Rendez-vous de l'info scientifique

Traitement de données avec Pandas & Jupyter notebooks



pandas $y_{it} = \beta' x_{it} + \mu_i + \epsilon_{it}$







Pablo Iriarte - pablo.iriarte@unige.ch / DIS

25 septembre 2024



Programme

Introduction

- Historique
- Excel et les erreurs scientifiques
- Reproducibility Crisis & Data deluge

Jupyter Notebooks

- Famille d'outils
- Accès au JupyterHub du cours ou installation via la distribution Anaconda
- Créer, organiser et partager des notebooks

Pandas

- Importer et exporter des données
- Manipuler et analyser les données
- Générer des graphiques



Historique

- iPython (2001->) https://ipython.org/
- Jupyter (2014 ->) https://jupyter.org/
- Famille d'outils
 - Jupyter Hub : https://jupyterhub.readthedocs.io/
 - Jupyter Lab : https://jupyterlab.readthedocs.io/
 - NB viewer : https://nbviewer.jupyter.org/
 - Binder : https://mybinder.org/



Historique : Jupiter

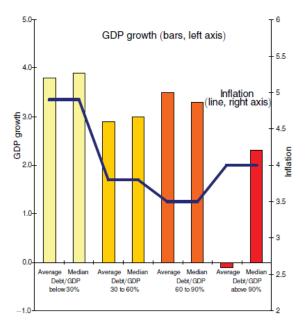


https://commons.wikimedia.org/wiki/File:Galileo manuscript.png

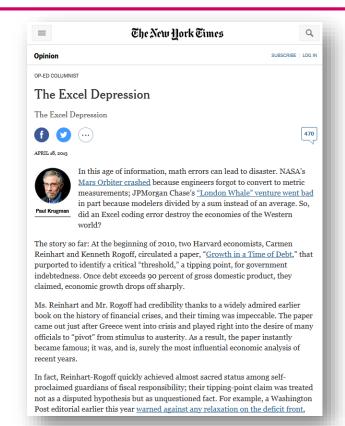


Excel et les erreurs scientifiques

L'exemple du «Reinhart-Rogoff error»



Reinhart, Carmen M., and Kenneth S. Rogoff. 2010. DOI:10.1257/aer.100.2.573

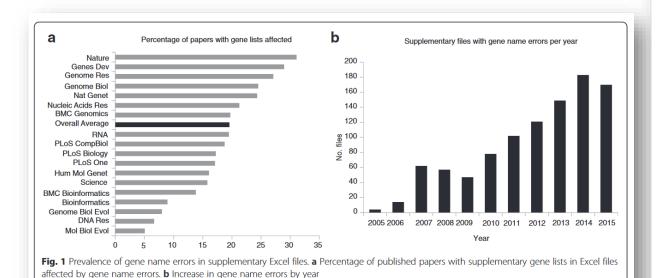


https://www.nytimes.com/2013/04/19/opinion/krugman-the-excel-depression.html



Excel et les erreurs scientifiques

L'exemple de la conversion des données



iemann et al. Genome Biology (2016) 17:177 OL 10 1185/s13059.016.1044.7

Genome Biology

COMMENT

Open Access

Gene name errors are widespread in the scientific literature



Mark Ziemann¹, Yotam Eren^{1,2} and Assam El-Osta^{1,3*}

Abstra

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbles. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain emoneous gene name conversions.

Keywords: Microsoft Excel, Gene symbol, Supplementary data

Abbreviations: GEO, Gene Expression Omnibus;

The problem of Excel software (Microsoft Corp., Redmond, WA, USA) inadvertently converting gene symbols to dates and floating-point numbers was originally described in 2004 [1]. For example, gene symbols such as SEPT2 (Septin 2) and MARCHI [Membrane-Associated Ring Finger (C3HC4) 1, E3 Ubiquitin Protein Ligase] are converted by default to '2-Sep' and '1-Mar,' respect ively. Furthermore, RIKEN identifiers were described to be automatically converted to floating point numbers (i.e. from accession '2310009E13' to '2.31E+13'). Since that report, we have uncovered further instances where gene symbols were converted to dates in supplementary data of recently published papers (e.g. 'SEPT2' converted to '2006/09/02'). This suggests that gene name errors continue to be a problem in supplementary files accompanying articles. Inadvertent gene symbol conversion is roblematic because these supplementary files are an important resource in the genomics community that are

*Correspondence: Assam£l-Osta@bakeridi.cedu.au 'baker ID Heart & Dubetes Innibitote, The Affred Medical Research and Education Precinct, Melbourne, Victoria 3004, Australia 'Certana' Clinical School, Faculty of Medicine, Monath University, Clyston, Victoria 3166, Australia frequently reused. Our aim here is to raise awareness of the problem.

We downloaded and screened supplem from 18 journals published between 2005 and 2015 using a suite of shell scripts. Excel files (.xls and.xlsx suffixes) were converted to tabular separated files (tsv) with ssconvert (v1.12.9). Each sheet within the Excel file was converted to a separate tsv file. Each column of data in the tsy file was screened for the presence of gene sym bols. If the first 20 rows of a column contained five or more gene symbols, then it was suspected to be a list of gene symbols, and then a regular expression (regex) search of the entire column was applied to identify gene symbol errors. Official gene symbols from Ensembl version 82, accessed November 2015, were obtained for Arabidopsis thaliana, Caenorhabditis elegans, Drosoph ila melanogaster, Danio rerio, Escherichia coli, Gallus gallus, Homo sapiens, Mus musculus, Oryza sativa and Saccharomyces cerevisiae [2]. The regex search used was similar to that described previously by Zeeberg and colleagues [1], with the added screen for dates in other formats (e.g. DD/MM/YY and MM-DD-YY). To expedite analysis of supplementary files from multi-disciplinary journals, we limited the articles screened to those that have the keyword 'genome' in the title or abstract (Science Nature and PLoS One). Excel files (xls andxlsx) deposited in NCBI Gene Expression Omnibus (GEO) [3] were also screened in the same way (files released 2005-2015). All URLs screened, results and scripts used in this study are currently available at SourceForge (https://sourceforge net/projects/genenameerrorsscreen/). Scripts were run on Ubuntu v14.04 LTS with GNU bash, version 4.3.11. These findings were verified manually by downloading and checking Excel files from every paper and GEO file suspected to include gene name errors.

Supplementary files in Excel format from 18 journals published from 2005 to 2015 were programmatically screened for the presence of gene name errors. In total, we screened 35,175 supplementary Excel files, finding 7467 gene lists attached to 3597 published papers. We

() BioMed Centra

6.2016 The Author(s). Open Access This article is distributed under the terms of the Creative Common Attribution 4.0 international Literature High/Ternationscriptments/high/40, which permits unrestricted use, distribution, and reproduction is any medium, provided you give appropriate credit to the original author(s) and the source, provides also the Creative Commons Scores, and indicate if changes were made. The Creative Commons Scores, and footbase of Author Author(s) and the source, provides also the Creative Commons Scores, and reduction with the Creative Commons Scores, and reduction with the Creative Commons Scores.

Ziemann et al. 2016. DOI:10.1186/s13059-016-1044-7

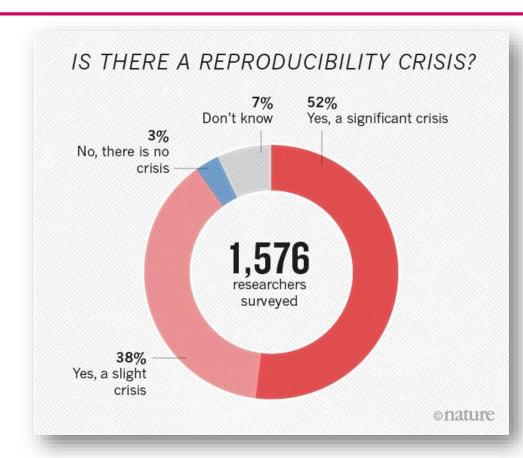


Reproductibilité et Open Science

La science en crise? 1,500 scientists lift the lid on reproducibility

Baker 2016, Nature 533

https://doi.org/10.1038/533452a

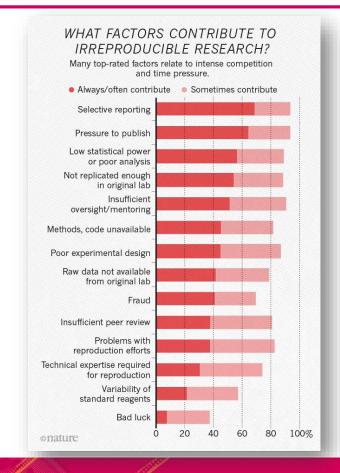




Reproductibilité et Open Science

La science en crise? 1,500 scientists lift the lid on reproducibility

Baker 2016, Nature 533 https://doi.org/10.1038/533452a





Reproductibilité et Open Science

Wired

https://www.wired.com/2017/04/want-fix-sciences-replication-crisis-replicate/

WANT TO FIX SCIENCE'S REPLICATION CRISIS? THEN REPLICATE





Big Data et Open Data

Quantifying the Data Deluge and the Data Drought

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=2984851

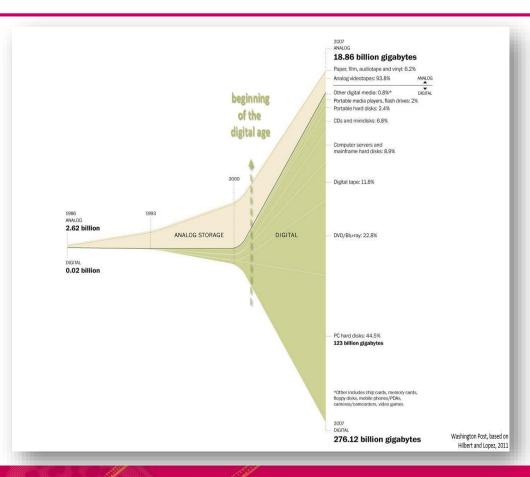
Nombreux réservoirs ouverts

Kaggle: https://www.kaggle.com

Github: http://github.com

WikiData: https://www.wikidata.org

Statistique historique : https://hsso.ch



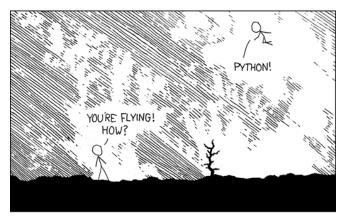


Excel: limitations

Liste complète :

https://support.office.com/en-us/article/excelspecifications-and-limits-1672b34d-7043-467e-8e27-269d656771c3







https://www.xkcd.com/353/











https://pandas.pydata.org



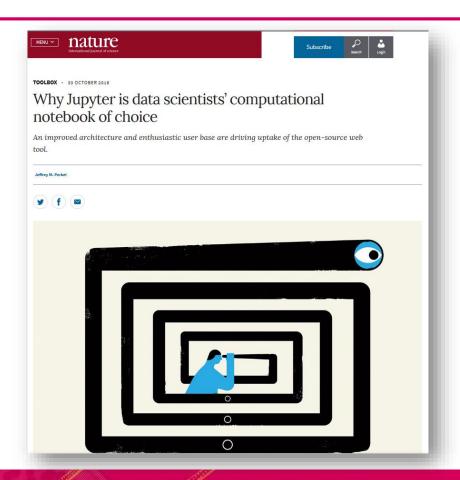
https://www.pinterest.ch/pin/155303887164507907/



Reproductibilité et Open Science

Nature

https://www.nature.com/articles/d41586-018-07196-1

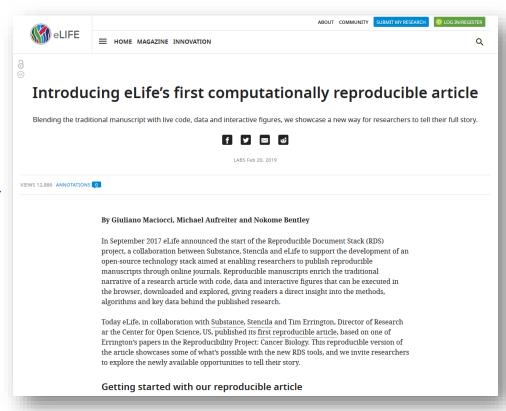




Reproductibilité et Open Science

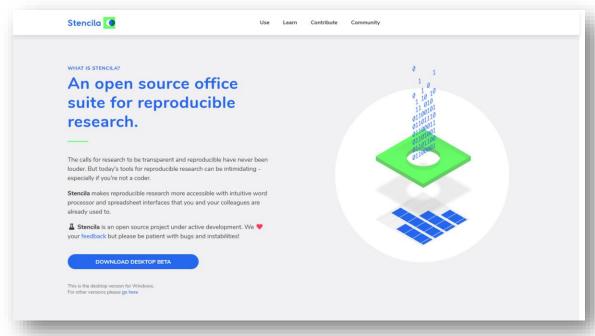
eLife

https://elifesciences.org/labs/ad58f08d/introducing-elife-s-first-computationally-reproducible-article



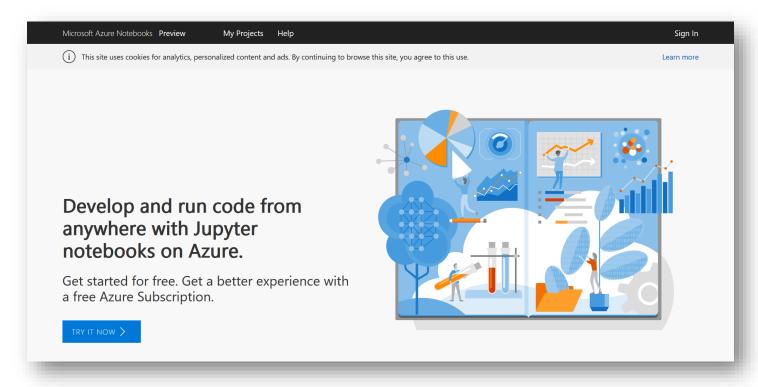


Reproductibilité et Open Science



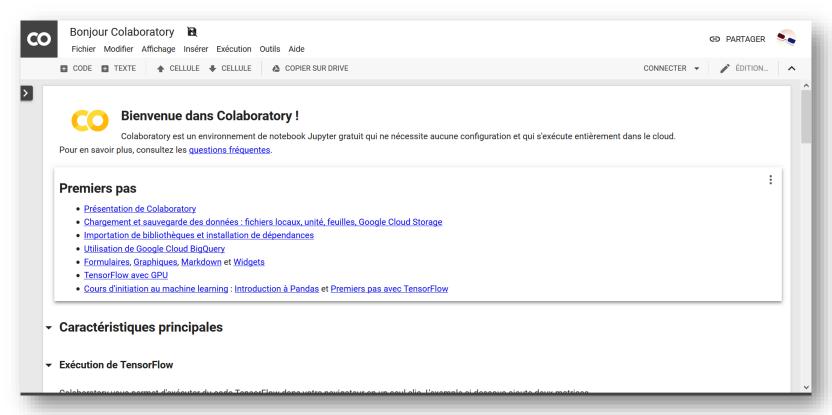
https://stenci.la





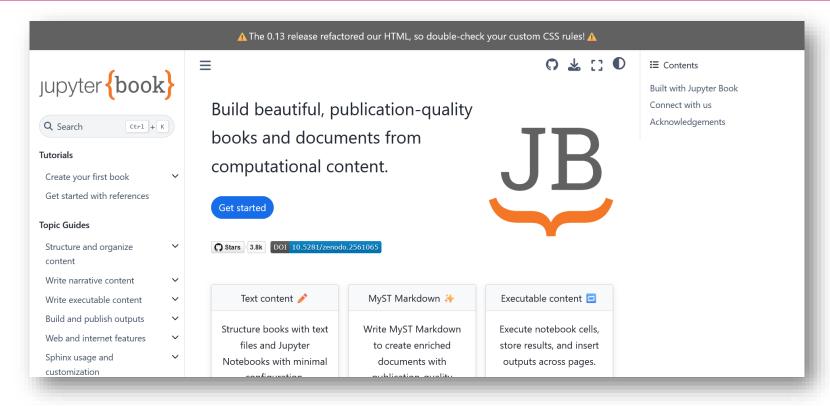
https://notebooks.azure.com/





https://colab.research.google.com



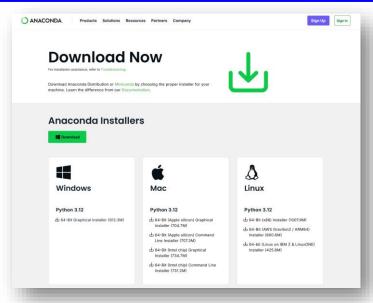


https://jupyterbook.org



Installer Jupyter Notebooks et Pandas sur son poste personnel avec la distribution « Anaconda» :

https://www.anaconda.com/download/





Travail sur le JupyterHub du cours

Se connecter sur cette adresse avec le login/pwd fourni pendant le cours :

https://learning.jupyterhub.unige.ch

over an unsecu	erHub seems to be served red HTTP connection. We mend enabling HTTPS for	;
Username:		
Password:		



Packages compris dans l'installation :

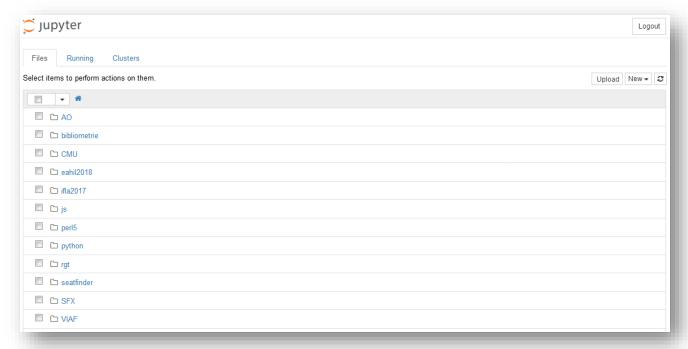
- Notebook (jupyter)
- Pandas
- NumPy
- Matplotlib
- NLTK
- ...

Liste complète : https://docs.anaconda.com/anaconda/pkg-docs/



Créer, organiser et partager des notebooks

Lancer Anaconda -> Jupyter Notebook



Si besoin : créer un lien symbolique entre le « home » et le dossier avec les notebooks

- 1. Avec le shell se positionner sur le «home»
- 2. Créer le lien avec la commande : mklink /D Nom-du-lien Dossier-de-destination

Aide: https://www.howtogeek.com/howto/16226/complete-guide-to-symbolic-links-symlinks-on-windows-or-linux/

Se familiariser avec les notebooks

Exercices

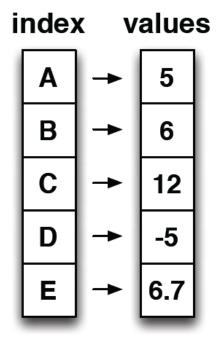
- 1. Ouvrir un notebook d'exemple (sur le dossier du cours)
- Créer un nouveau notebook et le renommer
- 3. Ajouter une cellule de texte (markdown)
- 4. Ajouter une cellule de code python (calcul simple)
- 5. L'exporter en format HTML

Aide markdown: https://guides.github.com/features/mastering-markdown/

Aide python: https://www.stavros.io/tutorials/python/

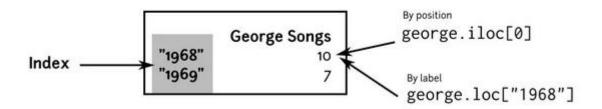


Series: 1 dimension

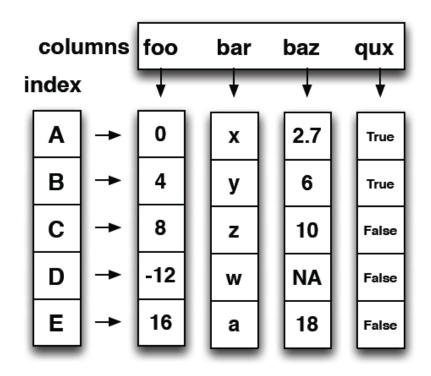


Index : afficher des données par la position ou le nom de l'index

Indexing

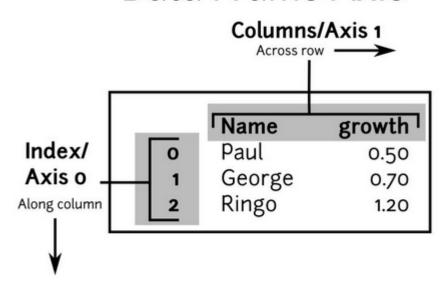


DataFrame: 2 dimensions



DataFrame: axes

Data Frame Axis





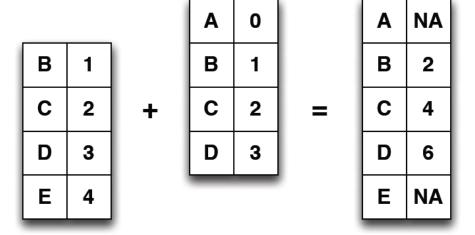
DataFrame: slices

Row & Column Slicing Examples

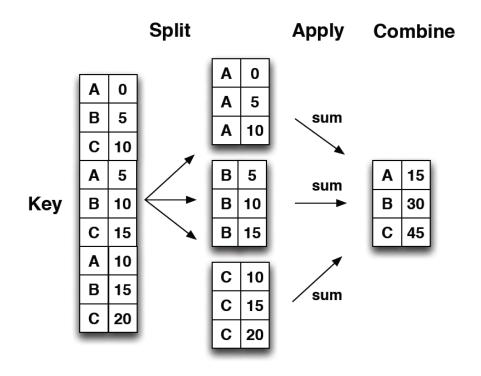
```
df.iloc[2:4, 0:1 → With a: return data frames Position - Half-open interval Without a: return series Label - Closed interval Rows Columns
```



Opérations facilitées par les index : jointures automatiques



Opérations : GroupBy

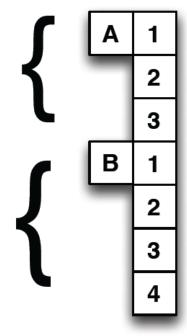


Opérations : GroupBy

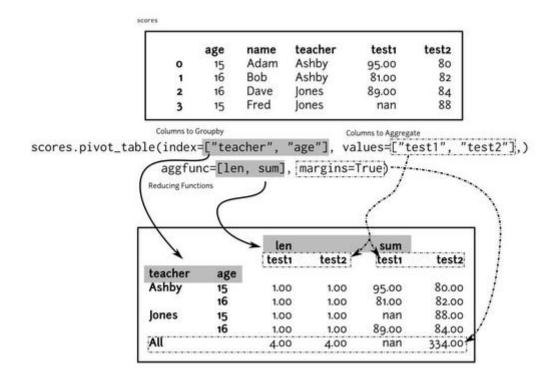
Method	Result
.all	Boolean if all cells in group are True
.any	Boolean if any cells in group are True
.count	Count of non null values
.size	Size of group (includes null)
.idxmax	Index of maximum values
.idxmin	Index of minimum values
.quantile	Quantile (default of .5) of group
.agg(func)	Apply func to each group. If func returns scalar, then reducing
.apply(func)	Use split-apply-combine rules
.last	Last value
.nth	Nth row from group
.max	Maximum value
.min	Minimum value
.mean	Mean value
.median	Median value
.sem	Standard error of mean of group
.std	Standard deviation
.var	Variation of group
.prod	Product of group
.sum	Sum of group



Index multidimensionnels



Pivoter les tables





Jointures (merge)

Visualizing Joins



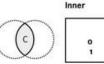


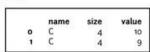


Dataset 2	

	name	value
3	C	10
1	C	9
2	D	8
4	D	7









Outer

	name	size	value
0	A	1.00	nan
1	В	2.00	nan
2	В	3.00	nan
3	C	4.00	10.00
4	C	4.00	9.00
5	D	nan	8.00
6	D	nan	7.00





	name	size	value
0	A	1	nan
1	В	2	nan
2	В	3	nan
3	C	4	10.00
4	C	4	9.00



Right

1		name	size	value
(() -)				
() 0 1	0	C	4.00	10
	1	C	4.00	9
***************************************	2	D	nan	8
	3	D	nan	7



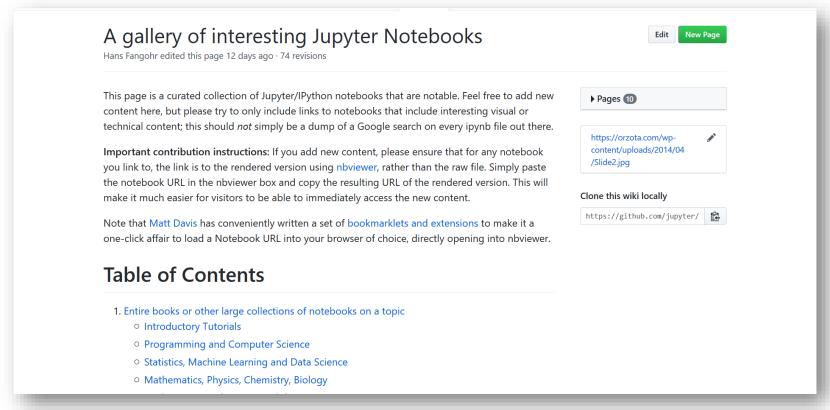
Pour avancer « pas à pas »



https://datacarpentry.org/python-socialsci/



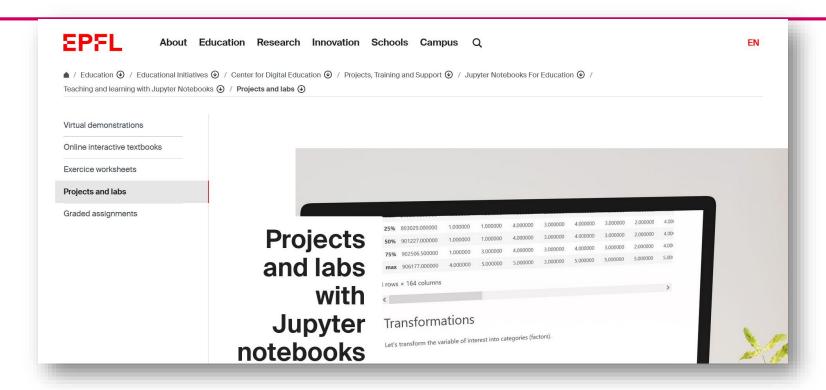
Pour aller plus loin



https://github.com/jupyter/jupyter/wiki#a-gallery-of-interesting-jupyter-notebooks



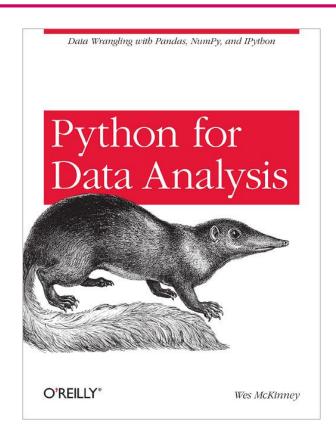
Pour aller plus loin

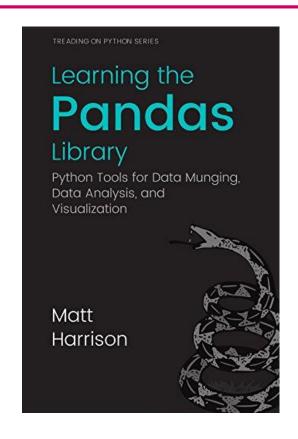


https://www.epfl.ch/education/educational-initiatives/jupyter-notebooks-for-education/teaching-and-learning-with-jupyter-notebooks/projects-and-labs-with-jupyter-notebooks/



Pour aller plus loin







Exercices pratiques disponibles ici :

https://github.com/dis-unige/formations

- 1. Importer des données
- 2. Analyser des données
- 3. Travailler avec différents types de données et des données manquantes
- 4. Exporter des données
- 5. Créer des graphiques simples

Aide Pandas: https://pandas.pydata.org/pandas-docs/stable/user_guide/10min.html



Sources

Cheat Sheets distribués dans le cours :

Jupyter notebook :

https://www.datacamp.com/cheat-sheet/jupyter-notebook-cheat-sheet

Markdown:

http://geog.uoregon.edu/bartlein/courses/geog607/Rmd/MDquick-refcard.pdf

Pandas :

https://pandas.pydata.org/Pandas_Cheat_Sheet.pdf

