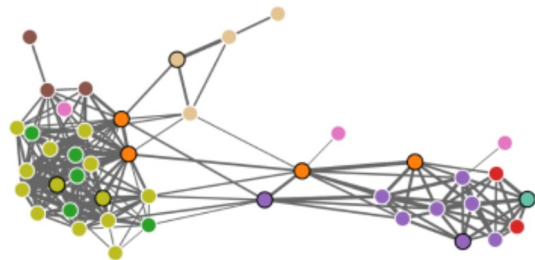
type: TF
Validation level: 6
Functional association: Regulator of anthocyanin synthesis. Berry color locus.
Paper references for functional association: Kobayashi et al., 2004
DOI of functional association: NULL
Paper references for family description: Wong et al. 2016 (DNA Res)
DOI of family description: doi.org/10.1093/dnares/dsw028
Phylogeny constructed: Maximum Likelihood (Bayesian)

Expression across SRA experiments (Updated to 28 April 2021)
Dots correspond to single SRA Runs selected according their metadata and found in the link below (manually curated when needed)

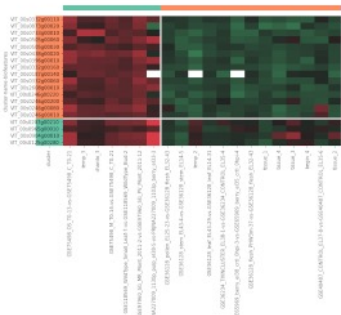
Download Metadata file



► Co-expression network



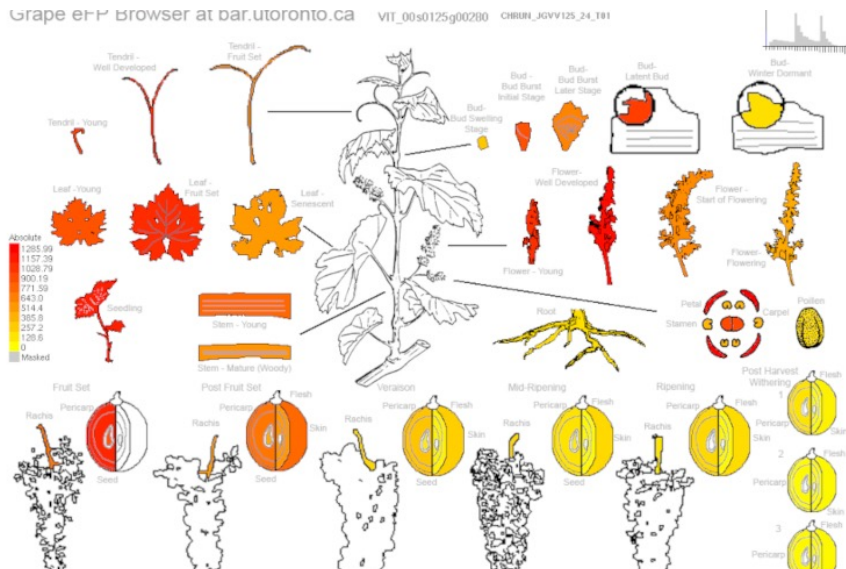
► Heatmaps



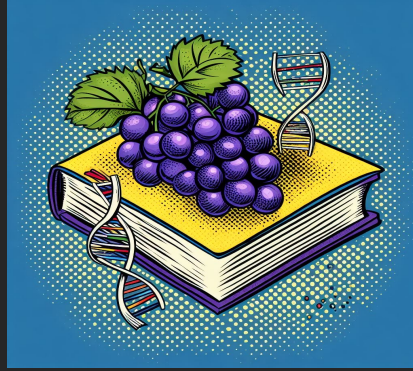
► Integrated Genome Browser



► Gene Expression Atlases



Dashboards - Implemented models within first release (Early 2024)



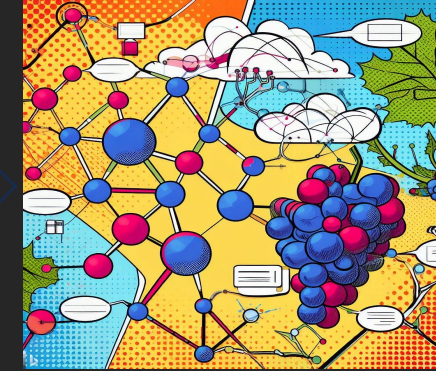
Genome JBrowser2



QTL Browser
Gene Catalogue/
Cards

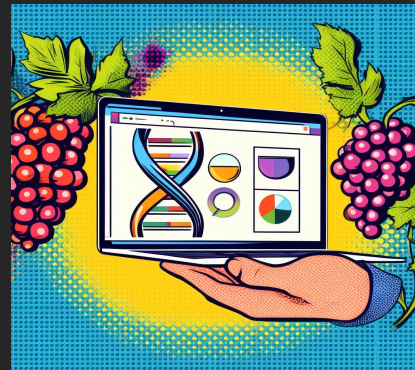


Expression
atlases



Co-expression &
regulatory
networks

Workflows (Nextflow)



Expression profiling,
gene annotation, others

Guidelines



& Curation /
Submission platforms

Funding

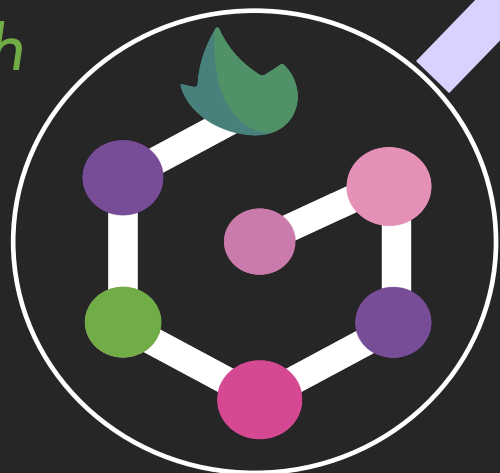
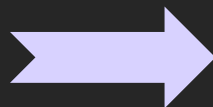
CIG Funding

Donations & Sponsoring

Own-funding resources

Public grant applications

*Establish
DB*



Commercial exploitation

*DB long-term
maintenance and
growth*

Services

Externalized

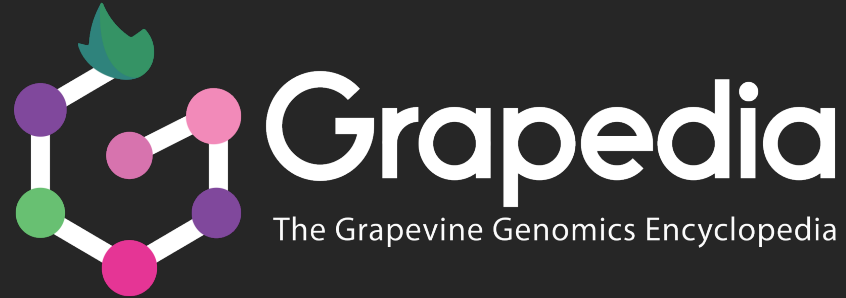
Tailored



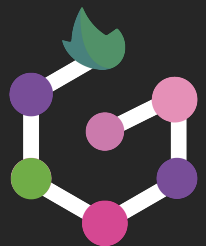
GRAPEDIA Annual Meeting, Valencia, Spain (2023)



TABLE GRAPE CONFERENCE, CAPE TOWN. 2023

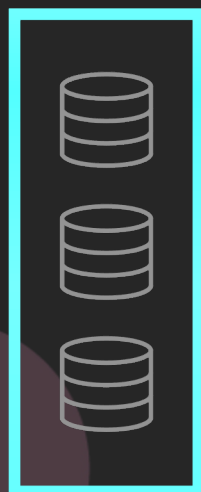






Federative Database System (FDBS)

SOURCE DATA & DATABASES



TRANSACTIONAL DATA
CURRENT DATA

DATA FEDERATION



VIRTUAL
DATABASES

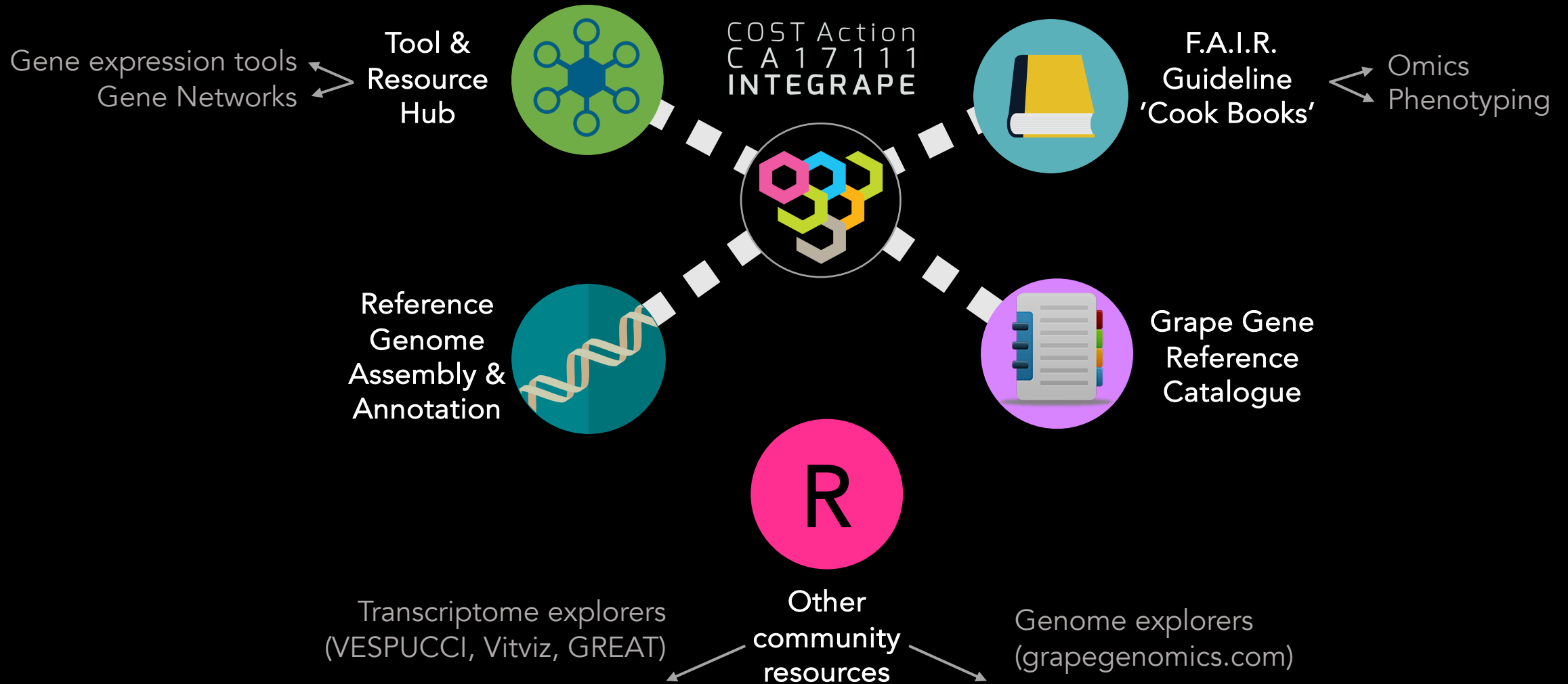
HISTORICAL DATA

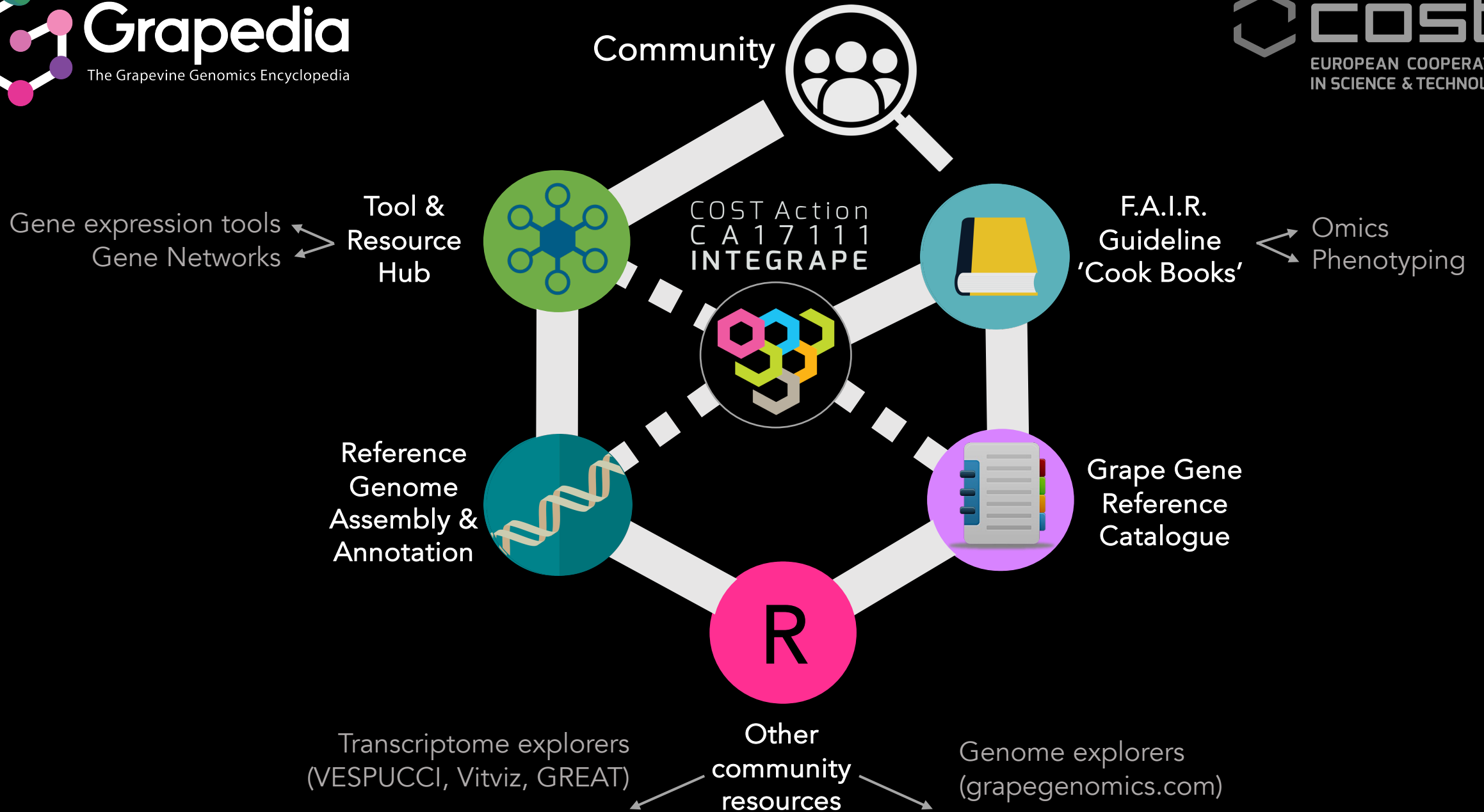
ETL

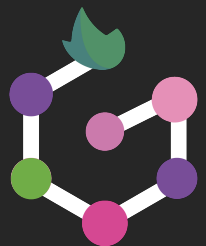


DATA WAREHOUSE
AND DATA MARTS









Commercial aspects

Services

DB long-term management



Externalized

Tailored

1. Link grapevine resources (API develop.)
2. Integrate Open Source tools
3. Develop Cloud Software
4. Customize algorithms
5. Ensure Security & Maintenance



AIR, Artificial intelligence RNAseq



GAIA, Metagenomics data analysis



GROWMICS, RNA analysis for agricultural R&D



GREEN GINO, Genomics data exploitation

Grapedia services



Clear interpretation
Unique perspectives
Applicable results



web



dashboard



workflow

Advanced UI

Responsive

Accessibility

- Data integration & visualization
 - Free custom
 - Open source (eg Jbrowse)
- Tools
 - Free custom (e.g Drago)
 - Open source (e.g BLAST)
- Upload, download, sharing sections
- User profile and data management

Free custom pipelines
to run bioinformatics
analysis

nextflow



docker



Community

To build GRAPEDIA by building a strong unified community

CIG tools offer



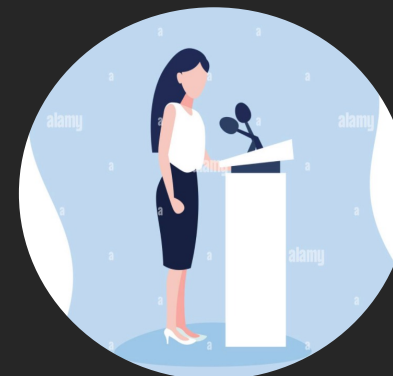
Working
Group
Meetings



Training
Schools
Hackathons



Short-term
Scientific
Missions



Dissemination
activities



Business
plan



COST Action Integrape CA17111



Mario Pezzotti
University of Verona
(Italy)



Anne-Francoise Adam-Blondon
INRAE Versailles
(France)

FUNDED BY



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EUROPEAN UNION



COST Innovators Grant IG17111

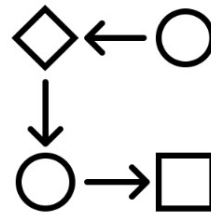
Grapedia Technology

Innovation at multiple levels

|0|0
|0|0

IT
infrastructure
Cloud and hybrid solution

Scalability
Flexibility
Reproducibility



Bioinformatics
algorithms
pipelines
database

Modularity
Precise
Versatile



Products
Custom & cloud SOFTWARE
Data delivery platform
Automated interpretation

Clear interpretation
Unique perspectives
Applicable results