Rendez-vous de l'info scientifique

Traitement de données avec Pandas & Jupyter notebooks



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







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16 avril 2025



Programme

Introduction

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

Jupyter Notebooks

- Famille d'outils
- Installation via la distribution Anaconda ou test en ligne via https://jupyter.org/try
- Créer, organiser et partager des notebooks

Pandas

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



Historique de deux outils *Open Source*

iPython (2001->) https://ipython.org/

"When I found out about IPP and LazyPython I tried to join all three into a unified system. I thought this could provide a very nice working environment, both for regular programming and scientific computing: shell-like features, IDL/Matlab numerics, Mathematica-type prompt history and great object introspection and help facilities. I think it worked reasonably well, though it was a lot more work than I had initially planned." Fernando Perez, graduate student at the University of Colorado, Boulder

Jupyter (2014 ->) https://jupyter.org/

Spin-off de l'Python appellé "Project Jupyter". l'Python continue en tant que Python shell et kernel sur Jupyter mais il n'est plus le seul langage supporté.



IPython ...

- Interactive Python shell at the terminal
- Kernel for this protocol in Python
- Tools for Interactive Parallel computing

Jupyter

- Network protocol for interactive computing
- Clients for protocol
 - Console
 - Qt Console
 - Notebook
- Notebook file format & tools (nbconvert...)
- Nbviewer



Language Agnostic

https://speakerdeck.com/fperez/project-jupyter?slide=5



Historique : Julia + Python + R & Hommage à Galileo





https://en.wikipedia.org/wiki/Project Jupyter



Famille d'outils

- Jupyter Notebook (le classique) : https://jupyter.org/
- Jupyter Lab (interface étendue) : https://jupyterlab.readthedocs.io/
- Jupyter Hub (version pour labos, etc.) : https://jupyterhub.readthedocs.io/
- Voilà (transforme le notebook en application Web) : https://voila-gallery.org/
- NB viewer (partage et visualisation) : https://nbviewer.jupyter.org/
- Binder (partage, visualisation et exécution) : https://mybinder.org/
- NotebookSharing.space (partage, visualisation, exécution et annotations):
 https://notebooksharing.space/
- GitHub (visualisation et versioning) : https://github.com
- Etc.



Pléthore de « librairies » python

- NumPy (scientific computing) : https://numpy.org/
- Pandas (analyse et manipulation de données) : https://pandas.pydata.org/
- Matplotlib (graphiques et visualisations) : https://matplotlib.org/
- Dask (parallélisme) : https://docs.dask.org
- Vaex (données massives, 10⁹ lignes par second!) : https://vaex.readthedocs.io
- Scikit-learn (Machine Learning): https://scikit-learn.org
- TensorFlow (Deep Learning) : https://www.tensorflow.org/
- PyTorch (Deep Learning) : https://pytorch.org/
- Etc.









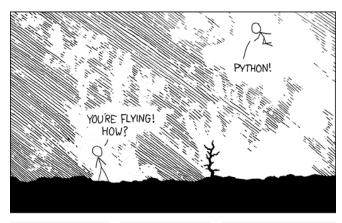


https://pandas.pydata.org



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





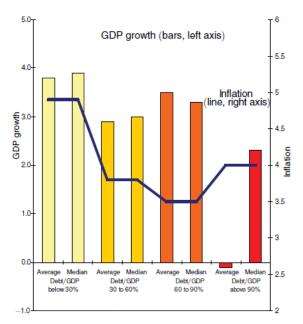


https://www.xkcd.com/353/

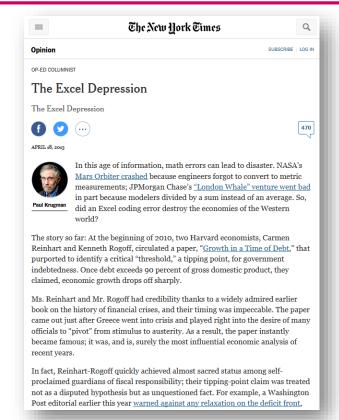


Excel et les erreurs scientifiques

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

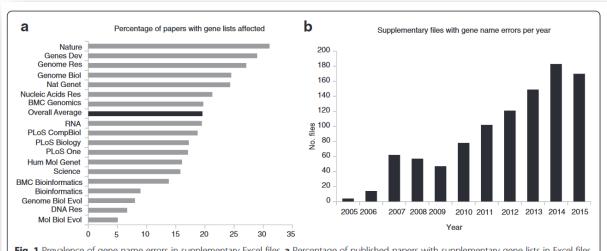


Fig. 1 Prevalence of gene name errors in supplementary Excel files. a Percentage of published papers with supplementary gene lists in Excel files affected by gene name errors. b Increase in gene name errors by year

emann et al. Genome Biology (2016) 17:177

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 numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

Keywords: Microsoft Excel, Gene symbol, Supplementary data

Abbreviations: GEO, Gene Expression Omnibus; JIF, journal impact factor

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: AssamEl-Osta@bakeridi.celu.au Baker ID Heart & Dubertes Inntitute; The Affred Medical Riesearch and Education Precision, Melbourne, Victoria 3004, Australia *Central Clinical School; Raculty of Medicine, Monayh University, Chyston, Victoria 3106, Australia Wichia School; Australia frequently reused. Our aim here is to raise awareness of

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



0.2016 The Authorids Open Access Tibs article is desiblated under the term of the Crediter Common Attitudion 40 International Enternational Enternational

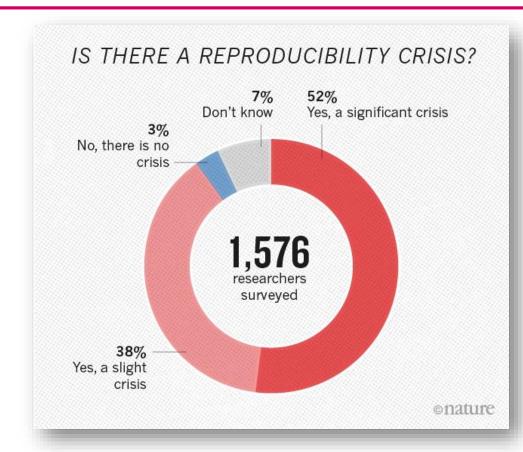
Ziemann et al. 2016. DOI:10.1186/s13059-016-1044-7



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

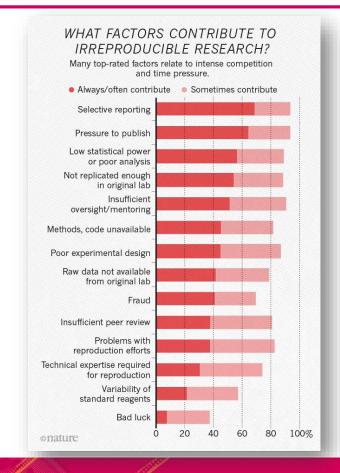




Reproductibilité et Open Science

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

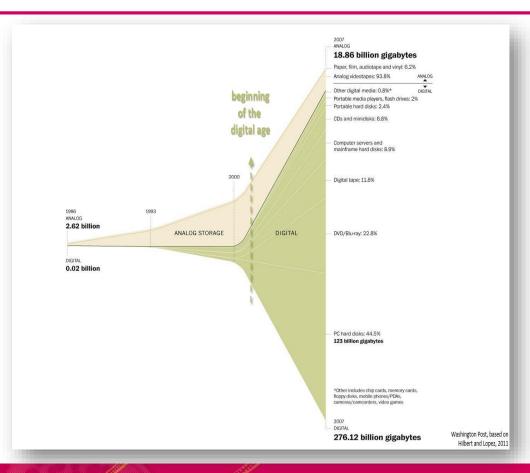
Nombreux réservoirs ouverts

Kaggle: https://www.kaggle.com

Github: http://github.com

WikiData: https://www.wikidata.org

Statistique historique : https://hsso.ch

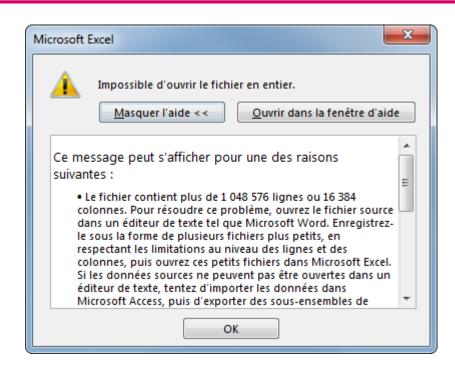




Excel: limitations

Worksheet and workbook specifications and limits

Feature	Maximum limit
Open workbooks	Limited by available memory and system resources
Total number of rows and columns on a worksheet	1,048,576 rows by 16,384 columns



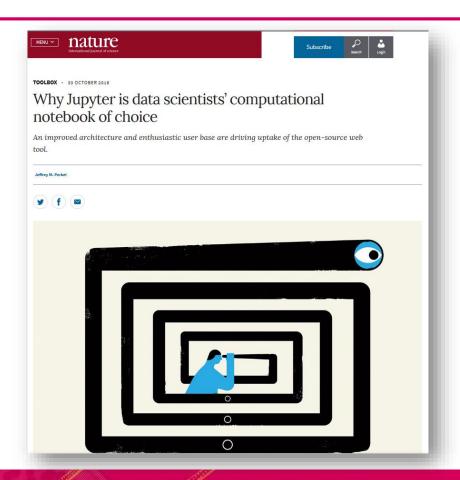
Liste complète des limites : https://support.office.com/en-us/article/excel-specifications-and-limits-1672b34d-7043-467e-8e27-269d656771c3



Reproductibilité et Open Science

Nature

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

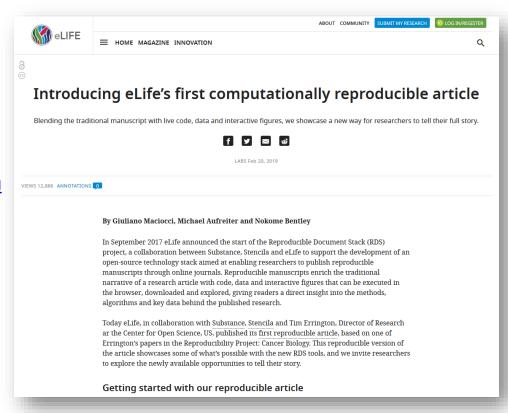




Reproductibilité et Open Science

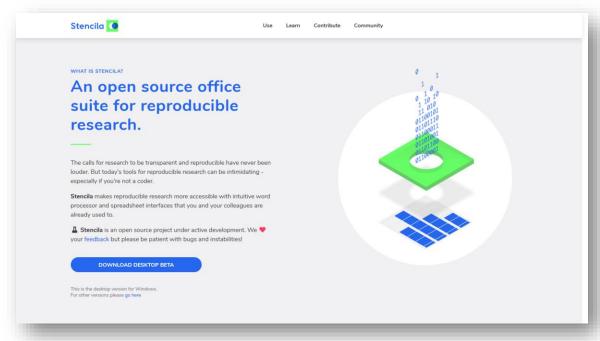
eLife

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



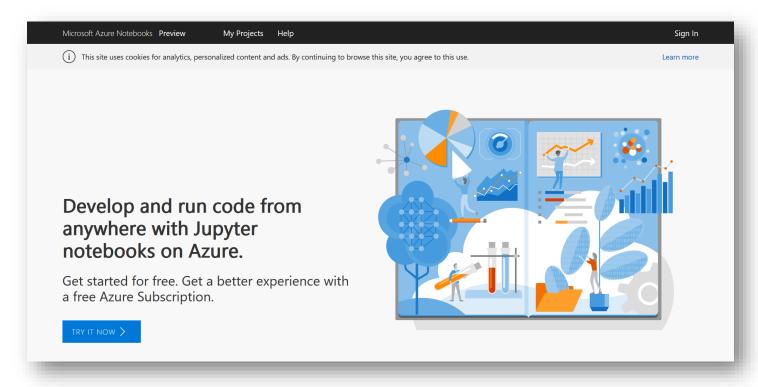


Reproductibilité et Open Science



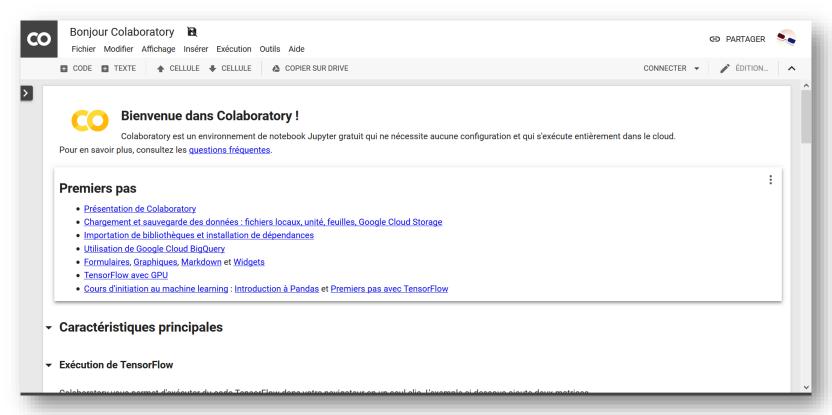
https://stenci.la





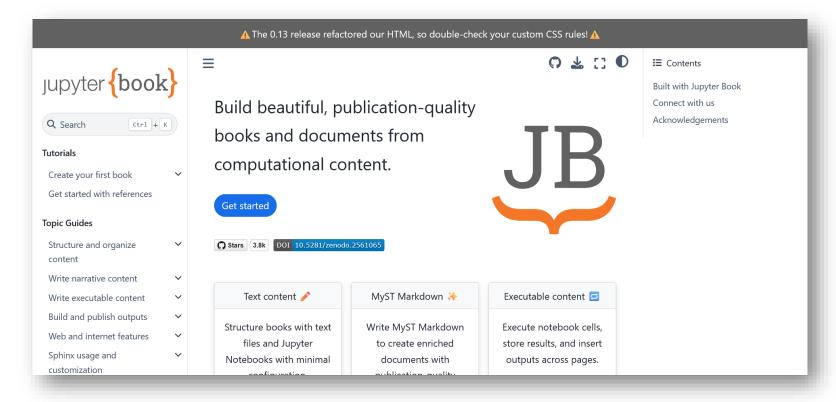
https://notebooks.azure.com/





https://colab.research.google.com



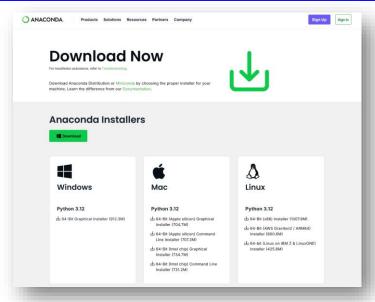


https://jupyterbook.org



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

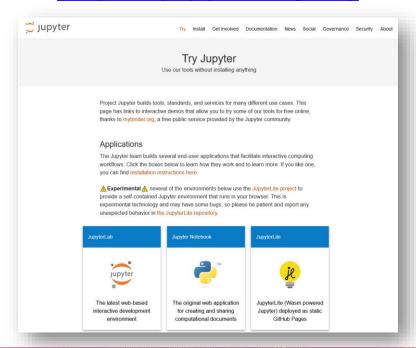
https://www.anaconda.com/download/





Ou utilisation sans installation possible sur «Try Jupyter»

https://jupyter.org/try





Packages importants (compris avec l'installation Anaconda):

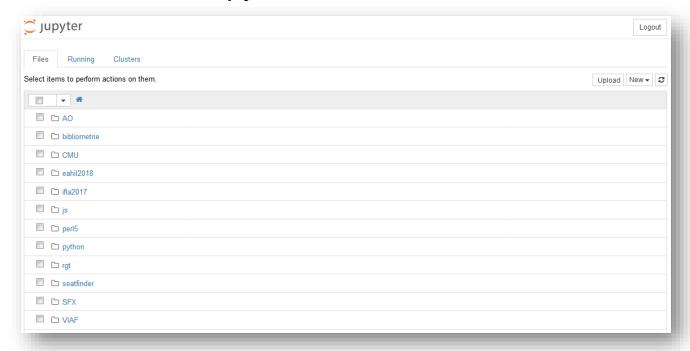
- Notebook (jupyter)
- Pandas
- NumPy
- Matplotlib
- NLTK
- ...

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



Créer, organiser et partager des notebooks

Lancer Anaconda -> Jupyter Notebook



Attention, le dossier par défaut à l'ouverture de Jupyter est le «home» du poste. Sur Windows c'est le dossier : C:\Users\[votre_id]

Ensuite on peut naviguer dans les sous-dossier mais pas en dehors!

Pour palier à ça il y a deux solutions :

- 1. définir l'emplacement du dossier avec la commande :
 - > jupyter notebook --notebook-dir=C:\[dossier souhaité]
- 2. créer un lien symbolique pour ajouter le dossier souhaité sur le «home» :
 - > mklink /D Nom-du-lien Dossier-de-destination



Exercices

Se familiariser avec les notebooks

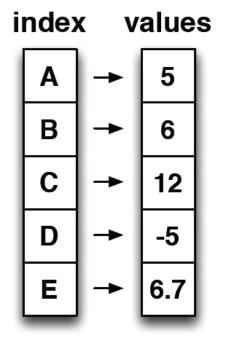
- 1. Ouvrir un notebook d'exemple (sur le dossier du cours)
- Créer un nouveau notebook et le renommer
- 3. Ajouter une cellule de texte (markdown)
- 4. Ajouter une cellule de code python (calcul simple)
- L'exporter en format HTML

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

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

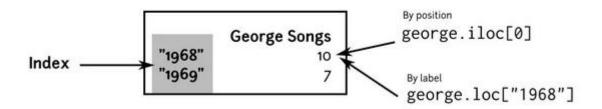


Series: 1 dimension

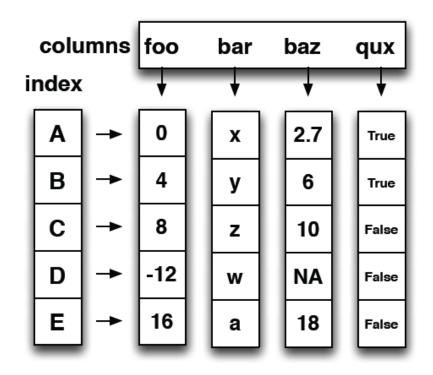


Index : afficher des données par la position ou le nom de l'index

Indexing

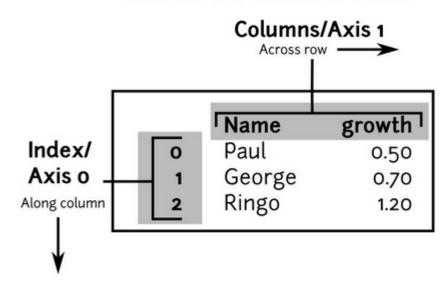


DataFrame: 2 dimensions



DataFrame: axes

Data Frame Axis





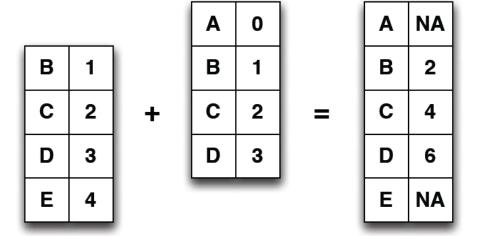
DataFrame: slices

Row & Column Slicing Examples

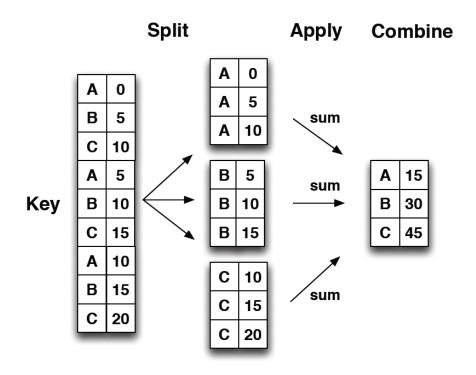
```
df.iloc[2:4, 0:1 → With a: return data frames Position - Half-open interval Without a: return series Label - Closed interval Columns
```



Opérations facilitées par les index : jointures automatiques



Opérations : GroupBy

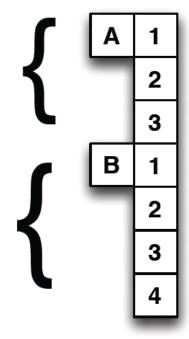


Opérations : GroupBy

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

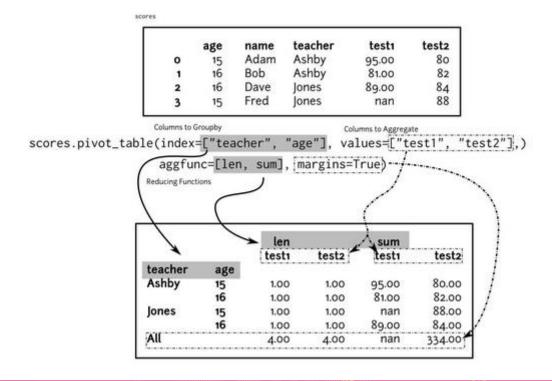


Index multidimensionnels





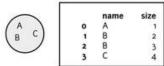
Pivoter les tables



Jointures (merge)

Visualizing Joins

Dataset 1





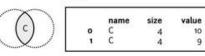
Dataset 2

Outer

Right

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





Inner



value size nan nan nan 10.00 9.00 8.00

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



	name	size	value
0	C	4.00	10
1	C	4.00	9
2	D	nan	8
3	D	nan	7



Exercices

Exemples 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
- Exporter des données
- 5. Créer des graphiques simples

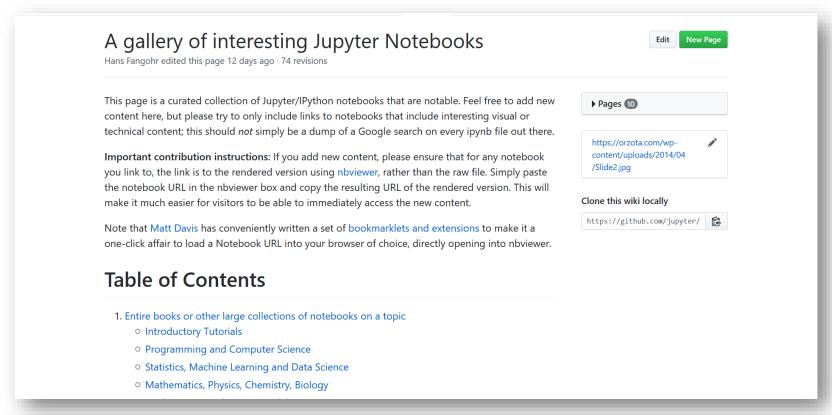
Aide Pandas: https://pandas.pydata.org/pandas-docs/stable/user_guide/10min.html





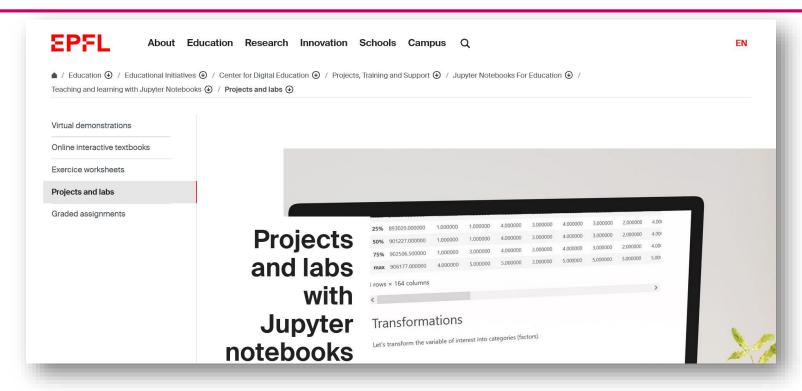
https://datacarpentry.org/python-socialsci/





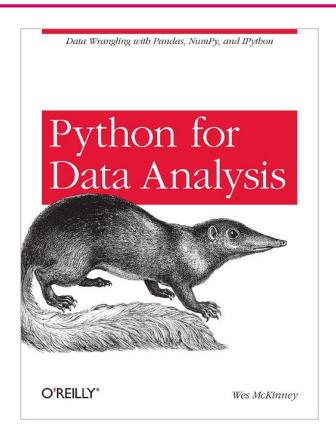
https://github.com/jupyter/jupyter/wiki#a-gallery-of-interesting-jupyter-notebooks

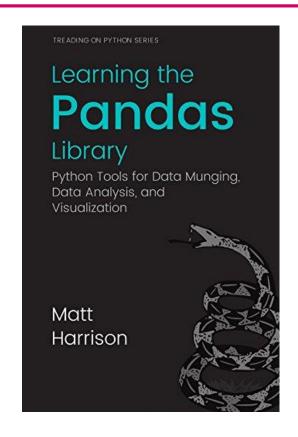




https://www.epfl.ch/education/educational-initiatives/jupyter-notebooks-for-education/teaching-and-learning-with-jupyter-notebooks/projects-and-labs-with-jupyter-notebooks/









Sources

Cheat Sheets:

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

