

Main-Title

Sub-Title

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A tagline for the report.

NBIS - National Bioninformatics Infrastructure Sweden
Science for Life laboratory

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1 Description

Delete this cell before converting to PDF.

Getting Started

This notebook is converted to PDF using ([ipypublish](#)). This requires a LaTeX installation. It is crucial that you show cell metadata, and edit the notebook metadata.

Metadata

There are three levels of metadata: - For notebook level: in the Jupyter Notebook Toolbar go to Edit -> Edit Notebook Metadata. **Edit this for every report.** - For cell level: in the Jupyter Notebook Toolbar go to View -> Cell Toolbar -> Edit Metadata and a button will appear above each cell. - For output level: using `IPython.display.display(obj,metadata={"ipub":{}})`, you can set metadata specific to a certain output. Options set at the output level will override options set at the cell level. For an example of this, see [Multiple Outputs from a Single Code Cell](#). - See [the full metadata definitions](#) to learn how to define different metadata blocks for your cells.

Outputting

To convert to pdf run `nbpublish -pdf -lb Example.ipynb --pdf-debug --clear-files - nbpublish -pdf -lb -f latex_ipypublish_nocode Example.ipynb --pdf-debug --clear-files`
#hides notebook code unless allowed (see below)

This permits merging multiple .ipynb into a single .pdf, preserving the metadata from the first notebook. See [ipypublish](#) for more info. If you want to merge notebooks and preserve cross-referencing between them consider using [bookbook](#).

To do

- Implement dynamic python markdown
- Edit TeX template to include NBIS logo and other info in front page
- Add xref in NBIS text.

2 Support Request

Some markdown text.

Description: (From redmine)

Work Log Detailed steps from contract, if possible

List:

- something
- something else

Numbered list

1. something
2. something else

3 Methods

3.1 Method Section 1

A great method description starts here... ^[1]

4 Results

4.1 Results 1

Some good results...

5 Closing procedures

You should soon be contacted by one of our managers, Jessica Lindvall (jessica.lindvall@nbis.se) or Henrik Lantz (henrik.lantz@nbis.se), with a request to close down the project in our internal system and for invoicing matters. If we do not hear from you within **30 days** the project will be automatically closed and invoice sent. Again, we would like to remind you about data responsibility and acknowledgements, see [Data Responsibilities](#) and [Acknowledgements](#).

You are naturally more than welcome to come back to us with further data analysis request at any time via [Support Web](#). **Thank you for using NBIS, we wish you the best of luck with your future research!**

6 Practical Information

Data responsibilities

Unfortunately, NBIS does not have resources to keep any files associated with the support request; we kindly suggest that you safely store the results delivered by us. In addition, we kindly ask that you remove the files from UPPMAX/UPPNEX. The main storage at UPPNEX is optimized for high-speed and parallel access, which makes it expensive and not the right place for long-term archiving. Please be considerate of your fellow researchers by not taking up this expensive space.

The responsibility for data archiving lies with universities and we recommend asking your local IT for support with long-term data storage. The [Data Center](#) at SciLifeLab may also be of help with discussing other options. Please note that special considerations may apply to human-derived, sensitive personal data. This should be handled according to specific laws and regulations as outlined at the [NBIS website](#).

Acknowledgments

If you are presenting the results in a paper, at a workshop or at a conference, we kindly remind you to acknowledge us according to the signed [NBIS User Agreement](#):

NBIS staff should be included as co-authors if the support work leads to a publication and when this is merited in accordance to the ethical recommendations for authorship, i.e. the [ICMJE recommendations](#).

If applicable, please include the NBIS expert as co-author.

If the above is not applicable, please acknowledge NBIS like so: *Support by NBIS (National Bioinformatics Infrastructure Sweden) is gratefully acknowledged.*

In addition, Uppmax kindly asks you to acknowledge UPPMAX and SNIC. If applicable, please add: *The computations were performed on resources provided by SNIC through Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX) under Project [User project number].*

In any and all publications based on data from NGI Sweden, the authors must acknowledge SciLifeLab, NGI and Uppmax, like so: *The authors would like to acknowledge support from Science for Life Laboratory, the National Genomics Infrastructure, NGI, and Uppmax for providing assistance in massive parallel sequencing and computational infrastructure.*

7 Markdown

Below we have the definitions for multiple figures, equations, tables, and so on. This is kept for ease of use.

7.1 Todo notes

an inline todo

Some text.

a todo in
the mar-
gins

7.2 Text Output

```
This is some printed text,  
with a nicely formatted output.
```

8 Images and Figures



Figure 8.1: A nice picture.

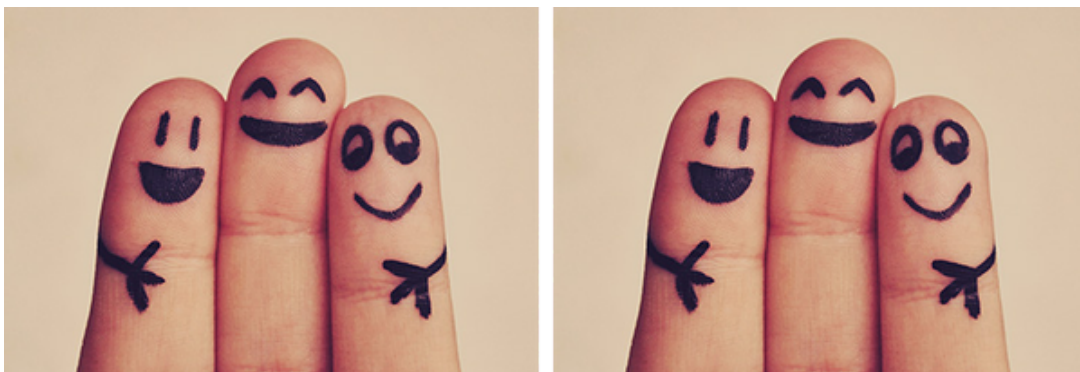


Figure 8.2: Horizontally aligned images.

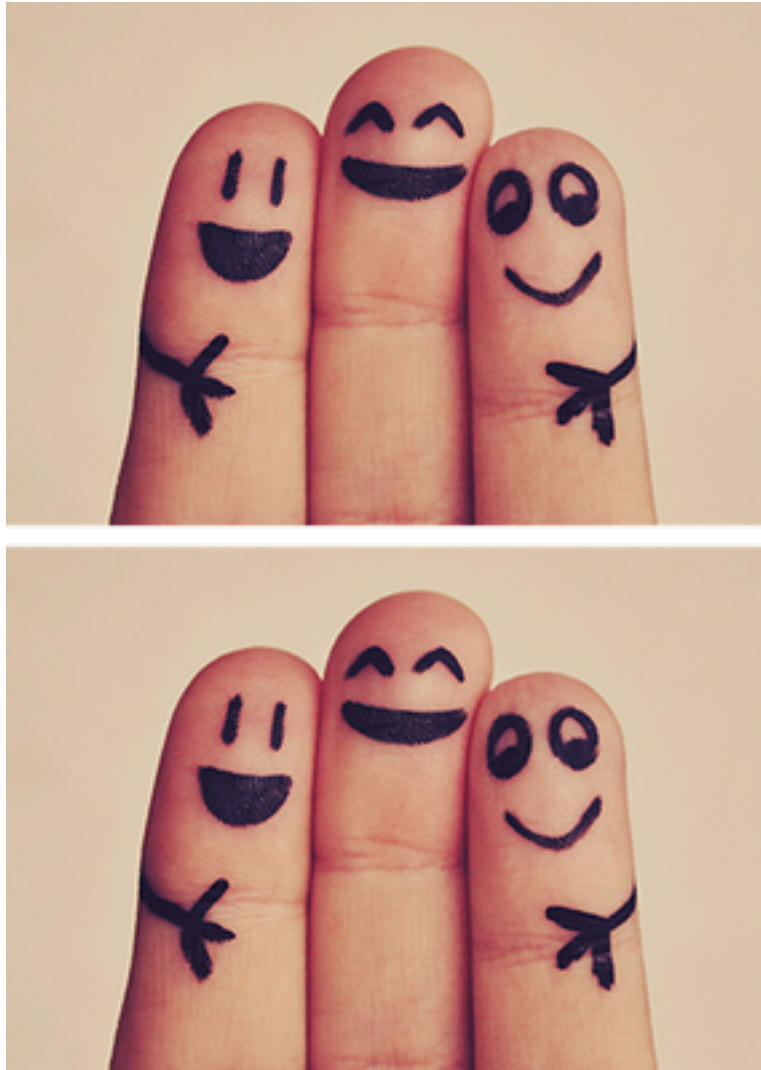


Figure 8.3: Vertically aligned images.

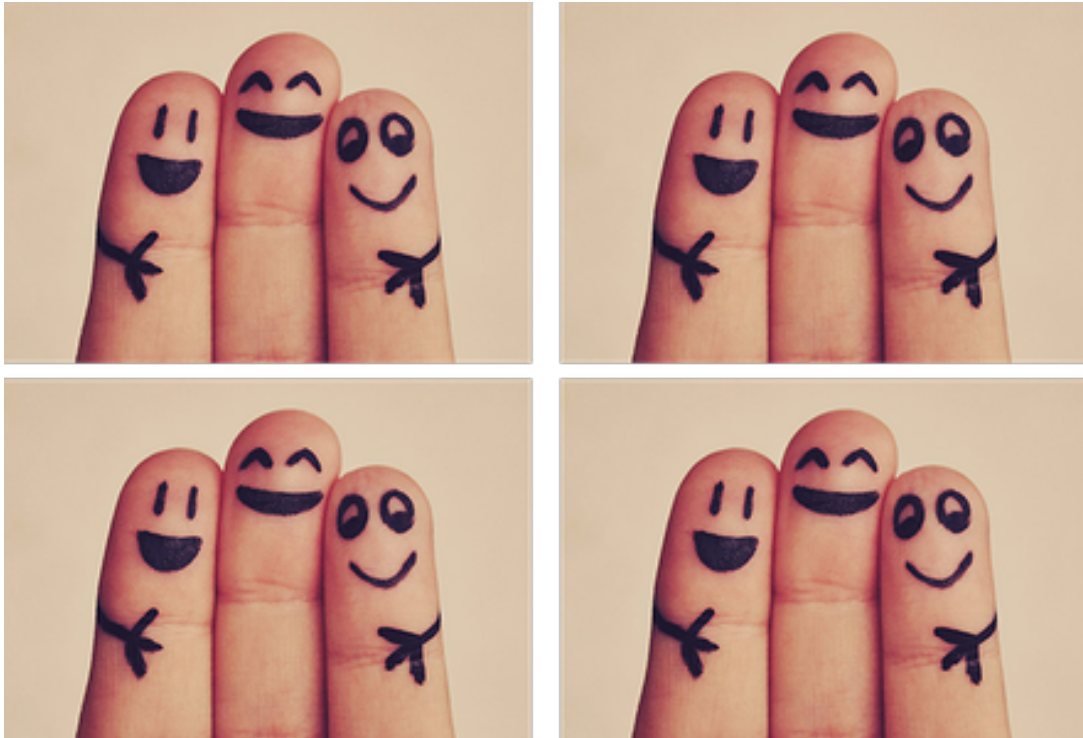


Figure 8.4: Images aligned in a grid.

8.1 References and Citations

To add citations and bibliography, use [Zotero's Firefox plugin](#) and [Zotero Better Bibtex](#). Don't worry if the next crossreferences are not rendered in the markdown, they are rendered on the final PDF.

References to fig. 8.1, table 9.1, eq. 10.2 and code 8.1.

Referencing multiple items: figs. 8.1 to 8.3.

A single^[2] or multiple latex citations^[2,3]

A html citation.^[3]

8.2 Displaying a plot with its code

Code 8.1: The plotting code for a matplotlib figure (fig. 8.5).

```
1 #note the "hideCode": false in the cell's metadata
2 import matplotlib.pyplot as plt
3 plt.scatter(np.random.rand(10), np.random.rand(10),
4             label='data label')
5 plt.ylabel(r'a y label with latex  $\alpha$ ')
6 plt.legend();
```

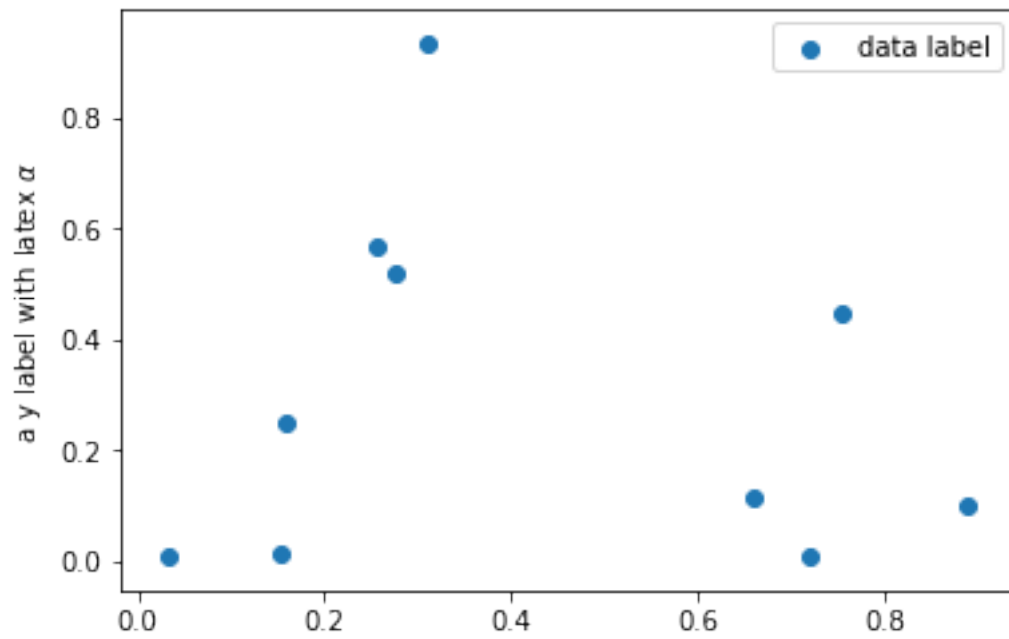


Figure 8.5: A matplotlib figure, with the caption set in the markdowncell above the figure.

8.3 Displaying a plot without its code

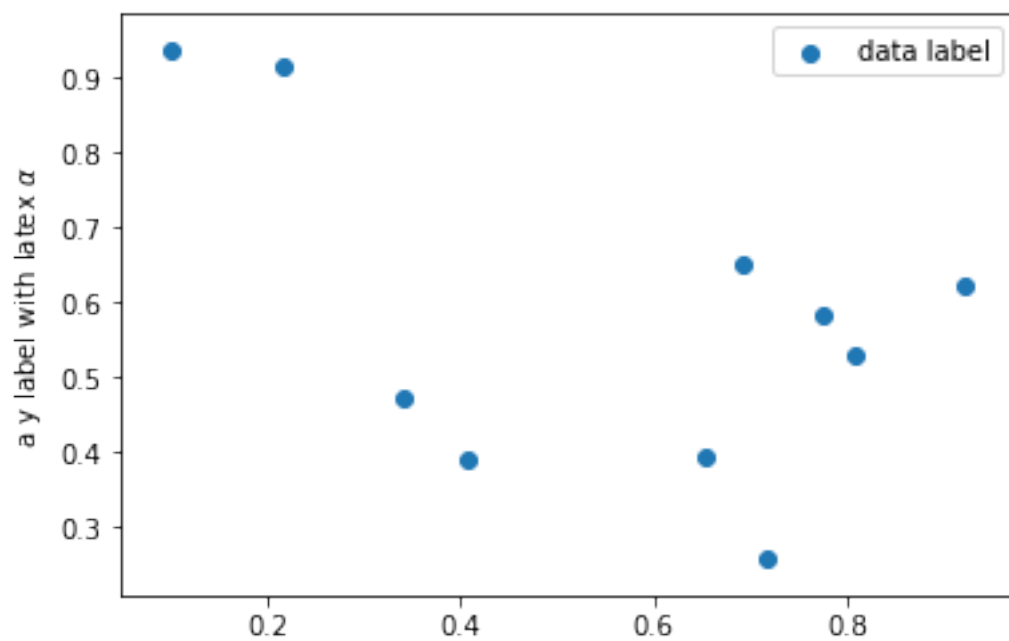


Figure 8.6: A figure with hidden code

9 Tables (with pandas)

Code 9.1: The plotting code for a pandas Dataframe table (table 9.1).

```
1 df = pd.DataFrame(np.random.rand(3,4), columns=['a', 'b', 'c', 'd'])
2 df.a = ['$\delta$', 'x', 'y']
3 df.b = ['l', 'm', 'n']
4 df.set_index(['a', 'b'])
5 df.round(3)
```

Table 9.1: An example of a table created with pandas dataframe.

	a	b	c	d
0	δ	l	0.583	0.279
1	x	m	0.914	0.021
2	y	n	0.333	0.116

10 Equations (with ipython or sympy)

$$a = b + c \quad (10.1)$$

Code 10.1: The plotting code for a sympy equation (eq. 10.2).

```
1 f = sym.Function('f')
2 y,n = sym.symbols('y \alpha')
3 f = y(n)-2*y(n-1/sym.pi)-5*y(n-2)
4 sym.rsolve(f,y(n),[1,4])
```

$$\left(\sqrt{5}i\right)^{\alpha}\left(\frac{1}{2}-\frac{2i}{5}\sqrt{5}\right)+\left(-\sqrt{5}i\right)^{\alpha}\left(\frac{1}{2}+\frac{2i}{5}\sqrt{5}\right) \quad (10.2)$$

11 Embed interactive HTML (like ipywidgets)

Interactive HTML was created using ipyvvolume and will render below in .html type outputs:

12 References

- [1] T. Rolland, M. Tasan, B. Charloteaux, S. J. Pevzner, Q. Zhong, N. Sahni, S. Yi, I. Lemmens, C. Fontanillo, R. Mosca, A. Kamburov, S. D. Ghiassian, X. Yang, L. Ghamsari, D. Balcha, B. E. Begg, P. Braun, M. Brehme, M. P. Broly, A. R. Carvunis, D. Convery-Zupan, R. Corominas, J. Coulombe-Huntington, E. Dann, M. Dreze, A. Dricot, C. Fan, E. Franzosa, F. Gebreab, B. J. Gutierrez, M. F. Hardy, M. Jin, S. Kang, R. Kiros, G. N. Lin, K. Luck, A. MacWilliams, J. Menche, R. R. Murray, A. Palagi, M. M. Poulin, X. Rambout, J. Rasla, P. Reichert, V. Romero, E. Ruysinck, J. M. Sahalie, A. Scholz, A. A. Shah, A. Sharma, Y. Shen, K. Spirohn, S. Tam, A. O. Tejada, S. A. Trigg, J. C. Twizere, K. Vega, J. Walsh, M. E. Cusick, Y. Xia, A. L. Barabasi, L. M. Iakoucheva, P. Aloy, J. De Las Rivas, J. Tavernier, M. A. Calderwood, D. E. Hill, T. Hao, F. P. Roth, and M. Vidal. A proteome-scale map of the human interactome network. *Cell*, 159(5):1212–26, November 2014. ISSN 1097-4172 (Electronic) 0092-8674 (Linking). doi:[10.1016/j.cell.2014.10.050](https://doi.org/10.1016/j.cell.2014.10.050).
- [2] P. J. Thul, L. Akesson, M. Wiking, D. Mahdessian, A. Geladaki, H. Ait Blal, T. Alm, A. Asplund, L. Bjork, L. M. Breckels, A. Backstrom, F. Danielsson, L. Fagerberg, J. Fall, L. Gatto, C. Gnann, S. Hober, M. Hjelmare, F. Johansson, S. Lee, C. Lindskog, J. Mulder, C. M. Mulvey, P. Nilsson, P. Oksvold, J. Rockberg, R. Schutten, J. M. Schwenk, A. Sivertsson, E. Sjostedt, M. Skogs, C. Stadler, D. P. Sullivan, H. Tegel, C. Winsnes, C. Zhang, M. Zwahlen, A. Mardinoglu, F. Ponten, K. von Feilitzen, K. S. Lilley, M. Uhlen, and E. Lundberg. A subcellular map of the human proteome. *Science*, 356(6340), May 2017. ISSN 1095-9203 (Electronic) 0036-8075 (Linking). doi:[10.1126/science.aal3321](https://doi.org/10.1126/science.aal3321).
- [3] M. Uhlen, C. Zhang, S. Lee, E. Sjostedt, L. Fagerberg, G. Bidkhori, R. Benfeitas, M. Arif, Z. Liu, F. Edfors, K. Sanli, K. von Feilitzen, P. Oksvold, E. Lundberg, S. Hober, P. Nilsson, J. Mattsson, J. M. Schwenk, H. Brunnstrom, B. Glimelius, T. Sjoblom, P. H. Edqvist, D. Djureinovic, P. Micke, C. Lindskog, A. Mardinoglu, and F. Ponten. A pathology atlas of the human cancer transcriptome. *Science*, 357(6352), August 2017. ISSN 1095-9203 (Electronic) 0036-8075 (Linking). doi:[10.1126/science.aan2507](https://doi.org/10.1126/science.aan2507).