The Digital Botanical Gardens Initiative

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Authors

- **The Digital Botanical Gardens Initiative Consortium** ✉
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Abstract

The Digital Botanical Gardens Initiative (DBGI) ambitions to explore innovative solutions for the collection, management and sharing of digital information acquired on living botanical collections. A particular focus will be placed on the large scale characterization of the chemodiversity of living plants collections through mass spectrometric approaches. The acquired data will be structured, organized and connected with relevant metadata through semantic web technology. The gathered knowledge will then inform ecosystem functioning research and orient biodiversity conservation projects. The DBGI initially aims to take advantage of the readily available living collections of Swiss botanical gardens to establish robust and scalable chemo- and biodiversity digitisation workflows. The ultimate goal is to apply these approaches in the field and at the global scale in wild ecosystems.

Goals

Figure 1: Main goals of the Digital Botanical Gardens Initiative.

The main goals of the DBGI are resumed in Figure 1 Some details are given hereafter:

1. Establish chemical extracts libraries of Swiss botanical gardens. These chemical libraries can be considered as complementary to herbarium samples. They are easily conserved over time and in a reasonable space. They represent the chemical diversity of a sample. They can be easily aliquoted. They can be screened for bioassays.

2. Digitize, through mass spectrometry, the chemodiversity of Swiss botanical gardens. Here high-resolution mass spectrometry is considered as a digital scanner allowing to capture the chemical fingerprint of the profiled sample. State-of-the-art computational metabolomics solutions are used to organize and annotate the acquired spectra with molecular data.

3. Gather chemical information and relevant samples metadata in a tailored knowledge graph. Chemical information acquired at the previous step (spectra and chemical structures) are connected to relevant samples metadata (taxonomy, phenology, geolocalisation, time of collection etc.). For this semantic web technologies (namely the RDF data model) are employed and a tailored knowledge graph is established.

4. Connect to existing ontologies (bio, chemo) and biodiversity digitization projects. Chemical and biological objects of the graph are connected to relevant pre-established ontologies (e.g. CHEBI, Plants Ontology) and data graphs (e.g. Wikidata). Connection with complementary biodiversity digitization efforts will be done (e.g BiCIKL, Dissco)

5. Establish web and programmatic interfaces for the query of the acquired knowledge. A web interface will allow a convenient access to the data acquired within the framework of the project. A dashboard will allow simple visualizations (e.g pie charts, barplots, treemap) to interpret the data. In addition a SPARQL endpoint and an application programming interface (API) will allow retrieval of data programmatically.

6. Illustrate the feasibility and advantages of an end-to-end Open Science project. The DBGI will strictly follow the Open Science guidelines by using open-source software and making available the acquired data and scripts under an open license agreement. In addition the DBGI results will be published at the moment they are acquired (previous to formal publication or even pre-prints) thus following the Open Notebook Science concepts.

7. Establish robust and scalable workflows for the digitization of wild ecosystems biodiversity. The DBGI, albeit ambitious, is a pilot project. The future objective is to propose digitization workflows for the characterization of the wild ecosystems chemodiversity, on a global scale. These workflow will be central to the future Earth Metabolome Initiative.

8. Provide "molecular arguments" for biodiversity conservation policies. The ultimate goal of DBGI is to use all the gathered metabolic information to support, extend or implement conservation efforts worldwide. We believe that by providing chemical maps of the landscape it will be possible to contribute to the prioritization of conservation and restoration targets . In other words, by establishing large scale chemical maps we expect to provide "molecular arguments" to biodiversity conservation endeavors (e.g. *"This piece of land has a high content of antibacterial scaffolds."* or *"This place might be poor in species diversity but rich in a rare chemodiversity"*.)

Background and context

Biodiversity is a major determinant of ecosystem stability [1]. Hundreds of studies spanning terrestrial and aquatic ecosystems support that higher levels of biodiversity, in all its forms, promote better ecosystem functions, such as carbon sequestration, underpinning human well-being [2,3]. Sadly, earth is experiencing a major biodiversity crisis and of the estimated nine million species of fungi, plants, and animals have been described [4], about a million species are currently at risk of extinction and may go extinct before the end of the century [5]. One major issue is that more than 80% of the estimated biodiversity still awaits to be described. We are in fact facing what is now called the Anthropocene extinction (sixth mass extinction) [6]. In order to try to deviate from these alarming trends, all possible efforts must be made by the responsible (i.e. our species) for the conservation of biodiversity. For this, the characterisation and documentation of biodiversity is a fundamental prerequisite. Over 3.5 billion years of evolution, natural selection, the craftsman of biodiversity, has created an overwhelming array of molecular entities. Myriad compounds are produced by all living organisms from bacteria to whales, forming the backbone of the ever-growing tree of life. Through the lens of chemistry, every species, biotic interaction, and community, reveals a unique ensemble of molecular structures: the metabolome. These chemical assemblages are a valuable, yet largely unexplored reflection of biodiversity and ecosystem functioning. To go beyond the simple quantitative representation of biodiversity provided by species inventories, and to reinforce our understanding of links between biodiversity and ecosystem functioning, we see chemical diversity as an alternative and highly complementary view of the diversity of our planet's ecosystems.

Rationale

With these urgent biodiversity characterization objectives in mind we are setting up the Digital Botanical Gardens Initiative (DBGI), which aims to develop robust and scalable workflows for the digitization of botanical gardens using several approaches. The central one being the use of analytical chemistry strategies to build information-rich chemical maps that will guide researchers focusing on biodiversity characterization and conservation.

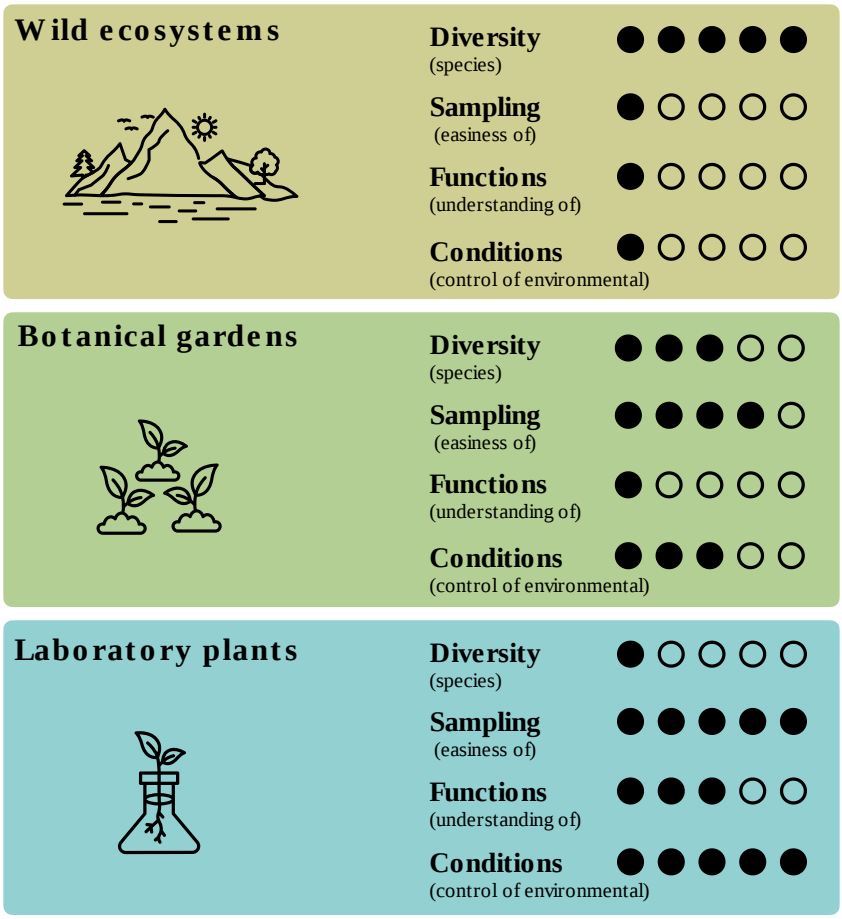

Figure 2: Characteristics of three main plant biodiversity sources for the scientist.

Sampling plants for chemical characterization can be done in three ways, either from natural living collections (botanical gardens), in the wild, or by growing plants in highly controlled settings (See Figure 2 for an overview of the advantages and inconveniences of each biodiversity source). For this first project, the sampling in botanical gardens is the chosen option, as within a very accessible location, thousands of species, which are already identified, labeled and organized, can be readily sampled.

Outline of the research

The aim of the DBGI is to characterize the chemodiversity of the all botanical gardens of Switzerland. This ambitious objective requires us to evaluate and test the entire workflow and methodology. For this, the initiators of the DBGI started gathering preliminary data from two botanical collections: the Jardin Botanique de l'Université de Fribourg (JBUF) and the Jardin Botanique de Neuchâtel (JBN). This choice was made for practical reasons (these are the respective working places of the DBGI initiators) but also because these two gardens each offer their unique characteristics. On one hand the JBUF presents over 5000 species systematically organized to reflect the Angiosperm Phylogeny Group (APG) system. The JBUF researchers are specialized in conservation biology. On the other hand, the JBN presents over 2000 species organized in 8 sub-gardens. The JBN has a focus on ethnomedicinal plants. Below, we will briefly outline the research workflow envisioned for the DBGI. The main steps have been schematized in Figure 3. The overall workflow can be divided into two main parts: one dealing with physical objects (upper part of Figure 3) and a second one dealing with data and metadata acquired from these objects (lower part of Figure 3).

Physical objects. Starting from a botanical garden (a living specimens collection), the aim is to sample each specimen and to build two libraries: a library of dried plant material and a library of chemical extracts. The dried plant material library will serve as a backup for extractions to be repeated, further characterization of compounds, or for orthogonal analysis (e.g. genetic sequencing). The chemical extracts library will be the source material for the mass-spectrometry digitization stage. This library will also be available for backups and orthogonal analysis (e.g. NMR profiling or bioassays campaigns). Complementary to herbarium, these two libraries offer an efficient way (reduced space, long term storage) to capture and conserve the chemistry of the botanical gardens.

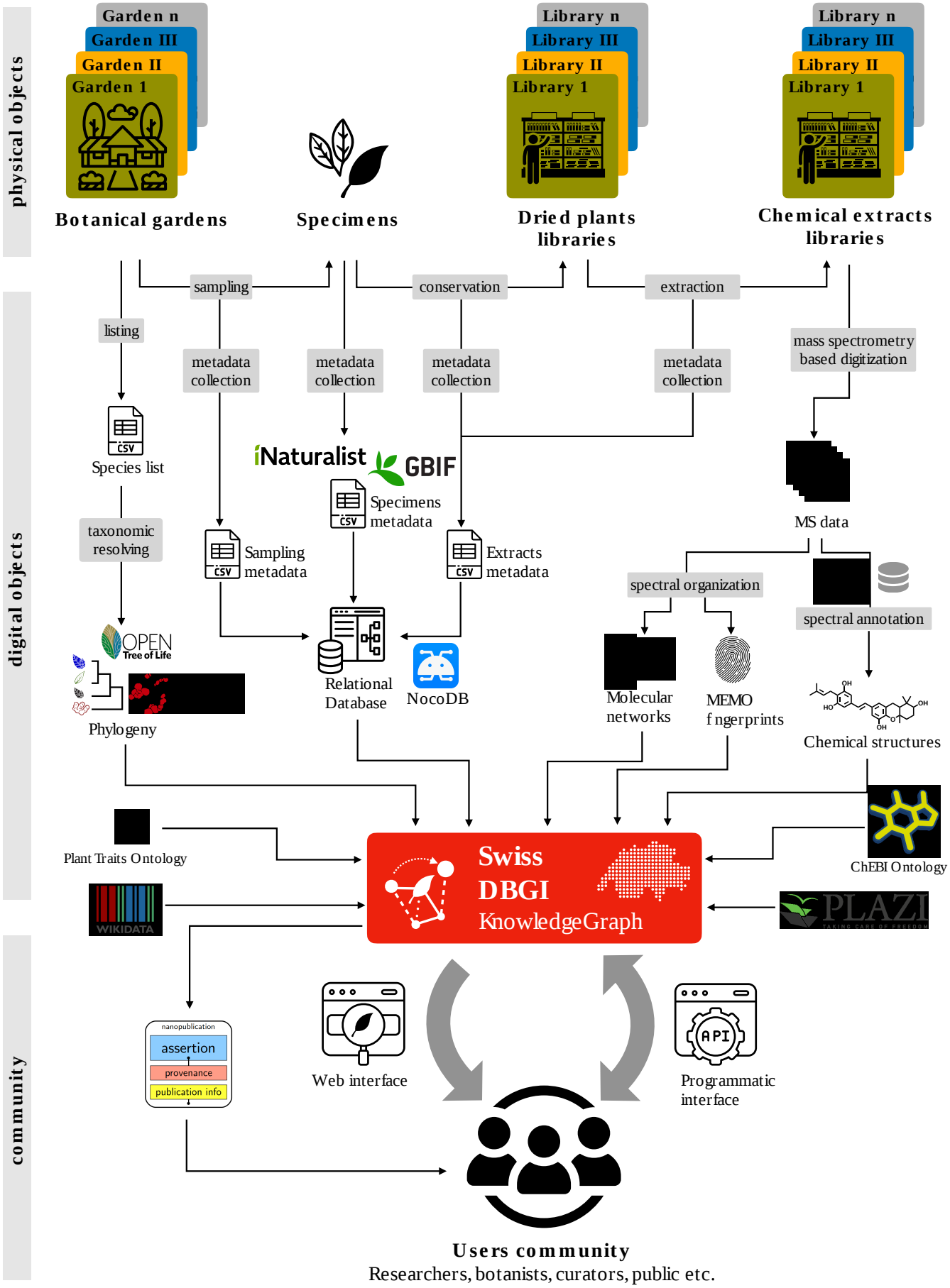

Figure 3: Data types and fluxes in the DBGI.

Digital objects. For all operations occurring on physical objects (sampling, conservation, extraction), metadata are collected to document the experiment. For each botanical garden, data collection is made at the species level. A species is collected for each garden, curated and taxonomically resolved (using the Open Tree of Life framework) in order to be compared across gardens. The Botalista platform will also be exploited at this step. For each collected sample, data are acquired at a finer granularity (namely at the specimen level). Here we take advantage of the iNaturalist platform and app. Using a smartphone, pictures of the sampled specimen (including eventual label in the botanical gardens, sampled organ and collection label), collector identity, date and geolocation are conveniently captured at the time of the collection. This data is then automatically collected by the iNaturalist DBGI project. The data of the project can then be programmatically accessed via the iNaturalist API. All species, specimens and experimental metadata will be collected and managed through an SQL database and accessed through a NocoDB instance for a convenient tracking of the samples by the DBGI participants.

The mass-spectrometry digitization then constitutes the core of the chemical information acquisition process. We use Ultra High Performance Liquid Chromatography coupled to High Resolution Mass Spectrometry (UHPLC-HRMS) to acquire fragmentation data in an untargeted fashion. Building on our computational metabolomics expertise we then organize and annotate the acquired pool of MS data. Here we will take advantage of five central tools (four of which were conceived by us). Molecular networking [7] will serve as a basis for spectral organization. The metabolite annotation will be performed by spectral matching against a theoretical natural products spectral database [8] and via a taxonomically informed scoring process [9] fed by the widest open resource of natural products biological occurrences (LOTUS [10]).

Dissemination of the results

The DBGI conducts this project following the Open Science principles, and by following the Open Notebook Science concepts. This approach allows all research artifacts (e.g. research proposals, drafts, ideas, source code, raw and processed data etc.) produced in the frame of the DBGI to be publicly available immediately, from the moment of their production, and not only after peer-reviewed publication. To implement the DBGI Open Notebook we employ Dendron, an open-source and lightweight note-taking and knowledge management software. Dendrons are built using an ingenious system of markdown files hierarchically organized based on their filename. This allows for extremely efficient note searching and refactoring of the hierarchies. Dendrons can be conveniently shared across members of the DBGI, versioned via git and automatically published as websites. The DBGI Dendron can be browsed at http://www.dbgi.org/dendron-dbgi/. Regarding raw data sharing, specimen-related information are hosted on the iNaturalist DBGI project home page and pictures are shared under a permissive CC0 license allowing further reuse in Wikidata for example. Mass spectrometry profiles and metabolite annotation files will be hosted on the MassIVE data platform where they will benefit from a permanent DOI.
All the code written in the frame of the DBGI will be publicly shared and versioned through the DBGI Github organization. Ideas, comments and issues will be collected using Github discussions.

DBGI Consortium

Note: the DBGI is welcoming any researchers interested to join the initiative. We expect people to participate according to their ressource/time/interest at the level they suit.

Initiators

- Pierre-Marie Allard (COMMONS Lab, University of Fribourg)
- Emmanuel Defossez (Institute of Biology, University of Neuchâtel & JBN)

Core team

We need you !
You have ca. 2 hours / week to dedicate to the DBGI plus time for 6 meetings a year ? You are willing to lead a group of Collaborators (see below) or gather Expert knowledge (see below) for the following areas.

Sampling & Collections Management

Metabolomics & Computational Mass Spectrometry

Linked data & Knowledge management

Open Science & Dissemination

Fundamental & Applied Research (from functional ecology to drug discovery)

Biodiversity Conservation

Collaborators

You are willing to put your hands in the dirt and concretely contribute to the DBGI under the following areas. We need you ! If you have expert knowledge to share but not that much time see Expert section Sampling & Collections Management Edouard Bruelhart (COMMONS Lab, University of Fribourg) Gregor Kozlowski (JBUF) ??? (to be contacted) Blaise Mulhauser (JBN) Nadir Alvarez (Université de Genève) Donat Agosti (Plazi) Cyril Boillat (Botalista) ??? (to be contacted) Laurent Kneubuhl (Botalista) ??? (to be contacted) Brian Sedio (University of Texas at Austin) Metabolomics & Computational Mass Spectrometry Ming Wang (University of Riverside) ??? (to be contacted) Gaétan Glauser (University of Neuchâtel) ??? (to be contacted) Brian Sedio (University of Texas at Austin) Linked data & Knowledge management ??? (to be contacted) Philippe Cudré-Mauroux (University of Fribourg) Christophe Dessimoz (University of Lausanne) Donat Agosti (Plazi) Cyril Boillat (Botalista) ??? (to be contacted) Laurent Kneubuhl (Botalista) ??? (to be contacted) Jakub Galgonek (Elixir Prague) ??? (to be contacted) Marco Pagni (SIB) Tarcisio Mendes (SIB) Ana-Claudia Sima (SIB) Open Science & Dissemination Christophe Dessimoz (University of Lausanne) Donat Agosti (Plazi) Henry Lütcke (ETHZ) Bernd Rinn (ETHZ) Caterina Barillari (ETHZ) Fundamental & Applied Research (from functional ecology to drug discovery) Sergio Rassmann (University of Neuchâtel) Thomas Walker (University of Neuchâtel) ??? (to be contacted) Patrice Descombes (University of Lausanne) ??? (to be contacted) Nadir Alvarez (Université de Genève) ??? (to be contacted) Brian Sedio (University of Texas at Austin) Biodiversity Conservation Gregor Kozlowski (JBUF) ??? (to be contacted) Patrice Descombes (University of

Lausanne) Experts You have expertise in the following areas and you are OK that we pick your brain for let's say … a one hour meeting each month. Sampling & Collections Management Gregor Kozlowski (JBUF) ??? (to be contacted) Blaise Mulhauser (JBN) Nadir Alvarez (Université de Genève) Donat Agosti (Plazi) Cyril Boillat (Botalista) ??? (to be contacted) Laurent Kneubuhl (Botalista) Metabolomics & Computational Mass Spectrometry Ming Wang (University of Riverside) ??? (to be contacted) Gaétan Glauser (University of Neuchâtel) ??? (to be contacted) Brian Sedio (University of Texas at Austin) Linked data & Knowledge management ??? (to be contacted) Philippe Cudré-Mauroux (University of Fribourg) Christophe Dessimoz (University of Lausanne) Donat Agosti (Plazi) Cyril Boillat (Botalista) ??? (to be contacted) Laurent Kneubuhl (Botalista) ??? (to be contacted) Jakub Galgonek (Elixir Prague) ??? (to be contacted) Marco Pagni (SIB) Tarcisio Mendes (SIB) Ana-Claudia Sima (SIB) Open Science & Dissemination Christophe Dessimoz (University of Lausanne) Donat Agosti (Plazi) Henry Lütcke (ETHZ) Bernd Rinn (ETHZ) Caterina Barillari (ETHZ) Fundamental & Applied Research (from functional ecology to drug discovery) Sergio Rassmann (University of Neuchâtel) Thomas Walker (University of Neuchâtel) ??? (to be contacted) Patrice Descombes (University of Lausanne) ??? (to be contacted) Nadir Alvarez (Université de Genève) ??? (to be contacted) Brian Sedio (University of Texas at Austin)

Biodiversity Conservation Gregor Kozlowski (JBUF) ??? (to be contacted) Patrice Descombes (University of Lausanne) Botanical Gardens Jardin Botanique de l'Université de Fribourg (JBUF) Jardin Botanique de Neuchatel (JBN) ??? Conservatoire et Jardins Botanique de Genève (CJBG) ??? Jardin Botanique de Lausanne (JBL)

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Basic formatting

Bold text

Semi-bold text

Italic text

Combined *italics and* ***bold***

~~Strikethrough~~

1. Ordered list item
2. Ordered list item
    a. Sub-item
    b. Sub-item
        i. Sub-sub-item
3. Ordered list item
    a. Sub-item

- List item

- List item
- List item

subscript: H_2O is a liquid

superscript: 2^{10} is 1024.

unicode superscripts^{0123456789}

unicode subscripts$_{0123456789}$

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Putting each sentence on its own line has numerous benefits with regard to editing and version control.

Line break without starting a new paragraph by putting
two spaces at end of line.

Document organization

Document section headings:

Heading 1

Heading 2

Heading 3

Heading 4

Heading 5

Heading 6

A heading centered on its own printed page

Horizontal rule:

`Heading 1`'s are recommended to be reserved for the title of the manuscript.

`Heading 2`'s are recommended for broad sections such as *Abstract*, *Methods*, *Conclusion*, etc.

`Heading 3`'s and `Heading 4`'s are recommended for sub-sections.

Links

Bare URL link: https://manubot.org

Long link with lots of words and stuff and junk and bleep and blah and stuff and other stuff and more stuff yeah

Link with text

Link with hover text

Link by reference

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Citation by DOI [11].

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Citation by PubMed ID [**pubmed:30718888?**].

Citation by Wikidata ID [13].

Citation by alias [14].

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Citation tags (i.e. aliases) can be defined in their own paragraphs using Markdown's reference link syntax:

Referencing figures, tables, equations

Figure 4

Figure 5

Figure 6

Figure 7

Table 1

Equation 1

Equation 2

Quotes and code

> Quoted text

> Quoted block of text
>
> Two roads diverged in a wood, and I—
> I took the one less traveled by,
> And that has made all the difference.

Code `in the middle` of normal text, aka `inline code`.

Code block with Python syntax highlighting:

```
from manubot.cite.doi import expand_short_doi

def test_expand_short_doi():
    doi = expand_short_doi("10/c3bp")
    # a string too long to fit within page:
    assert doi == "10.25313/2524-2695-2018-3-vliyanie-enhansera-copia-i-
        insulyatora-gypsy-na-sintez-ernk-modifikatsii-hromatina-i-
        svyazyvanie-insulyatornyh-belkov-vtransfetsirovannyh-geneticheskih-
        konstruktsiyah"
```

Code block with no syntax highlighting:

```
Exporting HTML manuscript
Exporting DOCX manuscript
Exporting PDF manuscript
```

Figures

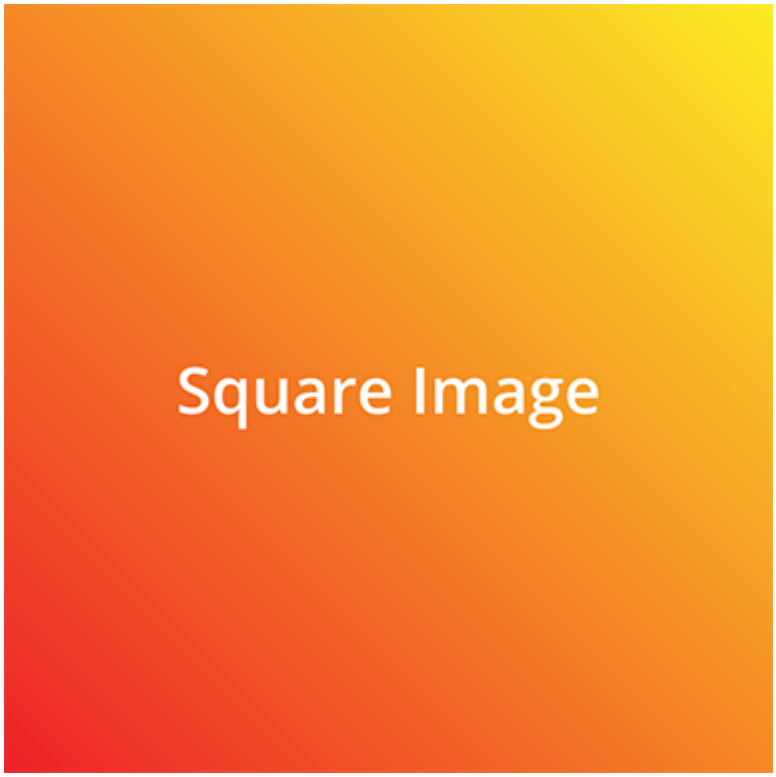

Figure 4: A square image at actual size and with a bottom caption. Loaded from the latest version of image on GitHub.

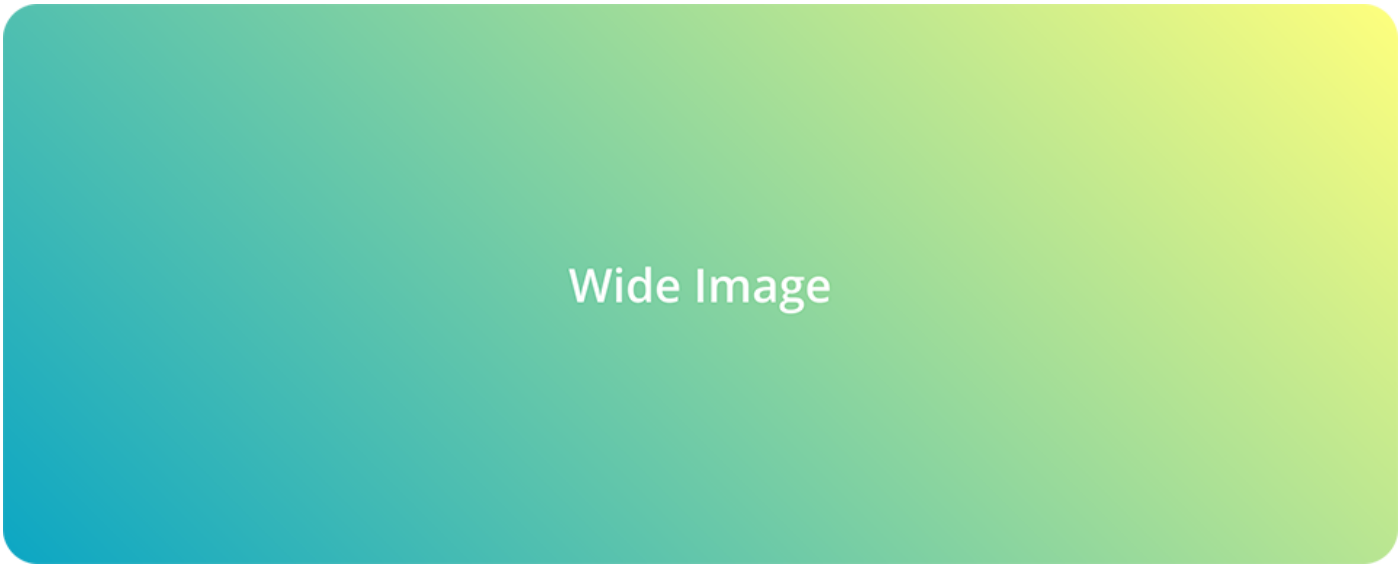

Figure 5: An image too wide to fit within page at full size. Loaded from a specific (hashed) version of the image on GitHub.

Figure 6: A tall image with a specified height. Loaded from a specific (hashed) version of the image on GitHub.

Figure 7: A vector `.svg` image loaded from GitHub. The parameter `sanitize=true` is necessary to properly load SVGs hosted via GitHub URLs. White background specified to serve as a backdrop for transparent sections of the image.

Tables

Table 1: A table with a top caption and specified relative column widths.

Bowling Scores	**Jane**	**John**	**Alice**	**Bob**
Game 1	150	187	210	105
Game 2	98	202	197	102
Game 3	123	180	238	134

Table 2: A table too wide to fit within page.

	Digits 1-33	**Digits 34-66**	**Digits 67-99**	**Ref.**
pi	3.14159265358979323 846264338327950	28841971693993751 0582097494459230	78164062862089986 2803482534211706	`piday.org`
e	2.71828182845904523 536028747135266	24977572470936999 5957496696762772	40766303535475945 7138217852516642	`nasa.gov`

Table 3: A table with merged cells using the `attributes` plugin.

	Colors	
Size	**Text Color**	**Background Color**
big	blue	orange
small	black	white

Equations

A LaTeX equation:

$$\int_0^\infty e^{-x^2} dx = \frac{\sqrt{\pi}}{2} \tag{1}$$

An equation too long to fit within page:

$$x = a + b + c + d + e + f + g + h + i + j + k + l + m + n + o + p + q + r + s + t + u + v + w + x + y + z + 1 + 2 + 3 + 4 + 5 + 6 + 7 + 8 + 9 \tag{2}$$

Special

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Light Grey Banner
useful for *general information* - manubot.org

Blue Banner
useful for *important information* - manubot.org

Light Red Banner
useful for *warnings* - manubot.org

References

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David Tilman, Forest Isbell, Jane M Cowles
Annual Review of Ecology, Evolution, and Systematics (2014-11-23) https://doi.org/gf5tpq
DOI: 10.1146/annurev-ecolsys-120213-091917

2. **Biodiversity and Ecosystem Functioning: Current Knowledge and Future Challenges**
M Loreau, S Naeem, P Inchausti, J Bengtsson, JP Grime, A Hector, DU Hooper, MA Huston, D Raffaelli, B Schmid, ... DA Wardle
Science (2001-10-26) https://doi.org/cnf65t
DOI: 10.1126/science.1064088 · PMID: 11679658

3. **Linking biodiversity to ecosystem function: implications for conservation ecology**
MW Schwartz, CA Brigham, JD Hoeksema, KG Lyons, MH Mills, PJ van Mantgem
Oecologia (2000-02-23) https://doi.org/cjwdg4
DOI: 10.1007/s004420050035 · PMID: 28308280

4. **Number of species on Earth tagged at 8.7 million**
Lee Sweetlove
Nature (2011-08-23) https://doi.org/djwm2d
DOI: 10.1038/news.2011.498

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IPBES
Zenodo (2019-05-04) https://doi.org/grbxsr
DOI: 10.5281/zenodo.6417333

6. **The misunderstood sixth mass extinction**
Gerardo Ceballos, Paul R Ehrlich
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DOI: 10.1126/science.aau0191 · PMID: 29880679

7. **Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking**
Mingxun Wang, Jeremy J Carver, Vanessa V Phelan, Laura M Sanchez, Neha Garg, Yao Peng, Don Duy Nguyen, Jeramie Watrous, Clifford A Kapono, Tal Luzzatto-Knaan, ... Nuno Bandeira
Nature Biotechnology (2016-08) https://doi.org/f8zxbs
DOI: 10.1038/nbt.3597 · PMID: 27504778 · PMCID: PMC5321674

8. **Integration of Molecular Networking and In-Silico MS/MS Fragmentation for Natural Products Dereplication**
Pierre-Marie Allard, Tiphaine Péresse, Jonathan Bisson, Katia Gindro, Laurence Marcourt, Van Cuong Pham, Fanny Roussi, Marc Litaudon, Jean-Luc Wolfender
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DOI: 10.1021/acs.analchem.5b04804 · PMID: 26882108

9. **Taxonomically Informed Scoring Enhances Confidence in Natural Products Annotation**
Adriano Rutz, Miwa Dounoue-Kubo, Simon Ollivier, Jonathan Bisson, Mohsen Bagheri, Tongchai Saesong, Samad Nejad Ebrahimi, Kornkanok Ingkaninan, Jean-Luc Wolfender, Pierre-Marie Allard
Frontiers in Plant Science (2019-10-25) https://doi.org/fm73
DOI: 10.3389/fpls.2019.01329 · PMID: 31708947 · PMCID: PMC6824209

10. **The LOTUS initiative for open knowledge management in natural products research**
Adriano Rutz, Maria Sorokina, Jakub Galgonek, Daniel Mietchen, Egon Willighagen, Arnaud Gaudry, James G Graham, Ralf Stephan, Roderic Page, Jiří Vondrášek, … Pierre-Marie Allard
eLife (2022-05-26) https://doi.org/gpzrr8
DOI: 10.7554/elife.70780 · PMID: 35616633 · PMCID: PMC9135406

11. **Sci-Hub provides access to nearly all scholarly literature**
Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene
eLife (2018-03-01) https://doi.org/ckcj
DOI: 10.7554/elife.32822 · PMID: 29424689 · PMCID: PMC5832410

12. **Reproducibility of computational workflows is automated using continuous analysis**
Brett K Beaulieu-Jones, Casey S Greene
Nature biotechnology (2017-04) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/
DOI: 10.1038/nbt.3780 · PMID: 28288103 · PMCID: PMC6103790

13. **Plan S: Accelerating the transition to full and immediate Open Access to scientific publications**
cOAlition S
(2018-09-04) https://www.wikidata.org/wiki/Q56458321

14. **Opportunities and obstacles for deep learning in biology and medicine**
Travers Ching, Daniel S Himmelstein, Brett K Beaulieu-Jones, Alexandr A Kalinin, Brian T Do, Gregory P Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M Hoffman, … Casey S Greene
Journal of The Royal Society Interface (2018-04) https://doi.org/gddkhn
DOI: 10.1098/rsif.2017.0387 · PMID: 29618526 · PMCID: PMC5938574

15. **Open collaborative writing with Manubot**
Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter
PLOS Computational Biology (2019-06-24) https://doi.org/c7np
DOI: 10.1371/journal.pcbi.1007128 · PMID: 31233491 · PMCID: PMC6611653