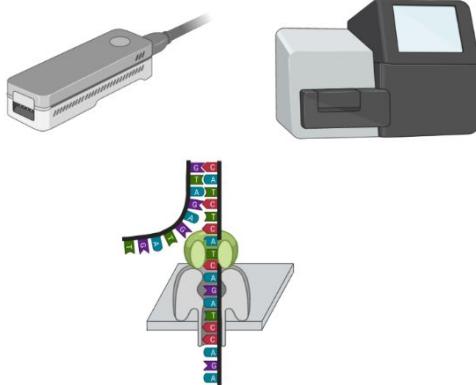
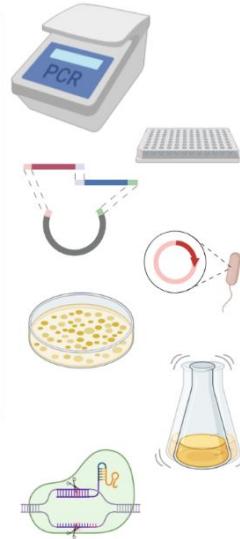
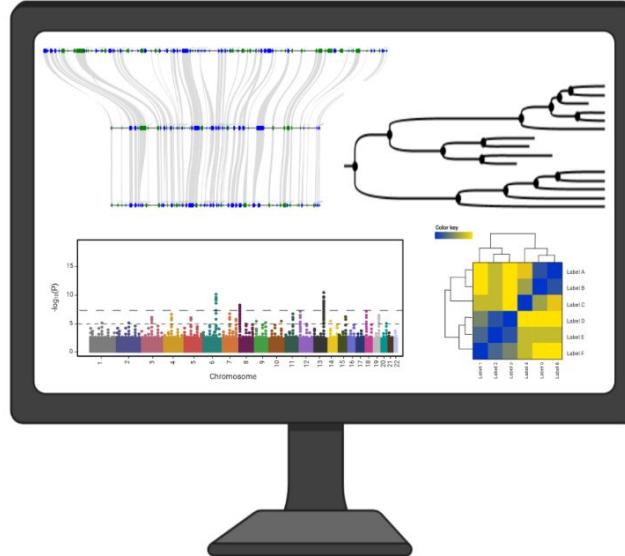




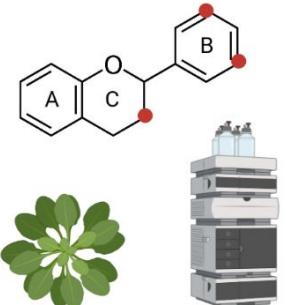
Technische
Universität
Braunschweig



Plant Biotechnology
and Bioinformatics



species biosynthesis proteins analysis different conditions
biosynthesis DODA bellman variants H23-MYB
within genes functional variants Col loco variant
dispersed site data divergent variants non-canonical
sequences KEGG multiple protein annotation level identified
single reference structure synthesis amino acid evolutionary
sites phylogenetic analysis pathway interaction
plants pigments model genome accessions systems biology long Canophylales
pigments Kewenta genes key against canonical Arabidopsis
flavonoid conservation sequencing for conserved Free thaliana
sites accessions identification gene read transcription synthesis evolution
plants plants sequencing sequencing MYB introns residues RNA-Seq



Submitting, publishing, and re-using data

Prof. Dr. Boas Pucker and Katharina Wolff
(Plant Biotechnology and Bioinformatics)

Availability of slides

- All materials are freely available (CC BY) - after the lectures:
 - StudIP: Data Literacy in Genomics
 - GitHub: <https://github.com/bpucker/teaching>
- Questions: Feel free to ask at any time
- Feedback, comments, or questions: b.pucker[a]tu-bs.de

My figures and content can be re-used in accordance with CC BY 4.0, but this might not apply to all images/logos. Some figure were constructed using bioRender.com.

Sharing data



OpenData

- Everyone can access and re-use these data sets
- Facts cannot be owned by someone
- Huge economic potential through re-use; advantages for society
- Possible restrictions: name author, share-alike
- Related initiative: open source, open content, open access, open education

OpenProtocols

- Enables others to reproduce experiments
- Protocols are precisely described and freely available to everyone
- DOIs can be assigned to protocols
- Protocols.io is a platform to support the exchange of protocols
- Example: gDNA extraction protocol



<https://www.protocols.io/welcome>

This screenshot shows a detailed view of a protocol titled 'Plant DNA extraction and preparation for ONT sequencing'. The page includes a profile picture of Boas Pucker, a timestamp of 'Mar 21, 2020', and a DOI link 'doi.org/10.17504/protocols.io.bcvyiw7w'. Below this, there are buttons for 'Run', 'Bookmark', 'Copy / Fork', and 'Share'. The main content area is divided into sections: 'ABSTRACT', 'Materials', 'Methods', 'Metrics', 'References', and 'Supplementary Information'. The 'ABSTRACT' section describes the protocol as a CTAB-based protocol for plant DNA extraction. The 'Materials' section lists various reagents like Tris-HCl, NaCl, and ethanol. The 'Methods' section contains detailed steps for extracting DNA from plant material. The 'Metrics' section includes a table of sequencing metrics. The 'References' section lists several scientific papers related to the protocol. The 'Supplementary Information' section provides additional details and figures.

doi:10.17504/protocols.io.bcvyiw7w

How to submit a protocol?

- Protocol submission:
 - Create a new protocol (can remain private; 5 in free version)
 - Assign a DOI to make it citable
 - Make protocol public
- PDF submission and conversion for \$50 (service fee)

The screenshot shows the protocols.io website interface. At the top, there's a file upload dialog box with options like 'New folder', '+ New protocol', and 'Upload files'. Below this, a banner reads 'A perfect fit, for any need' and 'From chemistry to computational workflows. Create a protocol that fits any need.' There are six categories of protocols displayed in a grid:

- Generic protocol
- Biology protocol
- Computational Workflow
- Chemistry method
- Collection of methods
- Document

Below the categories, there's a 'NEW STEP' button and a note: 'If you have an existing protocol you can [insert steps from a text file](#)'. To the right, there's a sidebar with various experimental parameters and units: Amount, Concentration, Temperature, Duration, Protocol, Document, Equipment, Reagent, Citation, Note, Safety Information, Expected Result, Ge Coordinates, Configuration, Smart Component, Shaker, Gels, pH, Cost, Pressure, Thickness, and Relative Humidity.

<https://www.protocols.io/>

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- CC BY: no restrictions, but name authors
- CC BY-SA: name authors and share results under same license
- CC BY-NC: name authors; only non-commercial use
- CC BY-NC-SA: name authors; only non-commercial use; share under same license

License stacking

- What happens if we combine different data sets?
- CC0 + CC BY
- CC0 + CC NC-SA
- CC BY + CC BY-NC
- ...

Software licenses

- MIT: leanest licence (everything is possible)
- Apache: similar to MIT, but lengthy
- GPL (General Public License): ensures that derived work remains open
- BSD (Berkeley Software Distribution): similar to MIT, but more cases specified

License	Commercial use	Distribution	Modification	Patent use	Private use	Disclose source	Licensing and copyright notice	Network use in distribution	Same license	State changes	Liability	Trademark use	Warranty
BSD Zero Clause License	●	●	●	●	●						●	●	
BSD 2-Clause License	●	●	●	●	●						●	●	
BSD 3-Clause License	●	●	●	●	●						●	●	
Apache License 2.0	●	●	●	●	●						●	●	
Artistic License 2.0	●	●	●	●	●						●	●	
BSD 2-Clause "Simplified" License	●	●	●	●	●						●	●	
BSD 3-Clause Clear License	●	●	●	●	●						●	●	
BSD 2-Clause "New" or "Revised" License	●	●	●	●	●						●	●	
BSD 2-Clause "Modified" or "OSI" License	●	●	●	●	●						●	●	
Boost Software License 1.0	●	●	●	●	●						●	●	
Creative Commons Attribution 4.0 International	●	●	●	●	●						●	●	
Creative Commons Attribution-NonCommercial 4.0 International	●	●	●	●	●						●	●	
Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International	●	●	●	●	●						●	●	
Creative Commons Attribution-NonCommercial-NoDerivs 4.0 International	●	●	●	●	●						●	●	
CC0 License	●	●	●	●	●						●	●	
CERN Open Source License Version 2.1	●	●	●	●	●						●	●	
CERN Open Hardware License Version 2.1	●	●	●	●	●						●	●	
Educational Software License v2.0	●	●	●	●	●						●	●	
EPIC License	●	●	●	●	●						●	●	
European Union Public License 1.1	●	●	●	●	●						●	●	
European Union Public License 1.2	●	●	●	●	●						●	●	
GNU General Public License v2.0	●	●	●	●	●						●	●	
GNU General Public License v3.0	●	●	●	●	●						●	●	
MIT License	●	●	●	●	●						●	●	
MIT No Attribution License	●	●	●	●	●						●	●	
MIT License	●	●	●	●	●						●	●	
Mozilla Public License 2.0	●	●	●	●	●						●	●	
Open Database License	●	●	●	●	●						●	●	
Microsoft Public License	●	●	●	●	●						●	●	
Mozilla Public License	●	●	●	●	●						●	●	
Mulan Permissive License - Version 2	●	●	●	●	●						●	●	
University of Illinois Open Source License	●	●	●	●	●						●	●	
Commons Open Source License v1.0	●	●	●	●	●						●	●	
SL Open Font License 1.1	●	●	●	●	●						●	●	
Open Software License 3.0	●	●	●	●	●						●	●	
PostgreSQL License	●	●	●	●	●						●	●	
The Unlicense	●	●	●	●	●						●	●	
Unlicense	●	●	●	●	●						●	●	
Do What The F*ck You Want To Public License	●	●	●	●	●						●	●	
40s License	●	●	●	●	●						●	●	

<https://choosealicense.com/appendix/>

Which license would you select and why?

- A script to analyze a gene family?
- A table with species observed in a particular forest?
- FASTQ files of a RNA-seq project?
- Genome sequence and the corresponding annotation?
- KM value and Vmax value of an enzyme?
- A protocol for efficient transformation of a plant species?

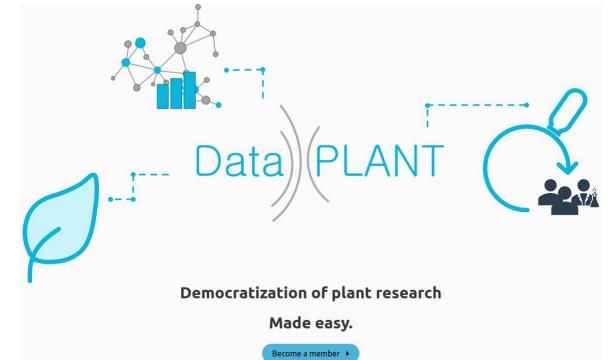


FAIR data

- Findable:
 - Globally unique and persistent identifier
 - Metadata must be available in connection to the identifier
- Accessible:
 - Retrieval based on the identifier
 - Protocol is open, free, and universally applicable
 - Authentication is possible where needed
 - Metadata are available even if data are restricted
- Interoperable:
 - Metadata use a formal, accessible, broadly accessible language
 - Vocabulary need to follow FAIR standards
- Re-usable:
 - Clear and accessible data usage license
 - Meet domain-relevant community standards

nfdi4plants

- NFDI = Nationale Forschungsdaten Infrastruktur e.V.
- Provide sustainable, annotated data management platform
- Pave way to pure data publications with research context
- Omics and imaging at petabyte size
- ARC = annotated research context
- Add user-oriented services to existing IT infrastructure (make submissions easy)



JSON

- JSON = JavaScript Object Notation
- File format for exchange between different tools
- File structure readable by many different tools & human-readable
- Attribute-value pairs (dictionary)

Plant genome sequence assembly in the era of long reads: Progress, challenges and future directions

Published online by Cambridge University Press: 11 March 2022

Boas Pucker , Iker Irisarri , Jan de Vries  and Bo Xu 

Show author details ▾

Article Figures Peer reviews Metrics

 Save PDF  Share  Cite

Abstract

Third-generation long-read sequencing is transforming plant genomics. Oxford Nanopore Technologies and Pacific Biosciences are offering competing long-read sequencing technologies and enable plant scientists to investigate even large and complex plant genomes. Sequencing projects can be conducted by single research groups and sequences of smaller plant genomes can be completed within days. This also resulted in an increased investigation of genomes from multiple species in large scale to address fundamental questions associated with the origin and evolution of land plants. Increased accessibility of sequencing devices and user-friendly software allows more researchers to get involved in genomics. Current challenges are accurately resolving diploid or polyploid genome sequences and better accounting for the intra-specific diversity by switching from the use of single reference genome sequences to a pangenome graph.

Keywords

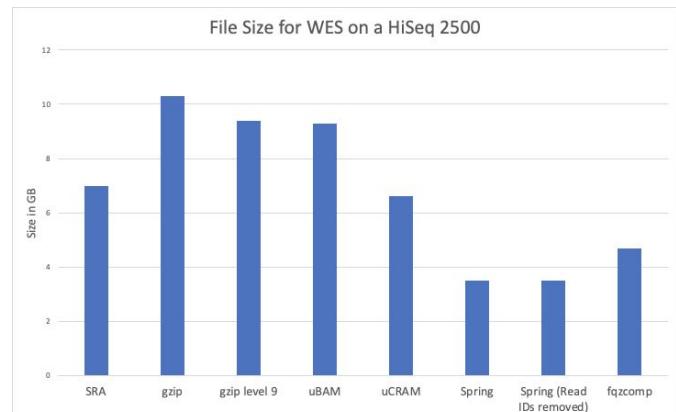
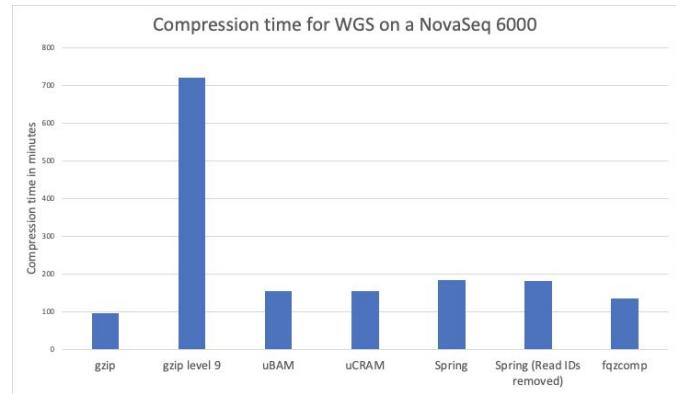
haplotyping long read sequencing Oxford Nanopore Technologies (ONT) Pacific Biosciences (PacBio)
plant genome assembly plant genomics

Type	Review
Information	<i>Quantitative Plant Biology</i> , Volume 3, 2022, e5 DOI: https://doi.org/10.1017/qpb.2021.18
Creative Commons	 This is an Open Access article, distributed under the terms of the Creative Commons Attribution licence (https://creativecommons.org/licenses/by/4.0/), which permits unrestricted re-use, distribution, and reproduction in any medium, provided the original work is properly cited.
Copyright	© The Author(s), 2022. Published by Cambridge University Press in association with The John Innes Centre

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3   [  
4     {  
5       "firstName": "Boas",  
6       "lastName": "Pucker"  
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8     {  
9       "firstName": "Iker",  
10      "lastName": "Irisarri"  
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18      "lastName": "Xu"  
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20  ],  
21  "title": "Plant genome sequence assembly in the era of long reads",  
22  "url": "https://doi.org/10.1017/qpb.2021.18",  
23  "doi": "10.1017/qpb.2021.18"  
24 }
```

Data compression

- Gzip is most frequently applied tool
- Different compression levels (default=6)
 - Level 1 = fast, but small size reduction
 - Level 9 = slow, but substantial size reduction
- File sizes can be reduced by 75%
- Gzip should always be used to reduce disk space requirements



tar

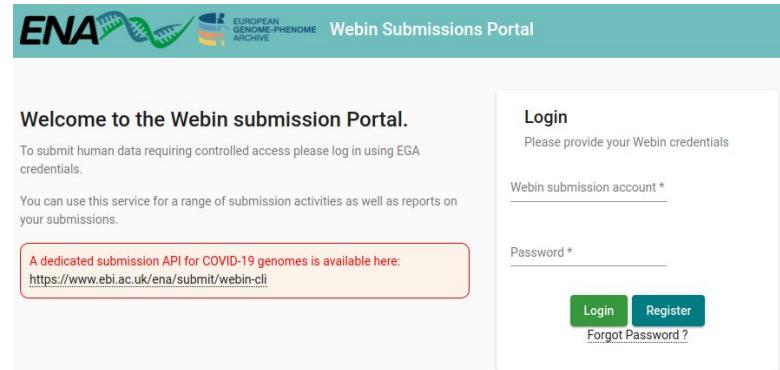
- Transfer to large numbers of files is a challenge
- Tar can be used to merge many files into a tar ball
- '.tar.gz' and '.tgz' are extensions of tarballs
- **Construct:** `tar -cavf archive.tar.gz content`
- **Extract:** `tar -xzvf archive.tar.gz`

sha256sum & md5sums

- Generate a digital fingerprint of a given file
- Md5sum is a 128-bit hash
- Md5sum is the standard in many bioinformatic workflows to ensure files have been transferred completely
- Sha256sum is recommended for security relevant purposes when malicious intent is expected

How to submit reads (to ENA)?

- Log into the submission portal
- Register study
- Register samples (spreadsheet upload option)
- Prepare and upload read files (via ftp)
- Submit sequence reads (spreadsheet upload option)



The screenshot shows the ENA Webin Submissions Portal login interface. At the top, there is a logo for "ENA" with a DNA helix icon, followed by "EUROPEAN GENOME-PHENOME ARCHIVE" and "Webin Submissions Portal". Below this, a teal header bar contains the text "Welcome to the Webin submission Portal." In the main content area, there is a message about submitting human data requiring controlled access using EGA credentials. It also states that the service is for a range of submission activities and reports on submissions. A red-bordered box highlights a link to a dedicated submission API for COVID-19 genomes: <https://www.ebi.ac.uk/ena/submit/webin-cli>. To the right, there is a "Login" form with fields for "Webin submission account *" and "Password *", and buttons for "Login", "Register", and "Forgot Password ?".

Accession	BioSample	Title
ERS3371290	SAMEA5569268	RNA-Seq Hypertelis bowkeriana flower
ERS3371289	SAMEA5569267	RNA-Seq Hypertelis bowkeriana leaf
ERS3371288	SAMEA5569266	RNA-Seq of Simmondsia chinensis flower
ERS2294062	SAMEA104692679	Corrigiola litoralis genome sequencing
ERS2294061	SAMEA104692678	Spergula arvensis genome sequencing
ERS2294060	SAMEA104692677	Simmondsia chinensis genome sequencing
ERS2294059	SAMEA104692676	Pharnaceum exiguum genome sequencing
ERS2294058	SAMEA104692675	Microtea debilis genome sequencing
ERS2294049	SAMEA104692666	Macarthuria australis genome sequencing
ERS2294048	SAMEA104692665	Limeum aethiopicum genome sequencing

How to submit reads (to ENA)? - read infos part 1

Submission of reads requires many details:

- Project_accession: accession assigned by ENA
- Project_alias: name assigned by user
- Sample_alias: accession assigned by ENA
- Experiment_alias: accession assigned by ENA
- Run_alias: XXX
- Library_name: User picks this name
- Library_source: GENOMIC
- Library_selection: RANDOM
- Library_strategy: XXX
- Design_description: XXX
- Library_construction_protocol: TrueSeq V2
- Instrument_model: Illumina HiSeq1500

How to submit reads (to ENA)? - read infos part 2

Submission of reads requires many details:

- File_type: FASTQ
- Library_layout: PAIRED
- Insert_size: 600
- Forward_file_name: fw_file.fastq.gz
- Forward_file_md5: jel9aks5joe8iaj1ie2lfk4jsk6flji
- Forward_file_unencrypted_md5:
- Reverse_file_name: rv_file.fastq.gz
- Reverse_file_md5: k1ea0wi7oji32so45jbae6fo81337xd
- reverse_file_unencrypted_md5

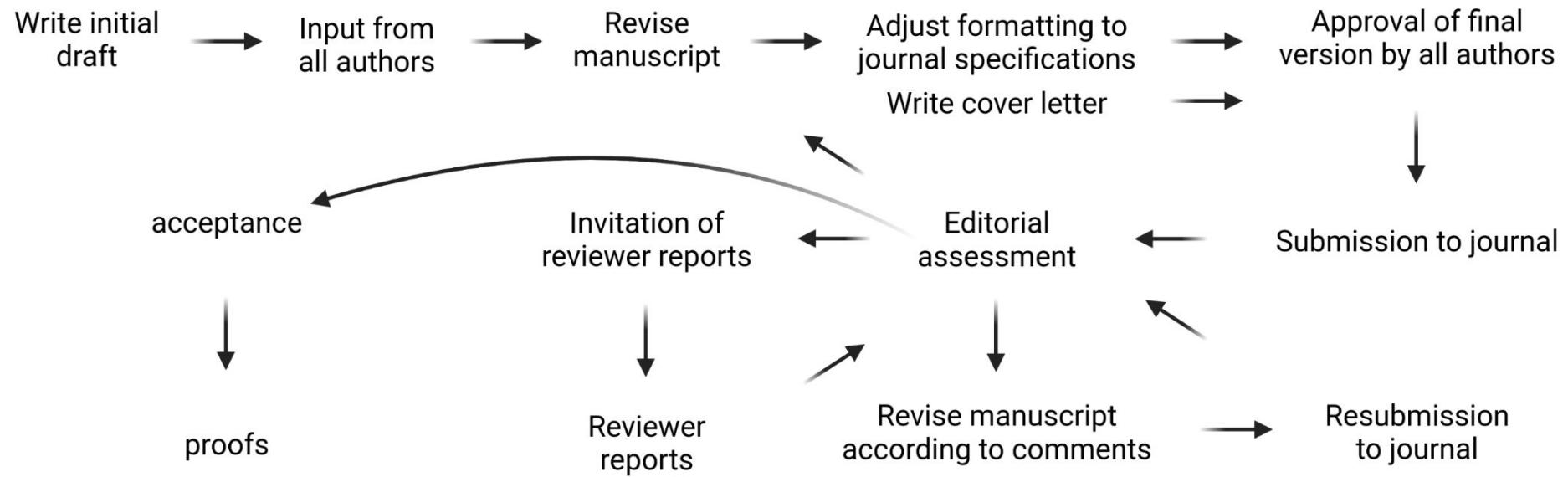
Publishing a research paper



Motivation

You have exciting findings that you would like to share with the scientific community or the whole world!

How to publish a paper - publication process



Authorship

- COPE: specifies criteria for authors (<https://publicationethics.org/>)
- Substantial contribution to
 - (1) data generation / analysis and
 - (2) data interpretation, and
 - (3) manuscript writing
- Order of authors indicates contribution to study:
 - First is best
 - Last is supervision of work + correspondence
- Example 1:
 - Head of an institute does not qualify (ghost authorship)
- Example 2:
 - Technician/undergrad contributing without scientific input does not qualify
- Example 3:
 - Student developing novel method, generating useful data, and contributing to the manuscript does qualify

Cover letter

- State title of the submission
- State article type (and special issue)
- Summarize the content of the submission
- Convince the editor of relevance
- State that the work has not been published (include link to preprint)
- Indicate previous interactions with journal



Institute for Plant Biology
Technische Universität Braunschweig

Plants
Editorial Office

Prof. Dr. Boas Pucker
Mendelsohnstr. 4
38106 Braunschweig
Germany

09. March 2022

Biochemistry and molecular basis of intracellular flavonoid transport in plants

Dear Editor, dear editorial team,

I am submitting the manuscript 'Biochemistry and molecular basis of intracellular flavonoid transport' by Boas Pucker and Dirk Selmar for publication in Plants as a review article in the Special Issue 'Evolution of Specialized Metabolism in Plants'.

Different subclasses of flavonoids play numerous important roles in plants. Examples are the coloration of flowers by anthocyanins, the pigmentation of seeds by proanthocyanins, and the protection against the consequences of UV radiation by flavonols. While the biosynthesis pathway is well understood due to investigations in many different plant species, the knowledge about the intracellular transport of flavonoids is sparse. In our review, we summarize the current state of knowledge and point out some questions for future studies.

We hope that you will find our manuscript suitable for publication and hereby confirm that it has not been submitted for publication elsewhere. However, there is a preprint available on Preprints.org (<https://www.preprints.org/manuscript/202203.0124/v1>) that already received some attention.

I have been in contact with [redacted] about this submission. She confirmed that no publication fees should be charged for the publication, because of my support of the journal as a guest editor.

Sincerely (on behalf of both authors),



Value of citations

- Currency of science: ‘Publish or perish’
- Important for scientific career: job applications, grant applications
- Quantity vs. quality
- Applications often require 3, 5, or 10 ‘most important’ publications

What is the h-index?



h-index

	Position	Citations
1	Genome-wide identification and characterisation of R2R3-MYB genes in sugar beet (<i>Beta vulgaris</i>) R Stracke, D Holzgräfe, J Schneider, B Pucker, T Rosleff Sørensen, ... BMC Plant Biology 14 (1), 1-17	77 2014
2	The evolution of betalain biosynthesis in Caryophyllales A Timoreira, T Feng, H Sheehan, N Walker-Hale, B Pucker, ... New Phytologist 224 (1), 71-85	56 2019
3	The negative regulator SMAX1 controls mycorrhizal symbiosis and strigolactone biosynthesis in rice J Choi, T Lee, J Cho, EK Servante, B Pucker, W Summers, S Bowden, ... Nature communications 11 (1), 1-13	44 2020
4	A De Novo Genome Sequence Assembly of the <i>Arabidopsis thaliana</i> Accession Niederenz-1 Displays Presence/Absence Variation and Strong Synteny B Pucker, D Holzgräfe, T Rosleff Sørensen, R Stracke, P Venhöver, ... PLoS One 11 (10), e0164321	34 2016
5	Evolution of L-DOPA 4,5-dioxygenase activity allows for recurrent specialisation to betalain pigmentation in Caryophyllales H Sheehan, T Feng, N Walker-Hale, S Lopez-Nieves, B Pucker, R Guo, ... New Phytologist 227 (3), 914-929	29 2020
6	A chromosome-level sequence assembly reveals the structure of the <i>Arabidopsis thaliana</i> Nd-1 genome and its gene set B Pucker, D Holzgräfe, KB Städemann, K Frey, B Huettel, R Reinhardt, ... PLoS one 14 (5), e0216233	29 2019
7	Genome-wide analyses supported by RNA-Seq reveal non-canonical splice sites in plant genomes B Pucker, SF Brockington BMC genomics 18 (1), 1-13	24 2018
8	High contiguity de novo genome assembly of trifoliate yam (<i>Dioscorea dumetorum</i>) using long read sequencing C Sladjic, B Pucker, P Venhöver, DC Albach, B Weisshaar Genes 11 (3), 274	23 2020
9	High quality de novo transcriptome assembly of <i>Croton tiglium</i> M Haak, S Vinke, W Keller, J Drost, C Rückert, J Kalinowski, B Pucker Frontiers in molecular biosciences 5, 62	23 2018
10	Auxotrophy to Xeno-DNA: an exploration of combinatorial mechanisms for a high-fidelity biosafety system for synthetic biology applications CM Whifford, S Dymek, O Kerkhoff, C März, O Schmidt, M Edich, J Drost, ... Journal of Biological Engineering 12 (1), 1-28	18 2018
11	Consideration of non-canonical splice sites improves gene prediction on the <i>Arabidopsis thaliana</i> Niederenz-1 genome sequence B Pucker, D Holzgräfe, B Weisshaar BMC Research Notes 10 (1), 1-6	17 2017
12	Automatic identification of players in the flavonoid biosynthesis with application on the biomedicinal plant <i>Croton tiglium</i> B Pucker, F Reither, HM Schilbert Plants 9 (9), 1103	16 2020
13	Comparison of read mapping and variant calling tools for the analysis of plant NGS data HM Schilbert, A Rempel, B Pucker Plants 9 (4), 439	15 2020
14	The R2R3-MYB gene family in banana (<i>Musa acuminata</i>): Genome-wide identification, classification and expression patterns B Pucker, A Pandey, B Weisshaar, R Stracke GigaScience 10 (1), 1-10	14 2020
15	Animal, fungi, and plant genome sequences harbor different non-canonical splice sites K Frey, B Pucker Cells 9 (2), 458	14 * 2020
16	The land plant-specific MIXTA-MYB lineage is implicated in the early evolution of the plant cuticle and the colonization of land B Xu, L Taylor, B Pucker, T Feng, BJ Glover, SF Brockington New Phytologist 229 (4), 2324-2330	11 2021
17	Integrating molecular biology and bioinformatics education B Pucker, HM Schilbert, SF Schumacher Journal of Integrative bioinformatics 16 (3)	11 2019
18	The reuse of public datasets in the life sciences: potential risks and rewards K Sielemann, A Rathner, B Pucker PeerJ 8, e9954	9 2020

h=14



What is the i10-index?



i10-index

Position	Citations	
1 Genome-wide identification and characterisation of R2R3-MYB genes in sugar beet (<i>Beta vulgaris</i>) R Stracke, D Hollgräfe, J Schneider, B Pucker, T Rosleff Sørensen, ... BMC Plant Biology 14 (1), 1-17	77	2014
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14 The <i>R2R3-MYB</i> gene family in banana (<i>Musa acuminata</i>): Genome-wide identification, classification and expression patterns B Pucker, A Pandey, B Weisshaar, R Stracke PLoS one 15 (10), e0239275	14	2020
15 Animal, fungi, and plant genome sequences harbor different non-canonical splice sites K Frey, B Pucker Cells 9 (2), 456	14 *	2020
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18 The reuse of public datasets in the life sciences: potential risks and rewards K Sielemann, A Rehner, B Pucker PeerJ 8, e9954	9	2020

Citations are career stage and field-dependent

Doctoral student

Young PI

Highly cited PI

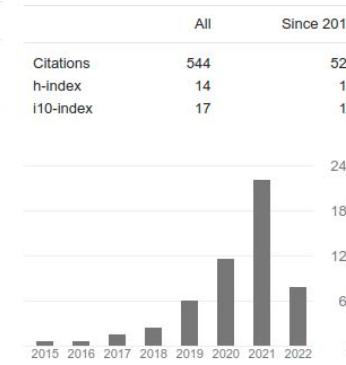
Pioneer and geneious

Researcher with 'hot topic'

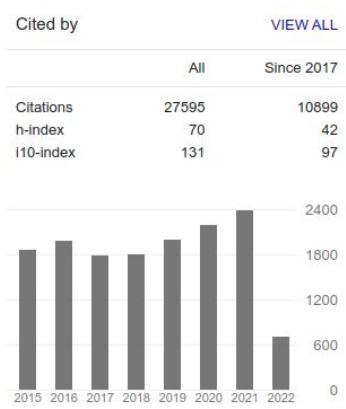
Zitiert von



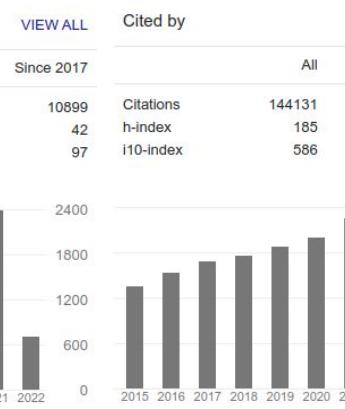
Cited by



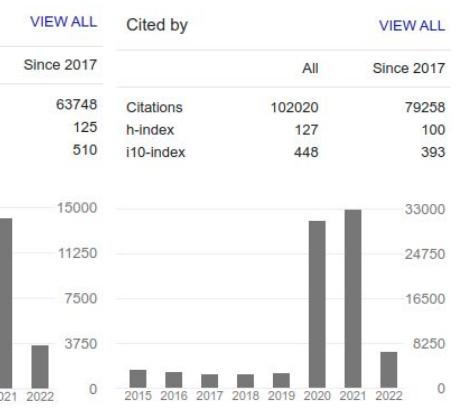
Cited by



Cited by



Cited by



Journal impact factor (IF)

- Journals like to present a journal impact factor (JIF or IF)
2-year-impact factor and 5-year impact factor
- IF = Average number of citations that each publication receives
- Number of citations per publication is extremely heterogeneous i.e. not an accurate reflection of article quality; publication-based metrics are more accurate
- Top journals: Nature, Science, Cell (30-50) (exciting story, ‘broad interest’)
- Good journals: New Phytologist, Genome Biology, Nucleic Acid Research ... (>8) (novel findings)
- Solid journals: 3-8 (technically solid)

Journal types

- Subscription: articles are paywalled
 - Readers have to pay for access
- Hybrid:
 - Authors can pay to get article open
 - Readers have to pay for most articles
- Open Access:
 - Articles are freely accessible
 - Author pay publication fees

The screenshot shows a journal article page from the **nature** website. The article title is **The growing inaccessibility of science**, written by Donald P. Hayes and published on 30 April 1992. The page includes metrics: 1015 accesses, 44 citations, and 27 Altmetric. Below the article summary, there are two main access options: "Rent or Buy article" and "Subscribe to Journal". The "Rent or Buy article" option is highlighted with a red circle and a price of \$8.99. The "Subscribe to Journal" option is also shown with a price of \$199.00 per year.

(Molecular) Plant Science Journals

- Nature/Science
- Nature Genetics / Nature Plants / Nature Communication
- New Phytologist
- Journal of Experimental Botany
- BMC Genome Biology / Genomics / Plant Biology / Plant Methods
- PLOS ONE / Genetics / Biology / Bioinformatics
- MDPI Plants / Genes / Agriculture / International Journal of Molecular Sciences
- Frontiers in Plant Sciences / Genetics / Molecular Sciences
- PeerJ
- Molecular Biology and Evolution, Genome Biology and Evolution
- Nucleic Acid Research
- Bioinformatics
- GigaScience
- The Plant Journal / Plant Cell
- ...

Data set publications

- Publications describing data sets without any novel insights
- Dedicated journals were established years ago, but many other are now happy to take everything ‘scientifically solid’
- Classic journals:
 - BMC Research Notes
 - Genome Announcements in many journals

Preprints

- bioRxiv: <https://www.biorxiv.org/> (Cold Spring Harbor Laboratory)
 - Recommended for original research
 - Does not accept reviews
- Preprints.org: <https://www.preprints.org/> (operated by MDPI)
 - Best place for reviews
 - Suggested by MDPI journals
- ResearchSquare: <https://www.researchsquare.com/> (supported by Springer Nature)
 - Should be avoided; suggested by Springer Nature journals

Reviewers

- Reviewers are picked based on qualifications and availability
- Qualifications = previous publications on a similar topic
- Lower quality journals have trouble finding reviewers (unqualified reviewers accepted)
- Review activity is documented via ORCID or Publons
- Some journals list reviewers and editors on publications (e.g. Frontiers)
- Getting review invitations is challenging for young scientists
- International visibility is important
- MDPI allows researchers to apply as reviewer for submissions
- Alternative reviewers can be suggested when rejecting an invitation

Review structure

- Summary of the submitted manuscript
- Evaluation of novelty and overall quality
- Major issues
 - Constructive comments about invalid methods
 - List missing controls
 - Point out cases of overstated conclusions
 - ...
- Minor issues (include line numbers)
 - Typos
 - Language issues

Rebuttal letter

- Authors write response to editorial decision
- Response to individual reviewer comments
- Authors' response should include references to the revised manuscript with line numbers
- Good rebuttal letter keeps reviewers from reading the manuscript again

Article Processing Charges

- DEAL: funding for all scholars at German research institutes for Springer Nature journals (except NatureComms + ScientificReports)
- OpenAccess Publication Funds of TU Braunschweig (only supports <2k € fees)
- Statement required: 'We acknowledge support by the Open Access Publication Funds of Technische Universität Braunschweig.'
- Funding for publications through DFG and other third party funded projects

TU Publication Fund

TU Publication Fund provides financial support for the publication of articles in Open Access Journals, Open Access Proceedings, articles / chapters in Open Access Volumes and complete Open Access Monographs. The financial support for the fund is provided by DFG and TU Braunschweig.

Funding requirements for articles in Open Access Journals:

- You are a researcher at TU Braunschweig and "Corresponding Author" of the submitted manuscript.
- Your article will be published in a Gold Open Access journal, i.e. all articles in this journal will be provided free-of-charge via the Internet immediately after publication. The majority of OA journals are listed in the [Directory of Open Access Journals \(DOAJ\)](#).
- The journal is peer-reviewed, i.e. it is verified on its quality by independent peer reviewers.
- The article processing fee (APC) is funded with a maximum of 2,000 EUR incl. VAT. If the APC should be higher, please contact us.

Are not eligible for funding:

- The fee-based "activation" of an article in a subscription-based journal (hybrid journal, "Open Choice" model). There are exceptions for publishers with whom it has been agreed that authors will not be charged for activation (such as Wiley and SpringerNature). Detailed information can be found under "Special conditions of individual publishers".
- Publications from third-party-funded projects, where the third-party funding provider covers the publication fees completely.

To submit your application, please use the [application form](#).

Funding conditions for Open Access monographs, contributions to Open Access Volumes, conference Papers, etc:

- Please contact [✉ openaccess\(at\)tu-braunschweig](mailto:openaccess(at)tu-braunschweig)

For information on the application process and billing, please see our [FAQs](#).

In case of a grant, we ask you to indicate the financial support from the Publication Fund in your publication in the following way:

- We acknowledge support by the Open Access Publication Funds of Technische Universität Braunschweig. (English publications)
- Diese Publikation wurde gefördert durch den Open Access-Publikationsfonds der Technischen Universität Braunschweig. (German publications)

<https://www.tu-braunschweig.de/en/ub/publishing-open-access/open-access-publishing>

ORCID

- ORCID = Open Researcher and Contributor ID
- Unique identifier for researchers (should be included in publications)
- ORCID can be used as SSO on many websites



1

REGISTER

Get your unique ORCID identifier. It's free and only takes a minute, so register now!

2

USE YOUR ORCID ID

Use your ID, when prompted, in systems and platforms from grant application to manuscript submission and beyond, to ensure you get credit for your contributions.

3

SHARE YOUR ORCID ID

The more information connected to your ORCID record, the more you'll benefit from sharing your ID - so give the organizations you trust permission to update your record as well as adding your affiliations, emails, other names you're known by, and more.

Data availability

- Open access journals require freely available data sets
- Established data repositories need to be used
 - Dryad
 - Zenodo
- Scripts have to be shared through suitable repositories
 - Github (codeberg)
 - Bitbucket

Flawed papers

- Typos e.g. comma misplaced
- Honest mistakes in analyses
- Scientifically wrong conclusions
- Fraud e.g. fabricated data sets or manipulated images

Retracted article

See the [retraction notice](#)

➤ [BMC Plant Biol.](#) 2020 Jul 31;20(1):361. doi: 10.1186/s12870-020-02566-2.

Contribution of anthocyanin pathways to fruit flesh coloration in pitayas

Ruiyi Fan ¹, Qingming Sun ¹, Jiwu Zeng ¹, Xinxin Zhang ²

Affiliations + expand

PMID: 32736527 PMCID: [PMC7394676](#) DOI: [10.1186/s12870-020-02566-2](#)

[Free PMC article](#)

Retraction in

[Retraction Note: Contribution of anthocyanin pathways to fruit flesh coloration in pitayas.](#)

Fan R, Sun Q, Zeng J, Zhang X.

[BMC Plant Biol.](#) 2021 May 20;21(1):225. doi: 10.1186/s12870-021-03005-6.

PMID: 34016048 [Free PMC article](#). No abstract available.

Correction

- Minor mistakes in articles can be solved by publishing a correction
- Mistakes must not affect any of the major conclusions of the article
- Examples: typos in numbers or mislabeled figures



Retraction

- Retraction is the removal of an article from the body of (valid) literature
- Retraction is done if a correction is not possible
- Retracted articles should not be cited (tools like Zotero can warn you)
- Errors can be propagated through the literature

Retracted article

See the [retraction notice](#)

› [BMC Plant Biol.](#) 2020 Jul 31;20(1):361. doi: 10.1186/s12870-020-02566-2.

Contribution of anthocyanin pathways to fruit flesh coloration in pitayas

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PMID: 34016048 [Free PMC article](#). No abstract available.

<https://pubmed.ncbi.nlm.nih.gov> › ... :

Contribution of anthocyanin pathways to fruit flesh ... - PubMed

by R Fan · 2020 · Cited by 11 — Conclusions: Collectively, our results suggest that anthocyanins partly contribute to color formation in pitaya fruit. Future studies aiming at ...

Are journals still relevant?

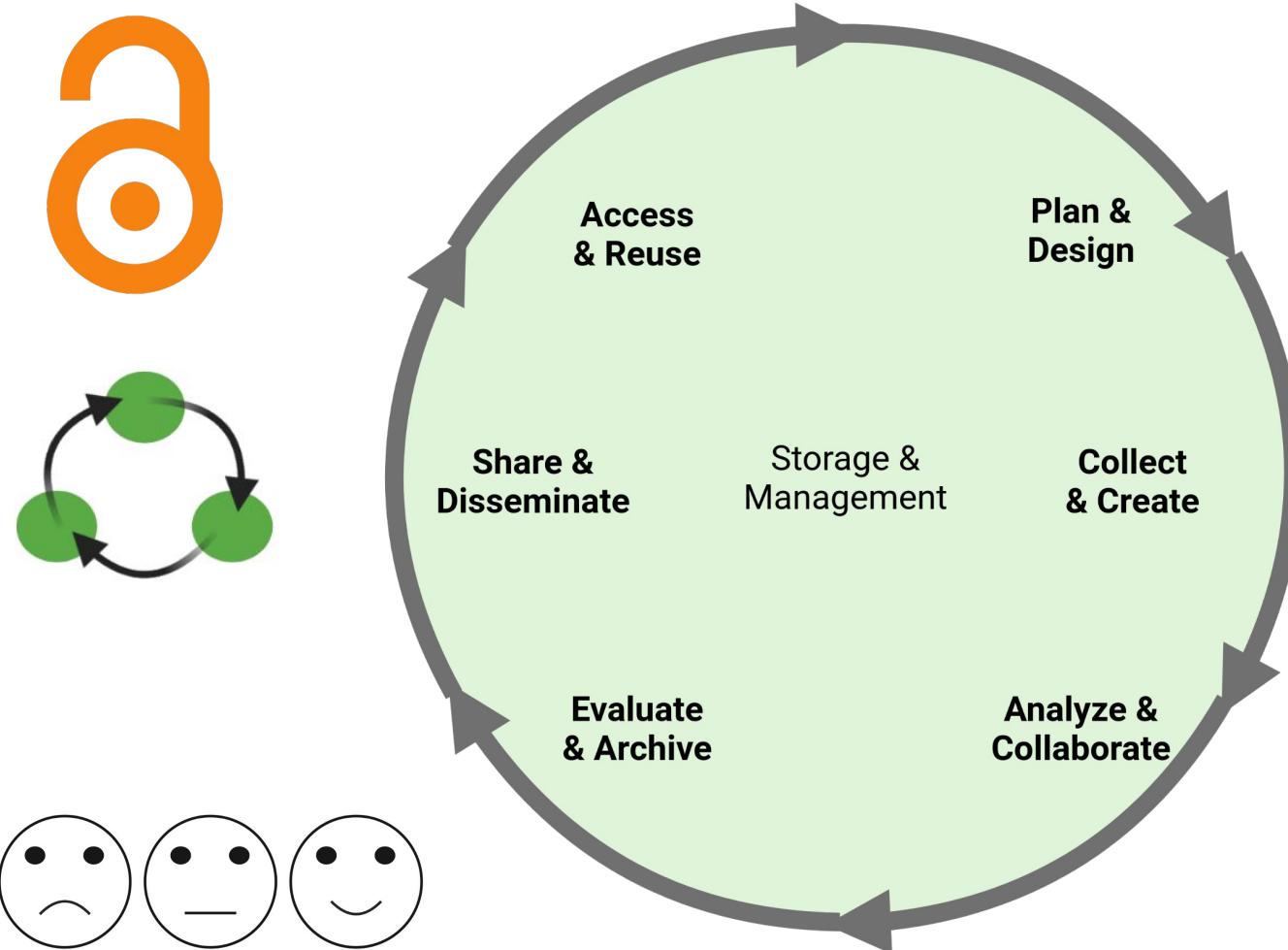
- Original function of journals is to share research with the community
- Research can be shared via preprints and through social media
- Article impact is measure by Altmetrics (alternative metrics):
 - Twitter
 - Blogs & news outlets
 - Reddit
 - CitationTools



Data life cycle



Data life cycle



PLAN



https://commons.wikimedia.org/wiki/File:RDM_02_Collect-and-Capture_frame01.svg
<https://www.picpedia.org/keyboard/a/analyze.html>



Plan & design

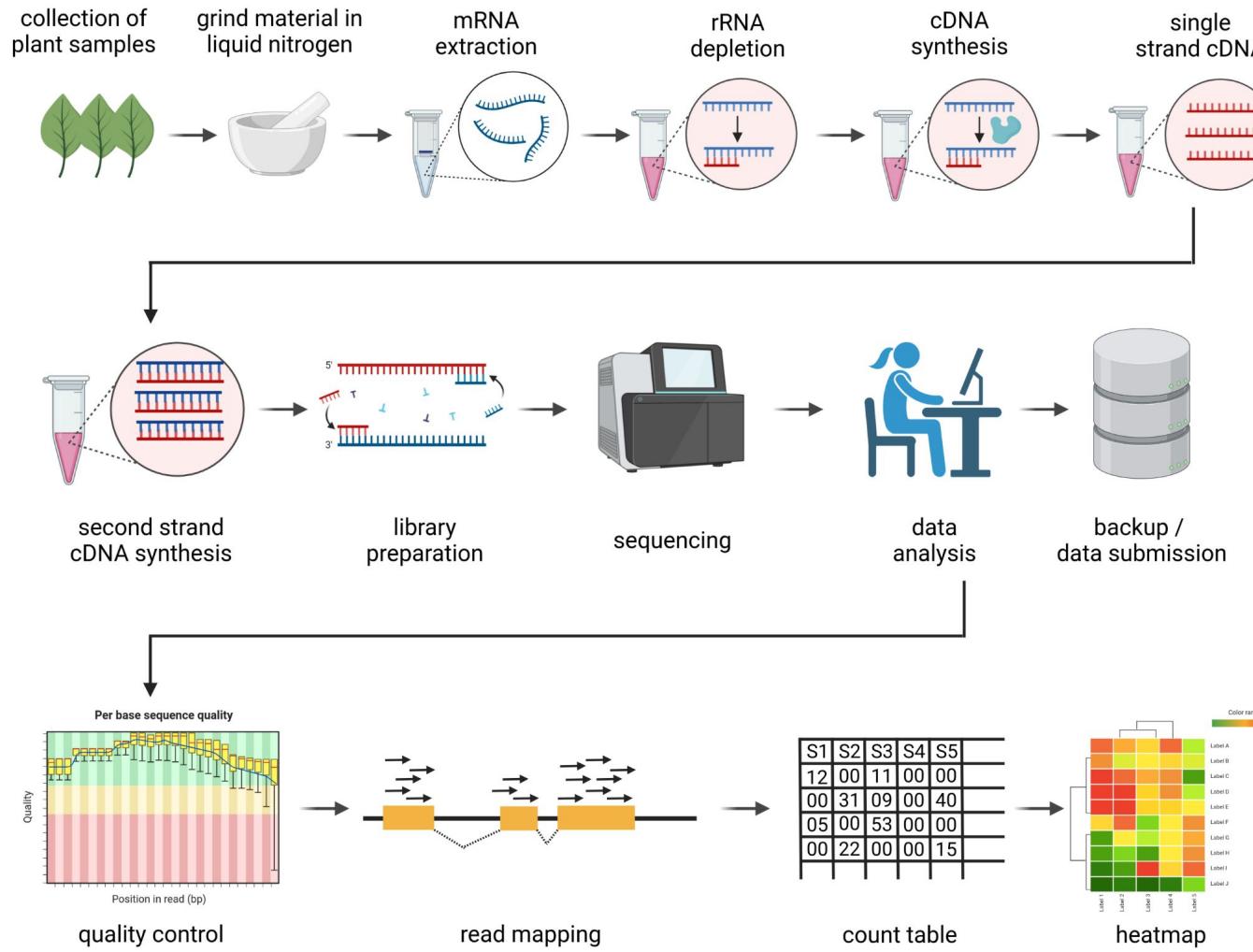
- What are the research questions/objectives?
- Plan analysis/experiment that will generate data OR use existing data sets
- How many replicates? Which statistical tests (power)?
- Data management plan
- How to ensure data safety (backups)?

EXAMPLE: Plan & design

- Research question: What are the molecular mechanisms explaining white and red pigmentation of flowers?
- Experiment:
 - RNA-Seq
 - ≥ 3 replicates per morphotype
 - paired-end sequencing
 - 30 million tags
- Data storage:
 - on a local hard drive
 - backup in cloud
 - cold storage



RNA-Seq



Data management plan

- Tools are available to generate data management plans
- Funder-specific differences in expectations
- Content:
 - Information about data and data format
 - method/time of collection; version control; backup
 - Metadata content and format
 - Policies for access, sharing, and reuse
 - Long-term storage
 - Budget: considerable costs might arise

Collect & create

- Perform planned experiment with replicates
- Document all steps
- Collect the results (data)
- Synchronize results across all storage/backup locations

EXAMPLE: Collect & create

- Grow plants under precisely controlled conditions
- Harvest material in a reproducible manner; replicates are important!
- Extract RNA and subject to RNA-seq experiment
- Store resulting FASTQ files



Synchronize & backup

- Synchronization of data between different locations:
 - \$ rsync <SOURCE> <TARGET>
- Backup solutions:
 - Desktop computers & laptops
 - External hard drives
 - Network drives
 - Central storage options (e.g. cold storage; tape storage)
 - Cloud storage
 - Optical storage
- 3 copies of data are recommended; one off-site

EXAMPLE: Synchronize & backup

- Sequencing data will be stored on local hard drive
- Copy will be uploaded to de.NBI cloud for analysis
- Backup of sequencing data in secure place after run completion

Analyze & collaborate

- Quality control
- Plausibility checks
- Sample identity checks
- Perform actual analysis alone/in collaboration
- Interdependence of collaborators possible

EXAMPLE: Analyze & collaborate

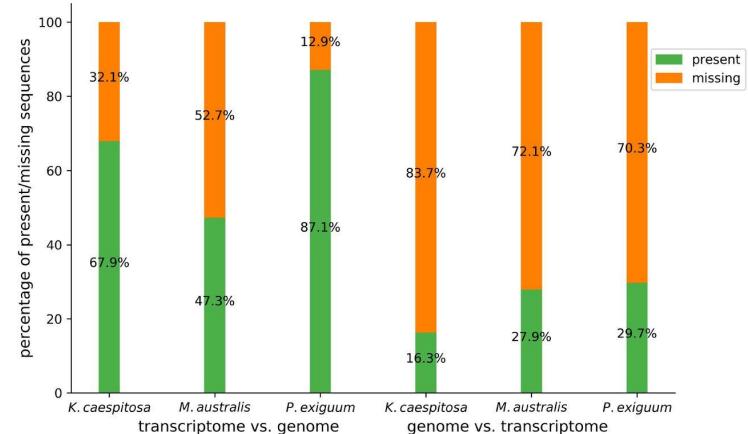
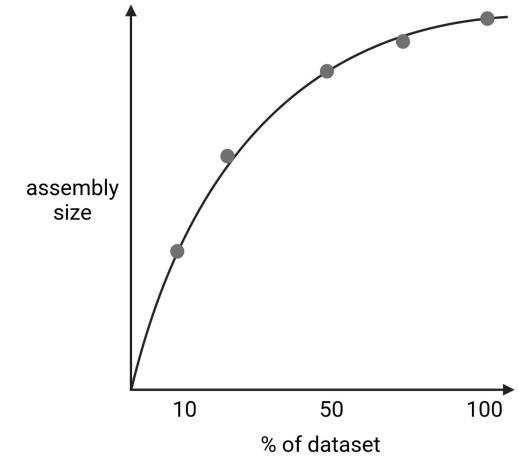
- Quality control via principal component analysis (PCA)
- Differential gene expression analysis (DESeq2)
- Pathway enrichment analysis (KEGG, GO)
- How to exchange files with collaborators
 - cloud
 - hard drives
- How to document collaboration
 - Documentation of meetings
 - Documentation of contributions to project
 - Documentation of progress
 - Writing reports for funding agencies

Evaluate & archive

- Are the data sets large enough?
- What could have been done better?
- Was the number of replicates sufficient?
- Are there clear differences between sample groups?
- Low variation between biological replicates?
- Archive all research data on tape storage for at least 10 years
- Off-site backups; Rsync to transfer only modified files
- Commercial clouds (Dryad, GigaDB); tape storage @ TUBS (contact GITZ)

Enough data?

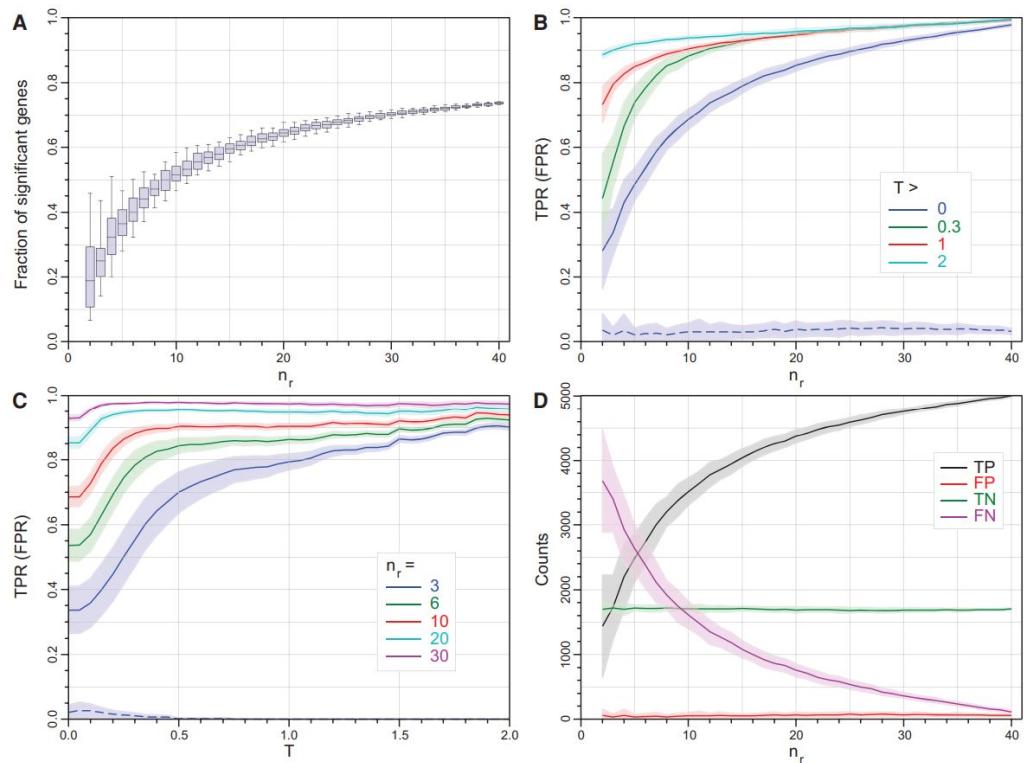
- Check if subsets lead to complete assemblies (saturation)
- Comparison of genome and transcriptome assembly
- Genome sequence assemblies cover lowly expressed genes
- Transcriptome assemblies can be advantageous for genes with large introns



Haak et al., 2018: 10.3389/fmbo.2018.00062
Pucker et al., 2019: 10.1101/646133

Sufficient replicates?

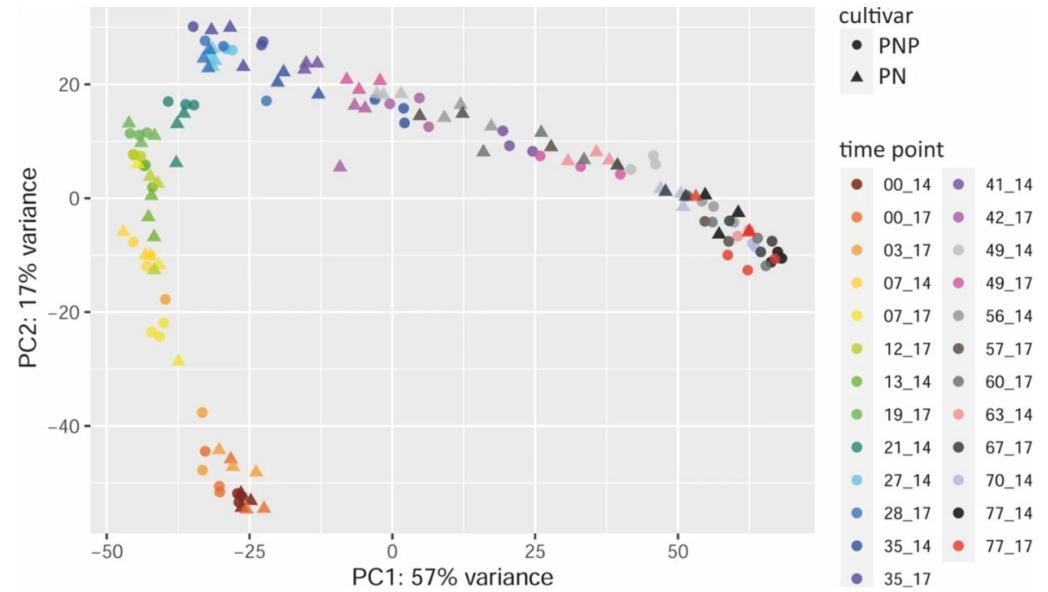
- More replicates allow the identification of a larger number of DEGs
- Reliability of gene classification increases with number of replicates
- Up to 40 replicates can boost signal strength



Schurch et al., 2016: 10.1261/rna.053959.115

Systematic differences between groups?

- Principal Component Analysis (PCA) separates RNA-seq samples based on gene expression patterns
- Similar samples are grouped together
- Principal Components (axes) are artificial axes



EXAMPLE: archive

- Submission of Nd-1 data sets to e!DAL
- Citable in corresponding publication via DOI
- Data are also archived on tape storage

The screenshot shows a detailed view of a dataset in the e!DAL repository. At the top, the e!DAL logo and the text "e!DAL - Plant Genomics & Phenomics Research Data Repository" are visible, along with the Leibniz Institute logo.

Citation: B. Pucker (2019-03-06): Chromosome-level Assembly Reveals the Niederenz (Nd-1) Genome Structure and Gene Set. DOI:10.5447/ipk/2019/4

Abstract: SMRT sequencing read assemblies of *Arabidopsis thaliana* ecotype Nd-1 and files of the gene predictions

License: CC0 1.0 Universal (Creative Commons Public Domain Dedication)

DOI: 10.5447/ipk/2019/4

Content: 5 Directories 38 Files (2.2 GB)

Files:

//dholtgra@cebitec.uni-bielefeld.de/Chromosome-level Assembly Reveals the Niederenz (Nd-1) Genome Structure and Gene Set [5 Directories 1 Files]

Up to parent directory

- falcon (377.2 MB)
- flye (370.2 MB)
- pangenomic (153.4 MB)
- canu (1000.7 MB)
- miniasm (378.7 MB)
- README.txt (446 B)

[Download as ZIP](#)

Metadata

CONTRIBUTOR:	Daniela Holzgräwe, Kai Bernd Stadermann, Bernd Weisshaar [Show full information]	COVERAGE:	none
CREATOR:	Boas Pucker [Show full information]	DATE:	Event: event CREATED: TimePoint: Wed Mar 06 12:15:16 CET 2019 UPDATED: TimePoint: Wed Mar 06 12:19:23 CET 2019
PUBLISHER:	Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Seeland OT Gatersleben, Correnstraße 3, 06466, Germany	LANGUAGE:	de_DE
SIZE:	2.2 GB	RELATION:	none
SUBJECT:	<i>Arabidopsis thaliana</i> ecotype Niederenz Nd-1, pseudochromosomes, chondrome, PacBio assembly, plastome sequence, gene prediction, Canu, Falcon, Flye, Miniasm	SOURCE:	none

Revision: 2 - CreationDate: Wed Mar 06 12:15:16 CET 2019 - RevisionDate: Wed Mar 06 12:19:23 CET 2019

Share & disseminate

- All data sets underlying a publication should be released
- Clearly refer to published data sets in data availability statement
- Submission of large data sets to suitable databases
- Select proper license for data sets
- Include all ‘customized scripts’ in publication

EXAMPLE: Share & disseminate

- Options to submit sequencing data:
 - European Nucleotide Archive (ENA)
 - Sequence Read Archive (SRA)
 - Gene Expression Omnibus (GEO)
- Submission of individual sequences: NCBI
- Options to share data sets (github, dryad, GigaDB, PUB, TUBS?)
- Scripts can be shared via github, bitbucket, gitlab, codeberg

The screenshot shows the ENA homepage with a header for 'European Nucleotide Archive'. It features a search bar with fields for 'Enter text search terms', 'Sample name, accessions', and 'Enter accession'. Below the search bar are links for 'Support' and 'Contact Us'. A message at the top states: 'Message updated 2022-05-13. Web submission services are back to normal after a brief downtime.' A note below says: 'We recommend that you subscribe to the ENA-newsletter making it easier to keep up-to-date with ENA news and developments.' Another note mentions: 'For SARS-CoV-2 data submissions, users should contact us in advance of submission at viruse-data@ebi.ac.uk for specific advice on options and to access the highest levels of support. We have also launched a Drag-and-Drop Data Submission Service (currently in Beta) suitable for certain SARS-CoV-2 submissions. We are inviting submitters to try this out. Please contact us at the email above for details.' The main content area is titled 'European Nucleotide Archive' with a sub-note: 'The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. More about ENA.' Below this are four teal buttons labeled 'Submit', 'Search', 'Rulespace', and 'Support'. To the right is a 'Tweets by @ENASequence' section with a small image of the ENA logo.

The screenshot shows the SRA landing page with a large blue circular graphic on the left. To the right, the title 'SRA - Now available on the cloud' is displayed in white. Below the title, a dark text box contains the following text: 'Sequence Read Archive (SRA) data, available through multiple cloud providers and NCBI servers, is the largest publicly available repository of high throughput sequencing data. The archive accepts data from all branches of life as well as metagenomic and environmental surveys. SRA stores raw sequencing data and alignment information to enhance reproducibility and facilitate new discoveries through data analysis.'

EXAMPLE: data availability statement

- Sequence read datasets generated and analyzed during this study were made available at ENA under the accession PRJEB35658. Individual run IDs are included in Additional file 1. The Col-0 genome sequence assembly of the GABI-Kat Col-0 genetic background (Col-0_GKat-wt) is available at ENA under the accession GCA_905067165.
- **Availability of supporting code and requirements**
 - Project name: KIPES3
 - Project home page: <https://github.com/bpucker/KIPES>
 - Operating system(s): Linux (website is platform independent)
 - Programming language: Python3
 - Other requirements: BLAST, MAFFT, FastTree2, dendropy, scipy
 - License: GNU General Public License v3.0
 - RRID: SCR_022370
- All data sets analyzed in this study are publicly available. Data sets generated as part of this study are shared via GitHub (<https://github.com/bpucker/KIPES>). A docker image is available via DockerHub (<https://hub.docker.com/r/bpucker/kipes>).

EXAMPLE: data publication

PUB - Publications at Bielefeld University

Arabidopsis thaliana methylation pattern analysis based on ONT sequence reads

Schilbert H, Kleinböltig N, Weisshaar B, Pucker B (2021)
Bielefeld University.

Research Data

Download [GK_040A12.vcf.gz](#) 176.58 MB
[GK_050B11.vcf.gz](#) 183.65 MB
[GK_082G09.vcf.gz](#) 185.46 MB

+ All

DOI <https://doi.org/10.4119/unibi/2956654>

Details Files Links

Creator

Schilbert, Hanna^[Unit]; Kleinböltig, Nils^[Unit]; Weisshaar, Bernd^[Unit]; Pucker, Boas^[Unit]

Department

Fakultät für Biologie > Genetik und Genomik der Pflanzen

Abstract / Notes

We sequenced the genomes of 14 Arabidopsis thaliana GABI-Kat T-DNA insertion lines (Col-0 background), which eluded flanking sequence tag-based attempts to fully characterize their insertion alleles, with Oxford Nanopore Technologies (ONT) long reads. Detailed information about each line, e.g., their T-DNA insertion site(s), have been described by Pucker et al. (BMC Genomics (2021) 22:599; <https://doi.org/10.1186/s12864-021-07877-8>). The DNA that has been sequenced is derived from a mixture of tissues as expected for DNA extracted from young plantlets. For 11 of the datasets from these lines, we called 5mC methylation patterns with the tool Megalodon v.2.2.9 provided by ONT (<https://github.com/nanoporetech/megalodon/>). Results of this analysis are available per line as individual VCF files. We are sharing unfiltered output files to grant full control over the down-stream analysis steps and to accelerate the research in epigenomics. We identified between 706,254 and 1,020,654 positions per line where at least 80% of 5 or more reads support a methylation site. The following datasets are available and the file names reveal the respective GK line:

1. GK_040A12.vcf
2. GK_050B11.vcf
3. GK_082G09.vcf
4. GK_290G05.vcf
5. GK_39C06.vcf
6. GK_410B07.vcf
7. GK_430F05.vcf
8. GK_433E06.vcf
9. GK_654A12.vcf
10. GK_767D12.vcf
11. GK_909H04.vcf

Keywords

long read sequencing; ONT; methylation; plant epigenomics; GABI-Kat; Megalodon

Year of Publication

2021

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Page URI

<https://pub.uni-bielefeld.de/record/2956654>

Cite this

AMA APA (6th ed.) Frontiers Harvard IEEE LNCs MLA

Schilbert H, Kleinböltig N, Weisshaar B, Pucker B. *Arabidopsis thaliana methylation pattern analysis based on ONT sequence reads*. Bielefeld University; 2021.

PUB - Publications at Bielefeld University

Arabidopsis thaliana methylation pattern analysis based on ONT sequence reads

Schilbert H, Kleinböltig N, Weisshaar B, Pucker B (2021)
Bielefeld University.

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[GK_082G09.vcf.gz](#) 185.46 MB

+ All

DOI <https://doi.org/10.4119/unibi/2956654>

Details Files Links

All files available under the following license(s):



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<https://creativecommons.org/licenses/by/4.0/legalcode>

Main File(s)

File Name [GK_040A12.vcf.gz](#) 176.58 MB
Access Level [Open Access](#)
Last Uploaded 2021-08-09T16:28:09Z
MD5 Checksum 5639514d2396b649688a1c08cb9b7ca7

File Name [GK_050B11.vcf.gz](#) 183.65 MB
Access Level [Open Access](#)
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Access Level [Open Access](#)
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Access Level [Open Access](#)
Last Uploaded 2021-08-09T16:28:09Z
MD5 Checksum df135692ca92ae1d4e1a0ff852c0691

File Name [GK_399C06.vcf.gz](#) 181.61 MB
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Access Level [Open Access](#)
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Access Level [Open Access](#)
Last Uploaded 2021-08-09T16:28:16Z
MD5 Checksum 4ecfa4ff5aa3585e5c8b851f7001dc1f

File Name [GK_654A12.vcf.gz](#) 187.28 MB
Access Level [Open Access](#)
Last Uploaded 2021-08-09T16:28:19Z
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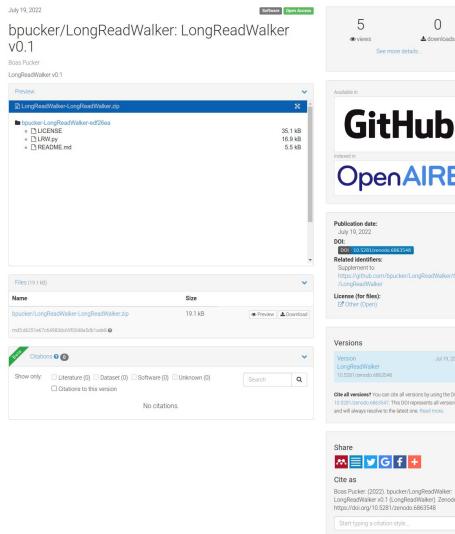
Schilbert et al., 2021: 10.4119/unibi/2956654



Technische
Universität
Braunschweig

EXAMPLE: publication of scripts

- Scripts should be shared through repositories:
 - Github
 - Bitbucket
 - Codeberg
 - Gitlab
- Archive repositories in Zenodo (DOI assignment)



bpucker trailing slash added to output directory aef0011 6 days ago 34 commits

- README.md documentation updated 23 days ago
- TBLASTN_check.py Add files via upload 6 months ago
- coexp3.py Add files via upload 23 days ago
- collect_best_BLAST_hits.py trailing slash added to output directory 6 days ago
- construct_anno.py Add files via upload 23 days ago
- exp_plots.py Add files via upload 5 months ago
- exp_plots_issue.py Add files via upload 23 days ago
- extract_red.py Add files via upload 6 months ago
- pairwise_comp3.py Add files via upload 23 days ago

README.md

DOI: 10.5281/zenodo.6112455

Apiaceae FNS I

These scripts were applied to study the evolution of *FNS I* in the Apiaceae. Please cite the corresponding publication when using these scripts.

Collect best BLAST hits

This script performs an automatic collection of sequences with some similarity to the bait sequences. Since BLAST does not allow the reliable identification of orthologs, a following validation through a phylogenetic analysis is necessary for most applications.

Usage:

```
python collect_best_BLAST_hits.py --baits <FILE> --out <DIR> [--subject <FILE>] [--subjectdir <DIR>]
```

Mandatory (option1):

- baits STR A multiple FASTA file.
- out STR Directory for temporary and output files.
- subject STR Subject sequence file.

Mandatory (option2):

- baits STR A multiple FASTA file.
- out STR Directory for temporary and output files.
- subjectdir STR Folder containing subject sequence files.

Optional:

- number STR Number of BLAST hits to consider.[10]

--baits FASTA file containing the bait sequences.

--out is the output folder. The folder will be created if it does not exist already.

--subject is the subject file for the screen via BLAST. Candidates will be identified in this collection of sequences.

--subjectdir is a folder containing the subject files. This option allows the automatic collection of sequences from multiple different species. This option prevents the need to run the analysis multiple times with different subject files.

--number defines how many different BLAST hits will be considered per query. A non-redundant set of sequences will be collected per subject sequence. Increasing this number make the search more sensitive, but also computationally more expensive. Default: 10.

<https://github.com/bpucker/ApiaceaeFNS1>

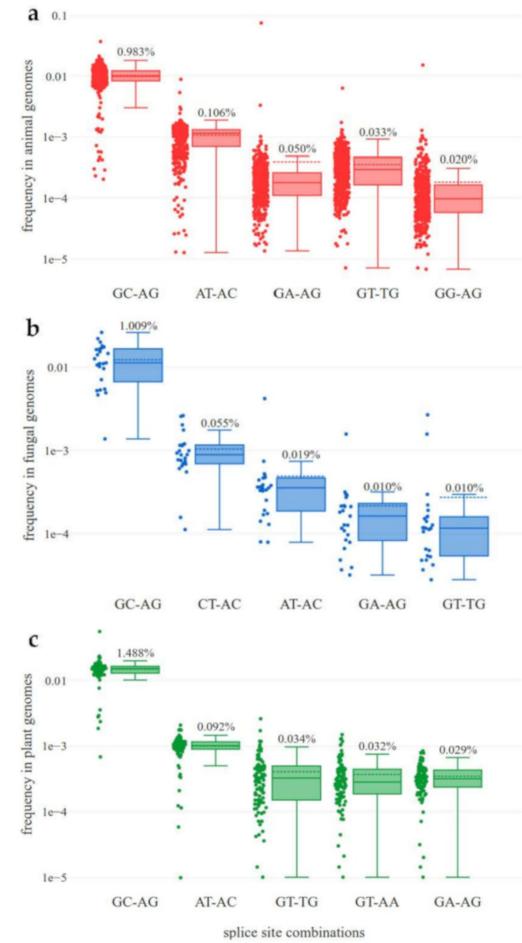
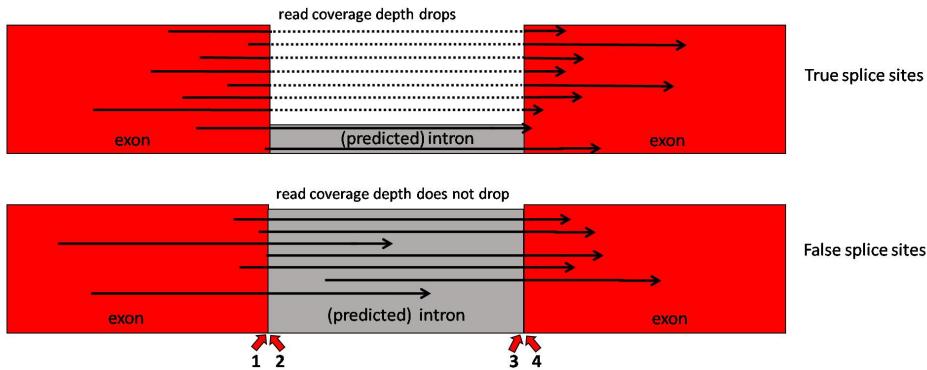


Access & reuse

- Data sets should be freely available to enable validation of findings
 - NOT: ‘Available upon reasonable request from the corresponding author’
- Public data sets are an excellent resource for re-use
- No costs for data generation
- Massive datasets can enable identification of small effect sizes
- Generation of novel hypothesis

EXAMPLE: access & reuse

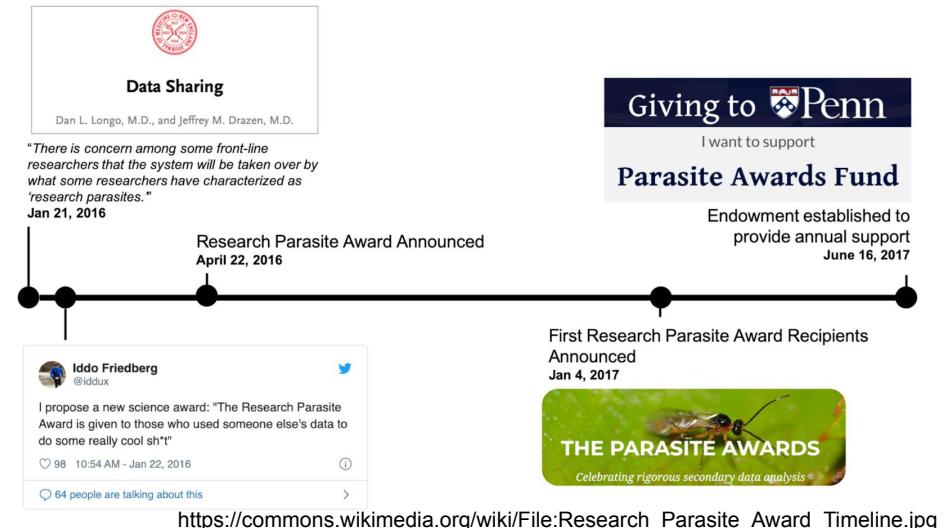
- Investigation of non-canonical splice sites in plants, animals, and fungi
- Screening genome sequences+annotations for splice sites
- Harnessing RNA-seq to quantify usage of (non-canonical) splice sites



Pucker & Brockington, 2018: 10.1186/s12864-018-5360-z
Frey & Pucker, 2020: 10.3390/cells9020458

The Parasite Awards

- Celebrates comprehensive secondary data analysis
- Novel insights inferred from existing (underutilized) data sets
- Supported by GigaScience/GigaByte



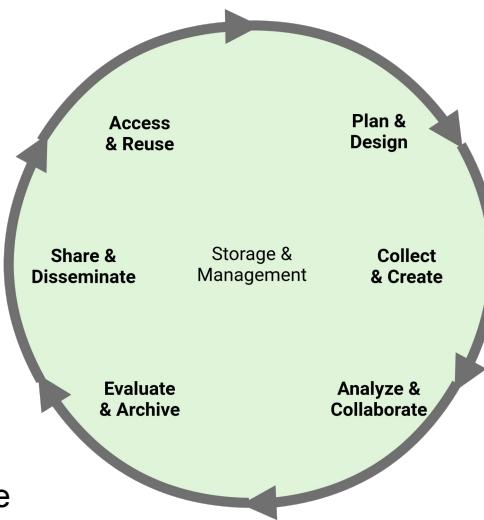
Full cycle: Nd-1

Data sets reused for variant caller benchmarking study

Publication about findings

data sets published at SRA

NGS not sufficient for complete genome sequence; on tape storage

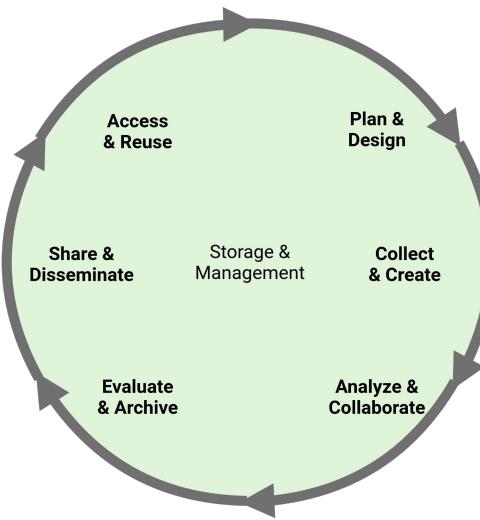


Sequence Nd-1 genome, because it is a parent of a mapping population

Sequencing on Roche 454, GAILx, & HiSeq1500

fastQC analysis, trimming with Trimmomatic, and assembly+annotation

Full cycle: *Croton tiglum*



Data reuse for validation of KIPEs

Publication about findings
data sets published at SRA

Evaluation to identify optimal parameters
Data stored via tape storage

Identify specific genes in *Croton tiglum*
via transcriptome assembly

RNA-seq with samples of different
tissues & normalized library

Transcriptome assembly and
characterization of candidate genes

Re-use



What are the advantages and challenges of re-use?

Advantages and challenges of data re-use

Advantage	Challenge
Cost-effective	Lacking metadata
Immediately accessible	Unknown details/issues
Extremely large data sets	Mislabeling possible
	Not perfectly matching needs
	Technology outdated

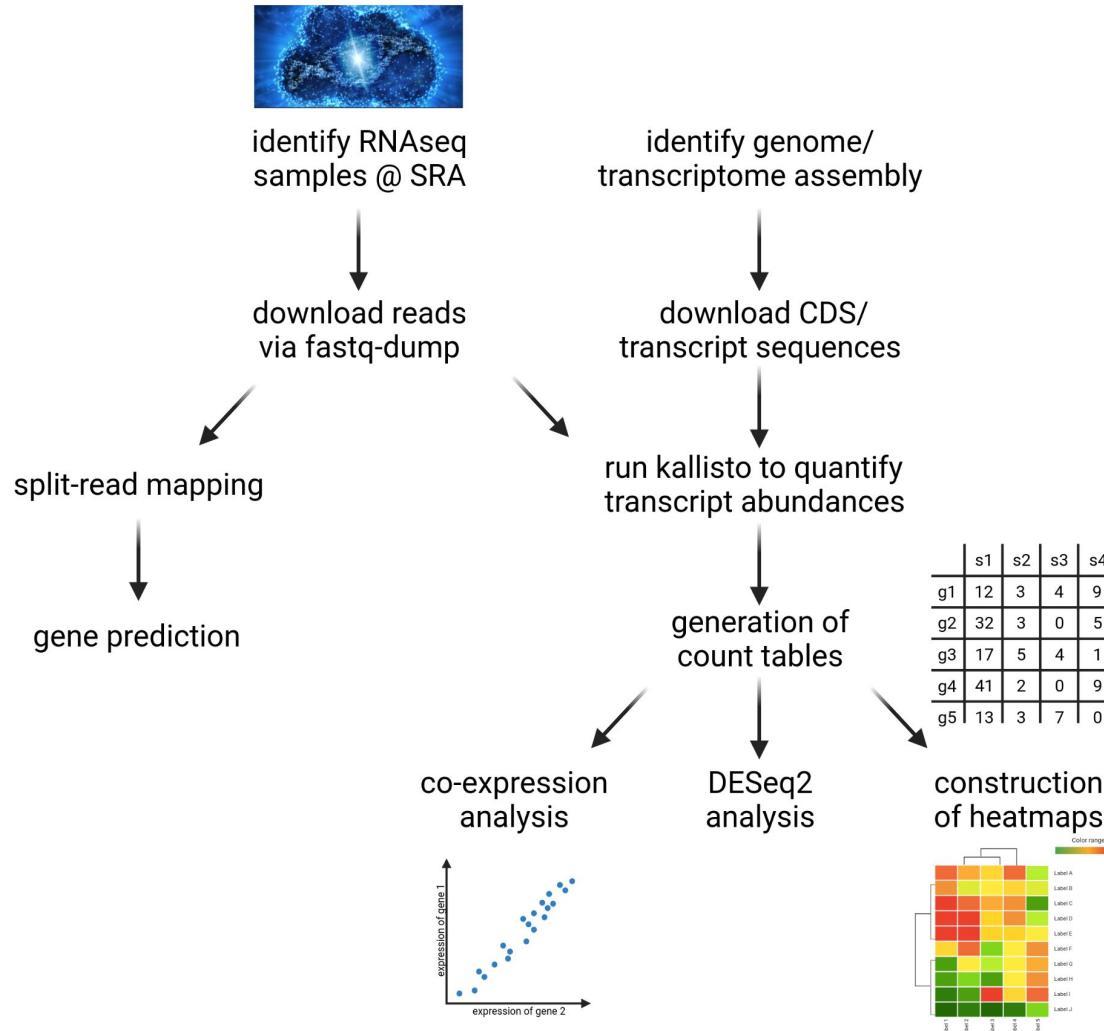
Find gene expression data sets

- SRA read selector
- Gene Expression Omnibus (GEO) search
- Publications: data availability statements & supplementary tables

How to retrieve data?

- Preprocessed data sets (count tables @ GEO)
- Cloud solutions (Galaxy)
- Fastq-dump

Workflow

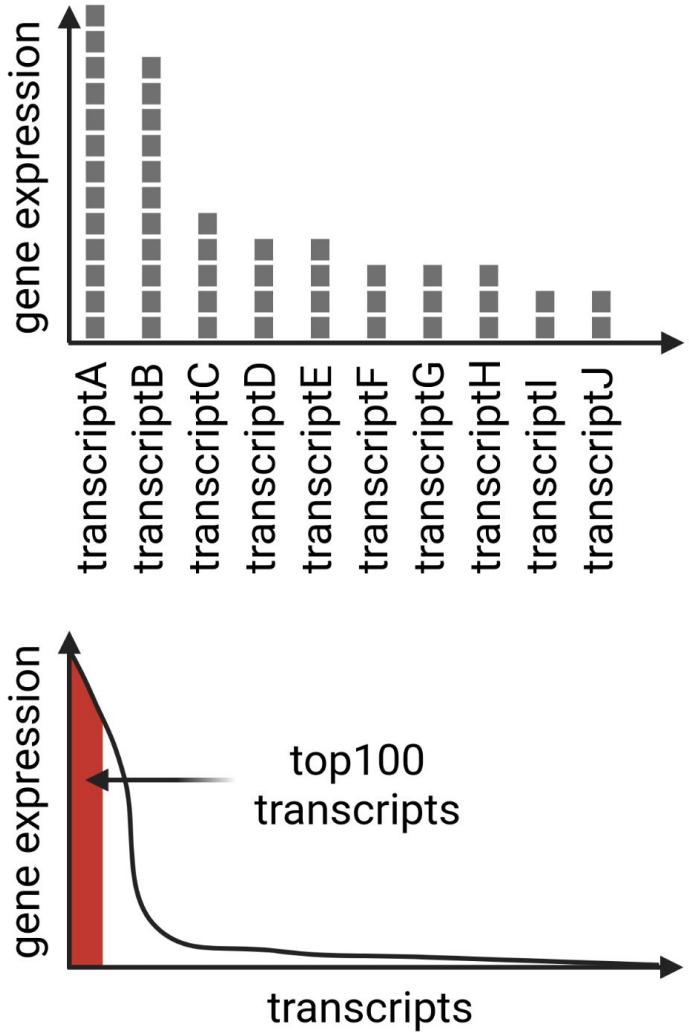


How to check RNA-seq data sets?



RNA-seq quality control

- Percentage of reads mapped to individual mRNA sequences
- Distribution of abundance across transcripts
 - Substantial coverage of top100 transcripts
- Metadata assessment / marker gene check
 - Highly expressed marker genes like RuBisCO



Managing references

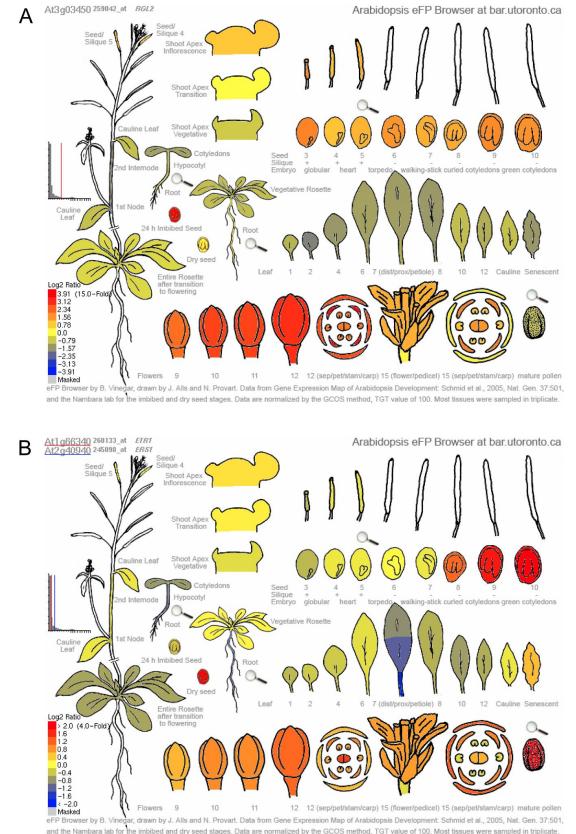
- Entries about publications / data sets are stored in a local database
- Convenient citation when writing manuscripts
- Support for comments and key words assigned to entries
- Examples:
 - Zotero: free
 - Mendeley: free, but belongs to Elsevier
 - Citavi: commercial, but campus license
 - EndNote: commercial

Data re-use examples



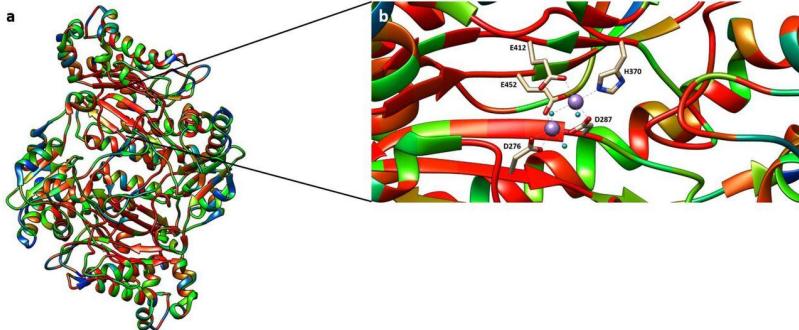
Electronic Fluorescent Pictograph browser

- Integration of existing microarray datasets
- Option to integrate other large scale datasets
- Basis for hypothesis generation
- Visualization of gene expression in many different plant tissues/conditions



Identification of conserved amino acid residues

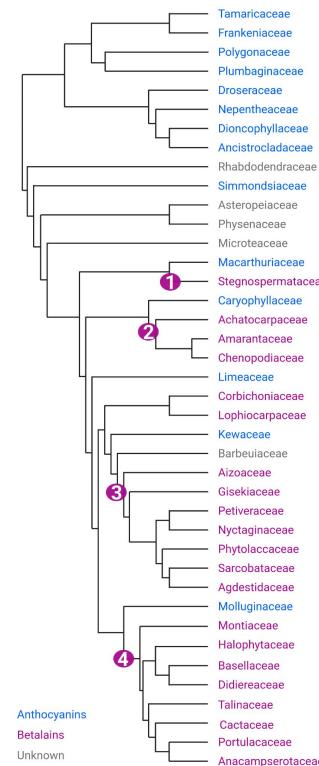
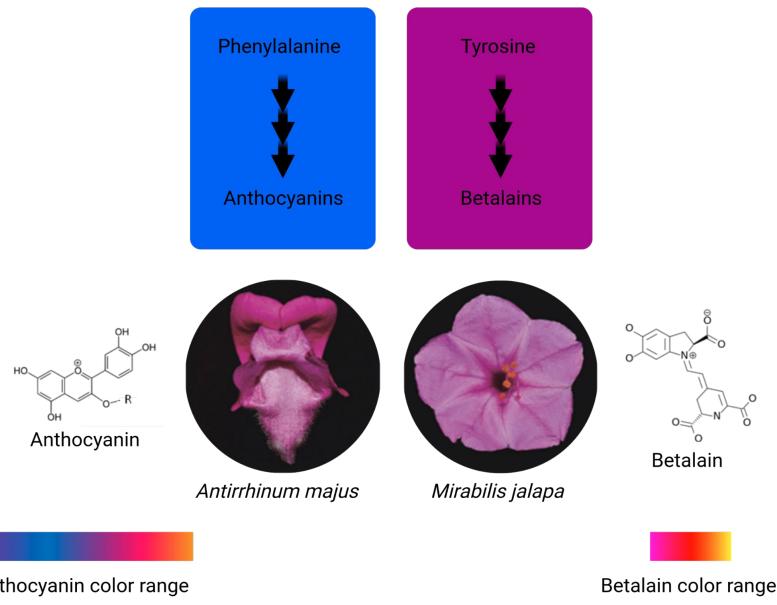
- Identification of orthologous sequences in hundreds of species
- Comparison of sequences to identify highly conserved amino acid residues
- 3D modeling based on known structures of homologs



	Animals	Plants	Fungi	Archaea	Bacteria
D276	94	99	100	100	100
D287	94	98	100	100	100
H370	94	98	100	100	100
E412	94	96	100	100	100
E452	91	97	100	100	100
T289	94	97	100	100	97
T410	93	96	100	79	100
H377	94	98	100	100	97
R398	93	98	89	10	57
W107	88	98	96	0	96
Y241	94	96	100	2	90
I244	93	98	97	88	100
H255	94	98	100	100	100
V376	89	1	38	81	94
C58	58	64	0	0	0
C158	40	1	0	0	0

Schilbert et al., 2018: 10.1101/423475

Complex pigment evolution in the Caryophyllales

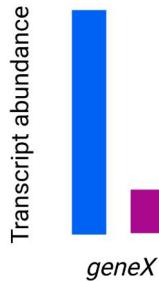


- Functional redundancy of anthocyanins and betalains
- At least four independent origins of betalain biosynthesis
- Mutual exclusion: anthocyanins and betalains were never observed in same (natural) plants

Timoneda *et al.*, 2019: 10.1111/nph.15980
Sheehan *et al.*, 2020: 10.1111/nph.16089

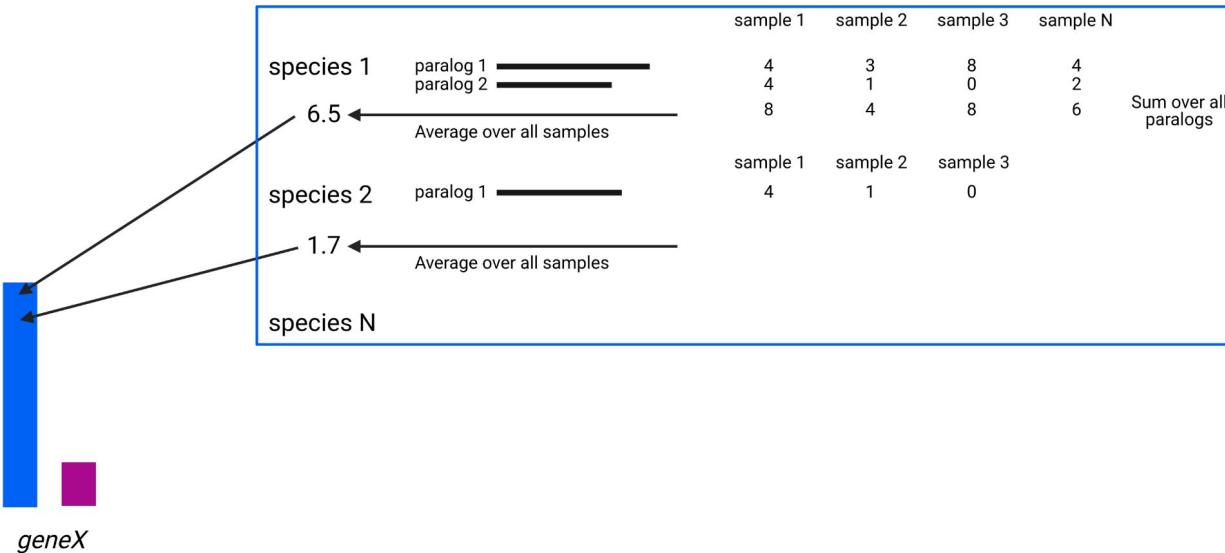
Cross species transcriptomics

		sample 1	sample 2	sample 3	sample N	
species 1	paralog 1	4	3	8	4	
	paralog 2	4	1	0	2	
		8	4	8	6	Sum over all paralogs
		6.5				Average over all samples



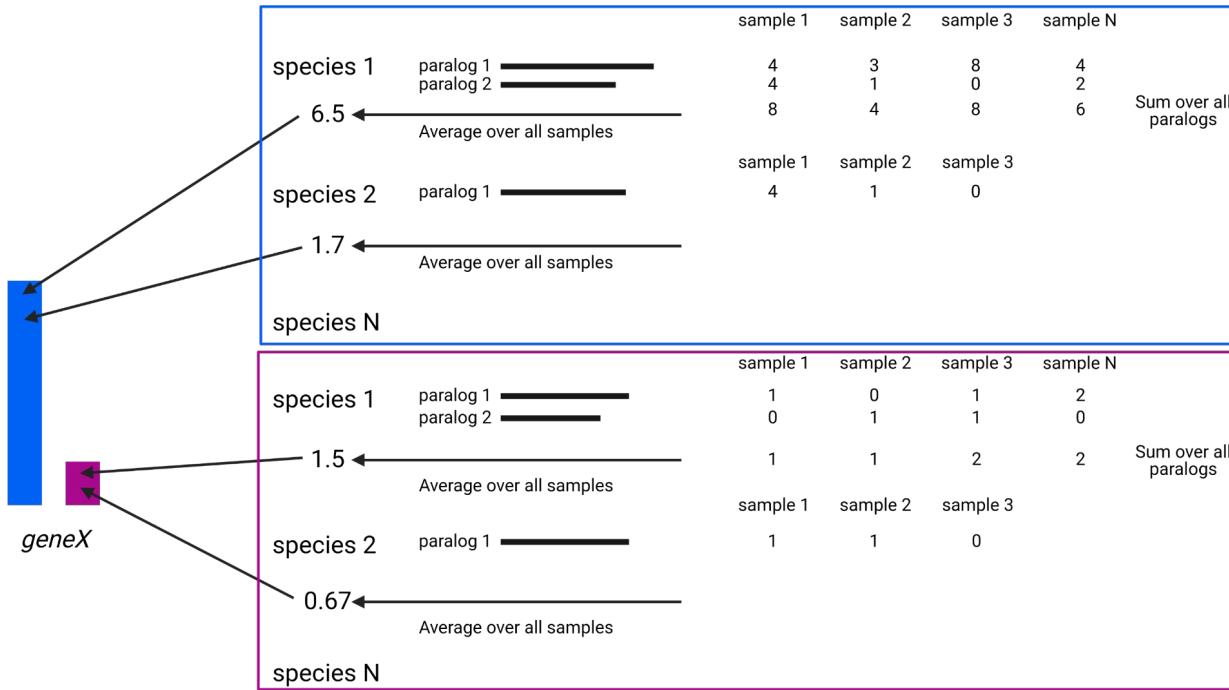
Cross species transcriptomics

Transcript abundance

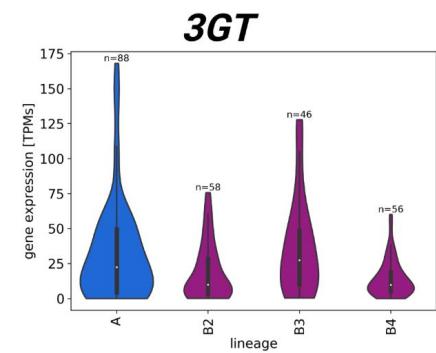
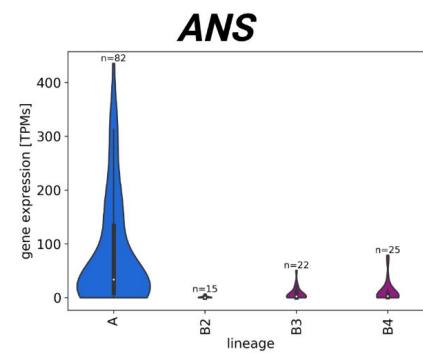
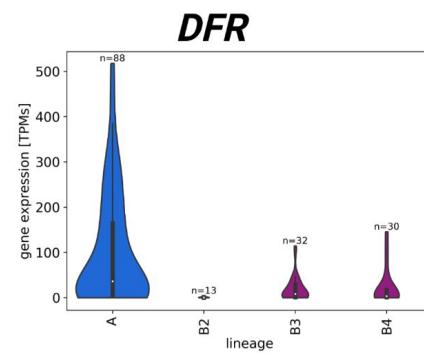
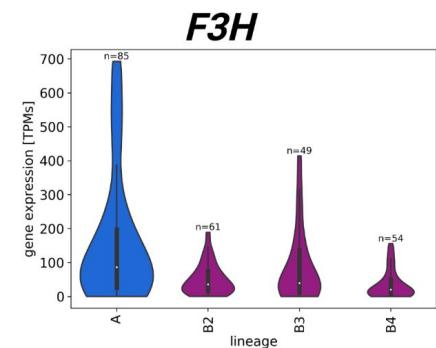
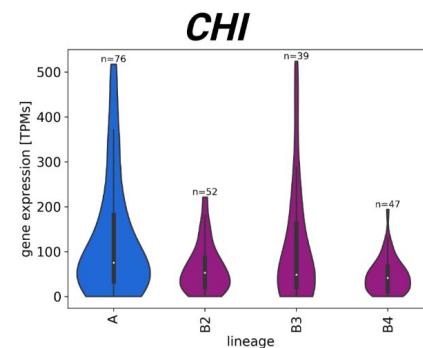
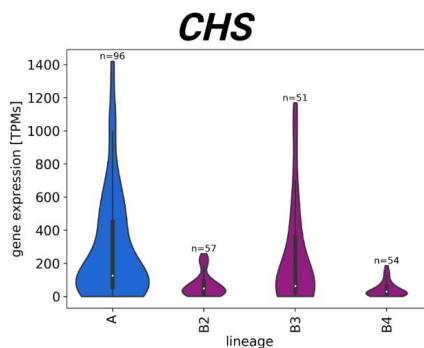
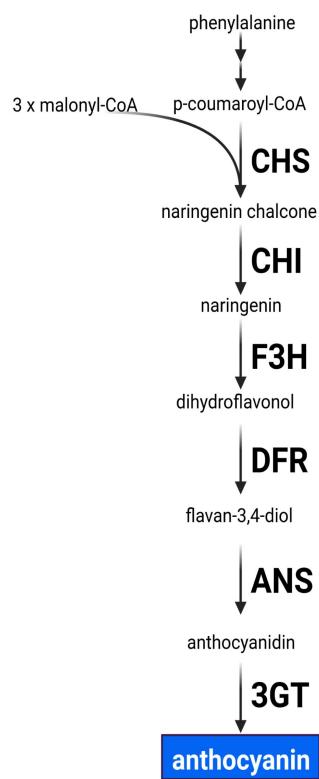


Cross species transcriptomics

Transcript abundance



Low transcriptional activity of anthocyanin biosynthesis genes



Summary

- Sharing protocols
- Licenses
- FAIR data
- ENA submission
- Scientific publication process
- Data life cycle
- Re-use

Time for questions!



Questions

1. Which licenses are available to share data sets / software?
2. What is license stacking and which issues result from it?
3. What is FAIR in data science?
4. How does a submission to ENA work?
5. Which steps and loops are part of a paper publishing process?
6. What elements are required in a cover letter?
7. What are h-index, i10-index, and (J)IF?
8. What are the advantages of preprints?
9. Which elements should be part of a review report?
10. Where would you deposit scripts/data sets?
11. What are the steps of a data life cycle?
12. What are the advantages and challenges of re-use?
13. Which options for QC and filtering of public RNA-seq data sets do you know?