

Data analysis and visualization (DAV)

Lecture 01

Łukasz P. Kozłowski

Warsaw, 2025

Data analysis and visualization (DAV)

Lecture 01

<https://www.mimuw.edu.pl/~lukaskoz/teaching/dav/>

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During the course, laboratories it is assumed that you use
Linux (Ubuntu/Debian)

(no help for Windows, Mac users will be provided)

The final score (grade) for the course depends on:

- 1) **Homeworks** - 50%,
- 2) **Project** (aka exam) – 50%,

The project: given the subject the student(s) will need to prepare the poster (static + animated) in which they:

- gather the data
- interpret the data
- present it using appropriate plots (static, interactive and animated)

To pass, you need at least 60% in both the syllabus and the project.

During last two-three laboratories students will present their topic in front of the class.

The homework: after (almost) each laboratory there will be home work which need to be sent before next unit. Total scores from home works will be scaled to 50% of the final grade

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The homework: after (almost) each laboratory there will be home work which need to be sent before next unit. Total scores from home works will be scaled to 50% of the final grade

During each laboratory there will be a list of presence
max 2 absences are allowed

(but this does not exempt you from submitting homework on time)

Lectures

- 1) Every Monday 14:15-16:00
- 2) The slides from the lectures will be provided at:

<https://www.mimuw.edu.pl/~lukaskoz/teaching/dav/>

and **Moodle:**

<https://moodle.mimuw.edu.pl/course/view.php?id=2388>

Key: k00Q6WbW

Homeworks

1) Frequently, there will homework after laboratory (it will be either the solutions from the laboratory itself or some extra exercise(s) similar to the one done during laboratories).

2) In order to pass given laboratory you need to send email with the solutions to lukaskoz@mimuw.edu.pl

(thus we will not use moodle for sending homeworks)

Homeworks

3) The email with homework need to have specific structure:

a) The subject: **DAV25_labN_hw_Surname_Name**

For instance:

DAV25_lab1_hw_Smith_John for homework from lab1 by Smith John

DAV25_lab2_hw_Kozlowski_Lukasz for homework from lab2 by Kozłowski Łukasz

DAV25_lab10_hw_Rodriguez_Jose for homework from lab10 by José Rodríguez

Note underscores, lack of special letters and the order of the parts

b) no text body in the email

c) single standard attachment with the same name compressed with 7z

For instance:

DAV25_lab1_hw_Smith_John.7z

DAV25_lab2_hw_Kozlowski_Lukasz.7z

DAV25_lab10_hw_Rodriguez_Jose.7z

The content and the structure of the attachment is laboratory specific and it will be explained separately

Homeworks

Deadline

For the homework the deadline (for all groups) is
Saturday 23:59 CET (GMT+1 Winter and GMT+2 Summer) – **one week***

* You can send delayed homework a week later, but it will be awarded by handicap/offset by -50% of the score (homework send later will not be graded)

Remember that you need on average 60% to pass

For reference, last year, students could earn up to 1,200 points, with each week's workload worth approximately 100 points.

- optimize the size of files
- do not use special letters in file names e.g. Polish
- do not use Polish (everything should be in English)
- always add legends and descriptions for the plots

follow the golden rule:

one plot, one (python) script

Thus:

- do not overuse jupyter
- do not overuse any web browser solutions

follow the golden rule:

one plot, one (python) script

Thus:

- do not overuse jupyter
- do not overuse any web browser solutions
- make proper project structure

Be prepared to present everything as static file
(preferably pdf)


```
(base) lukaskoz@x230:/tmp/project1$ tree
```

```
.  
├── data  
│   ├── dataset1.json  
│   └── dataset2  
│       ├── test.csv  
│       ├── train.csv  
│       └── validate.csv  
├── images  
│   ├── fig1.png  
│   └── fig2.gif  
└── scripts  
    ├── fig1.py  
    └── fig2.py
```

- make proper project structure

Be prepared to present everything as static file
(preferably pdf)

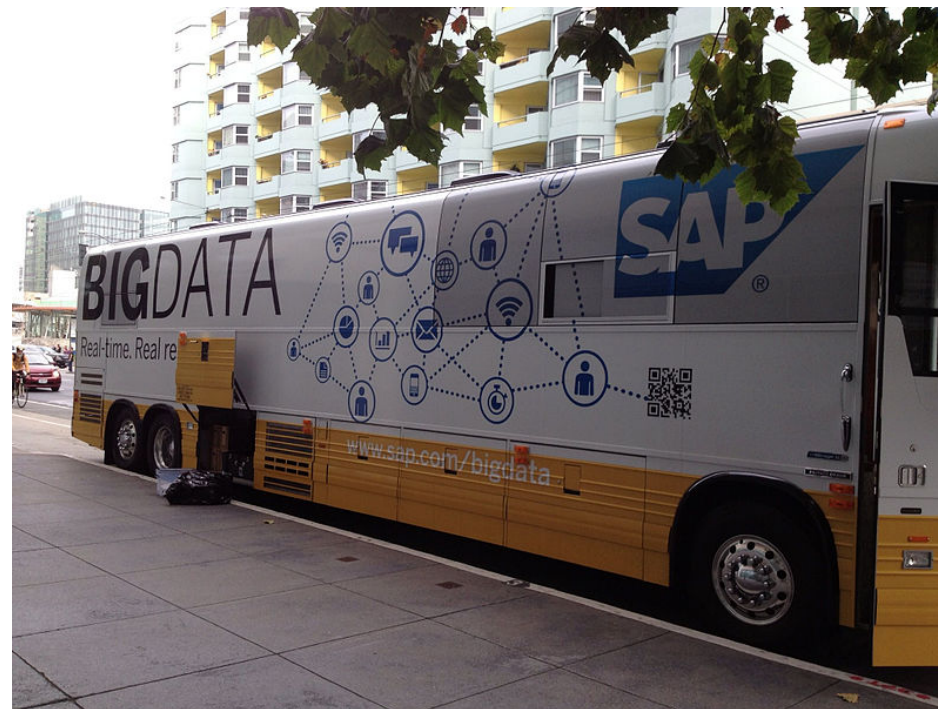
DATA

Data analysis is a process of inspecting, cleansing, transforming and modeling data with the goal of discovering useful information, informing conclusion and supporting decision-making.

Wikipedia

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Wikipedia



BIGDATA

We will be working with **Big Data** in **Bioinformatics**

This means that you will need to have solid background in basic biology or refresh it (there will no time to do it during the course)

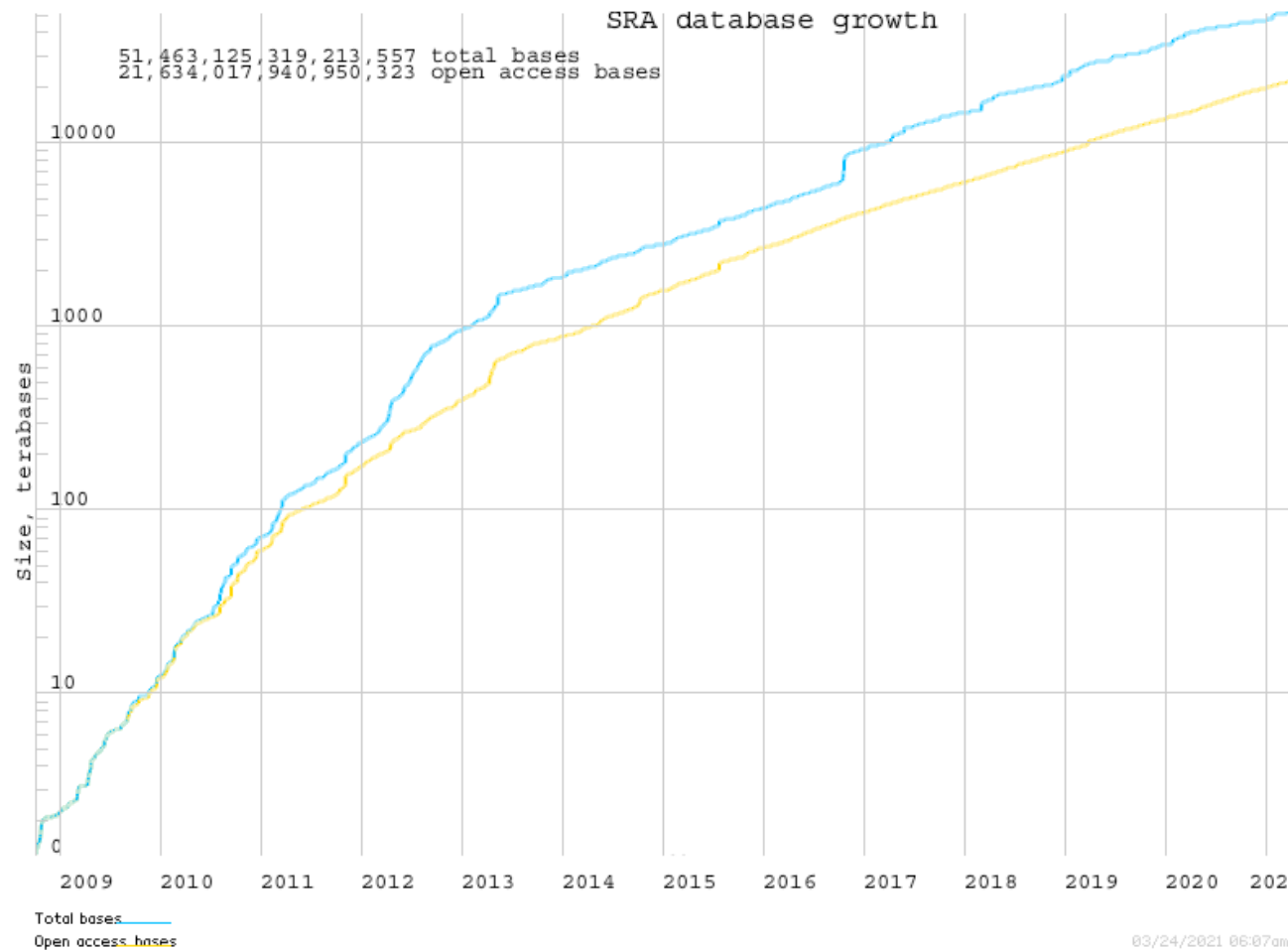
We will be working with **Big Data** in **Bioinformatics**

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DIY (biology)

you need to know what is DNA, RNA, protein, what are their letters (ATGCN, AUTCN, VXCDBFMOLNYIQTGHWESKPAUR) and know basic facts from genetics (such as genetic code, gene, genome, proteome, cell structure, organism kingdoms, tree of life, etc.).

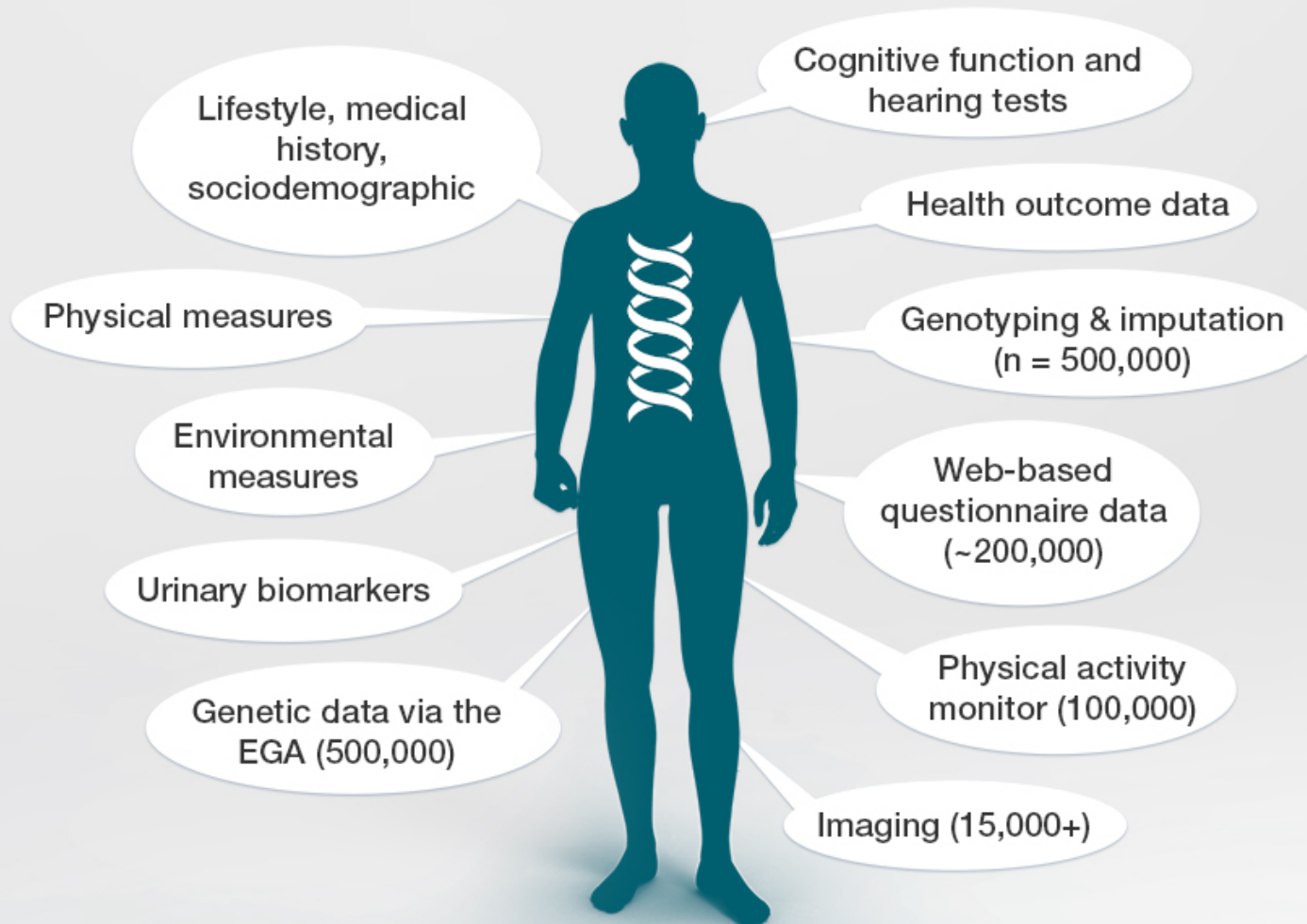
Sequence Read Archive (SRA)



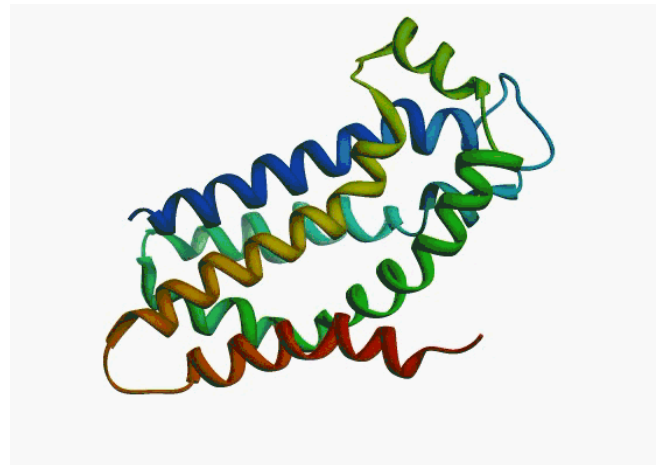
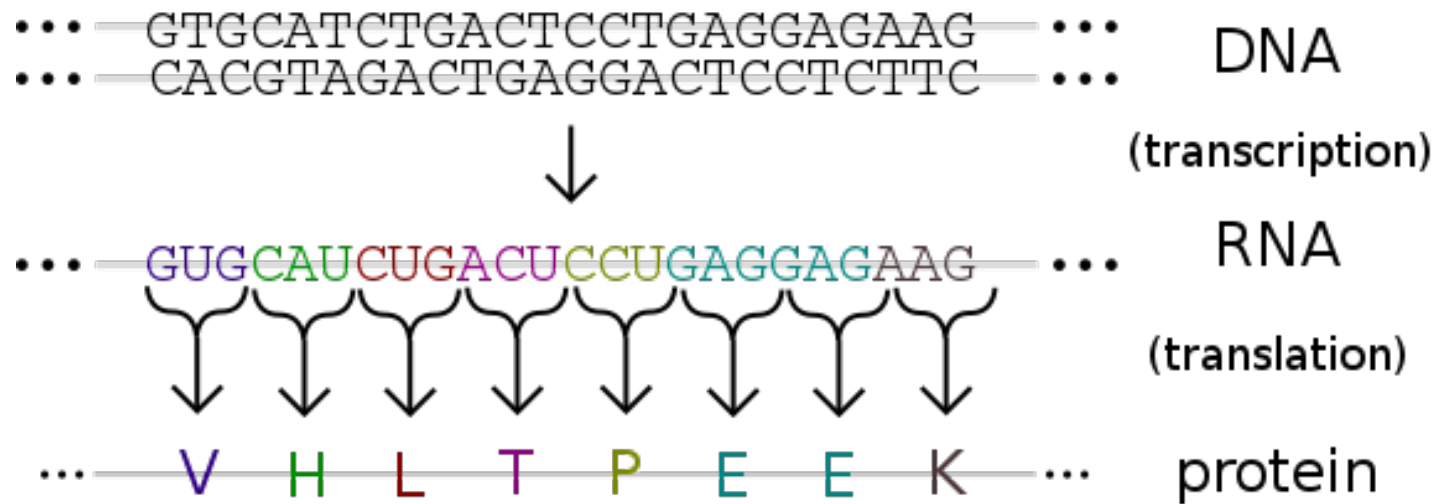
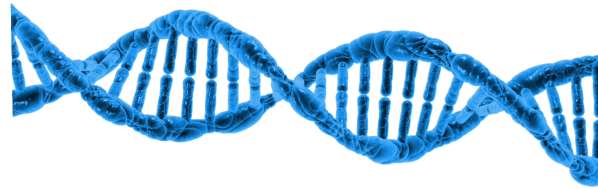


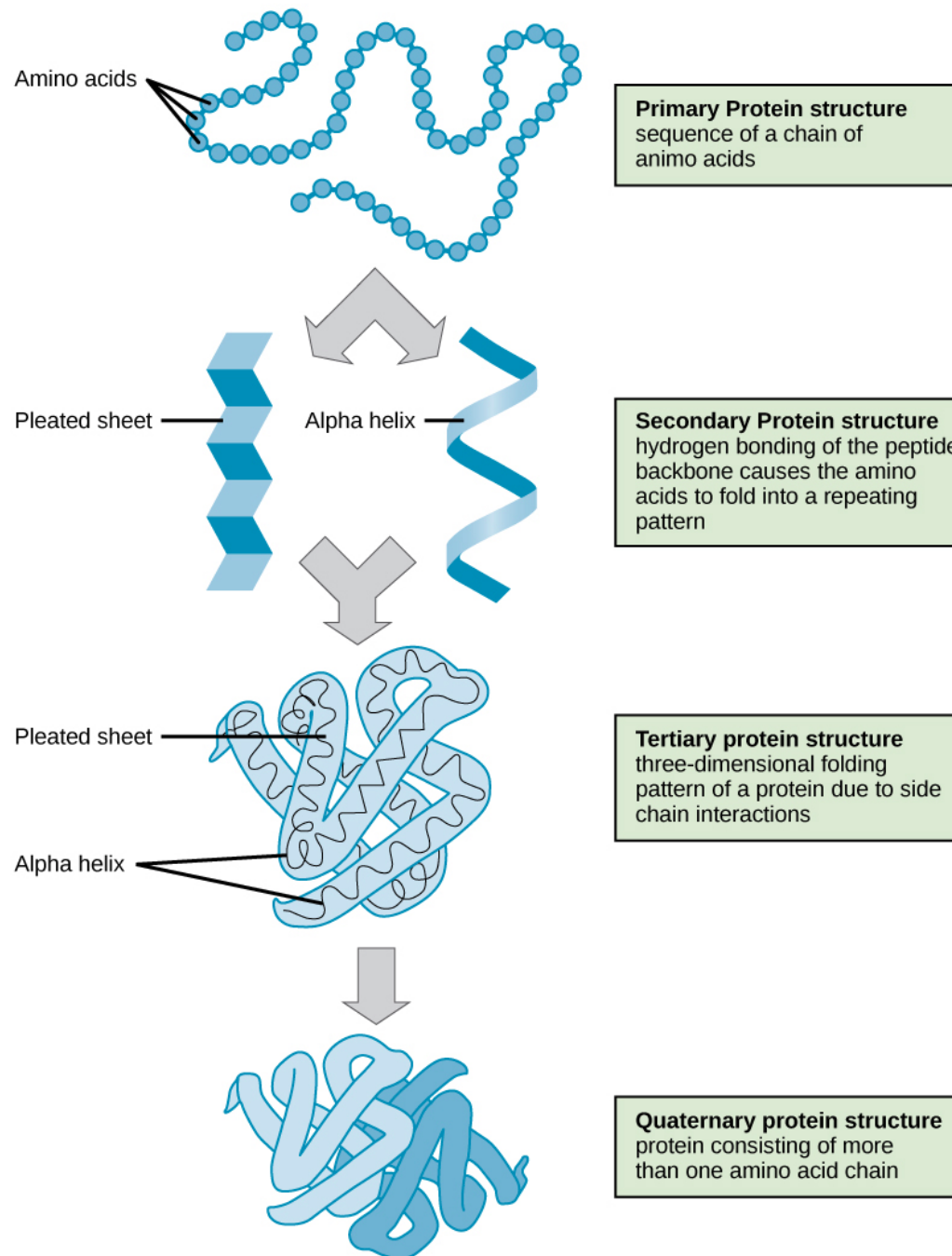
Enabling scientific discoveries that improve human health

Data on UK Biobank participants



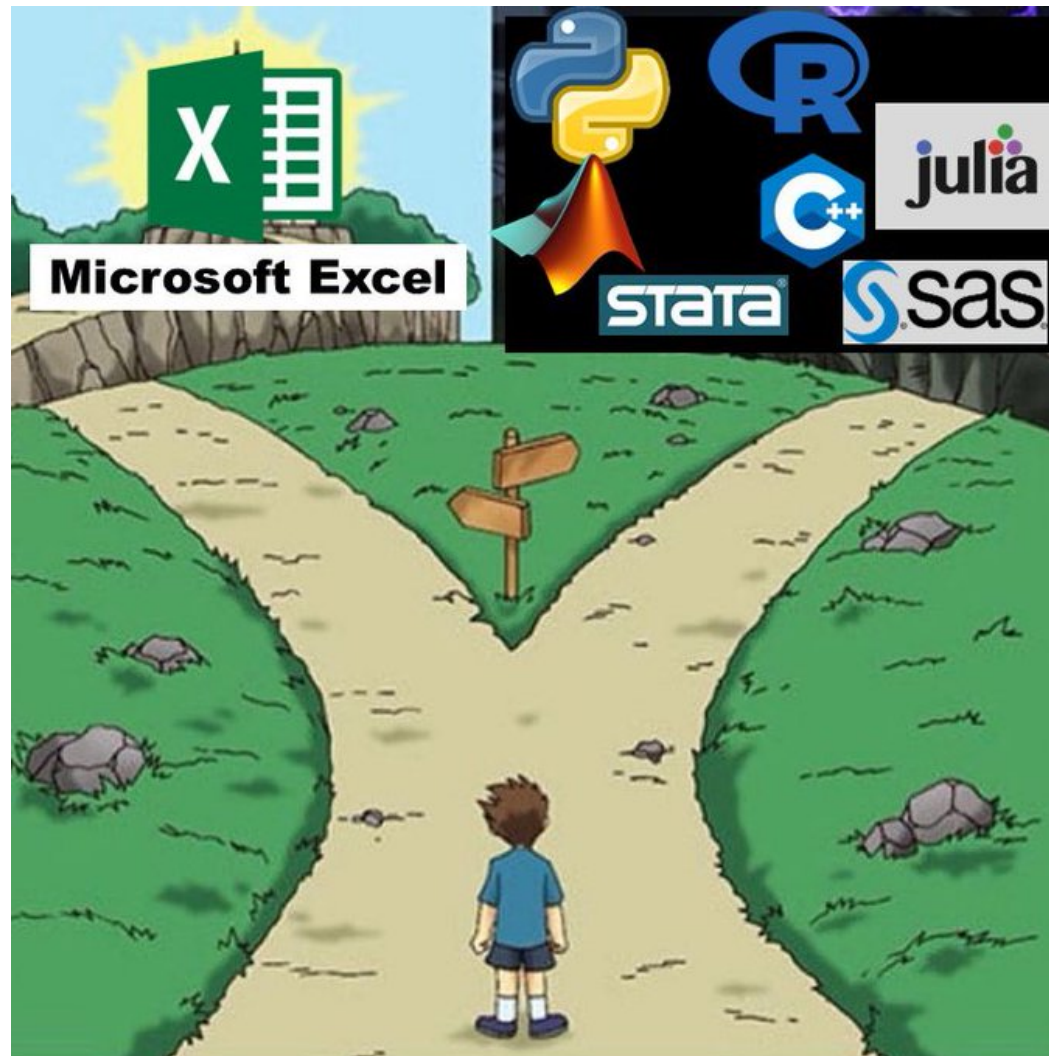
<https://www.ukbiobank.ac.uk/>

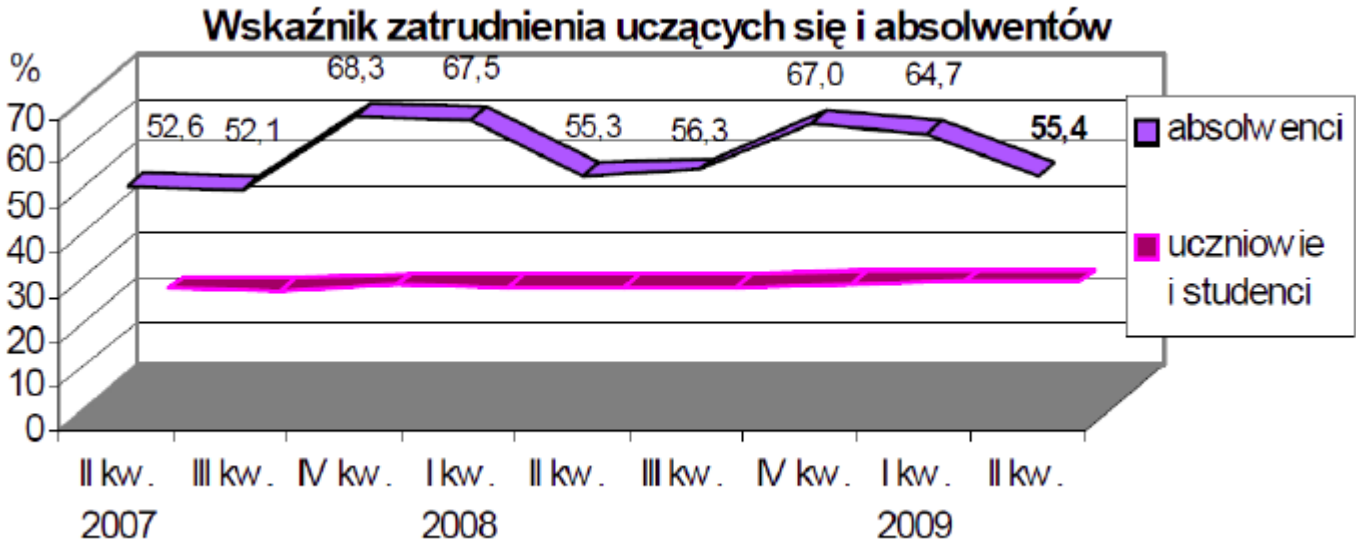


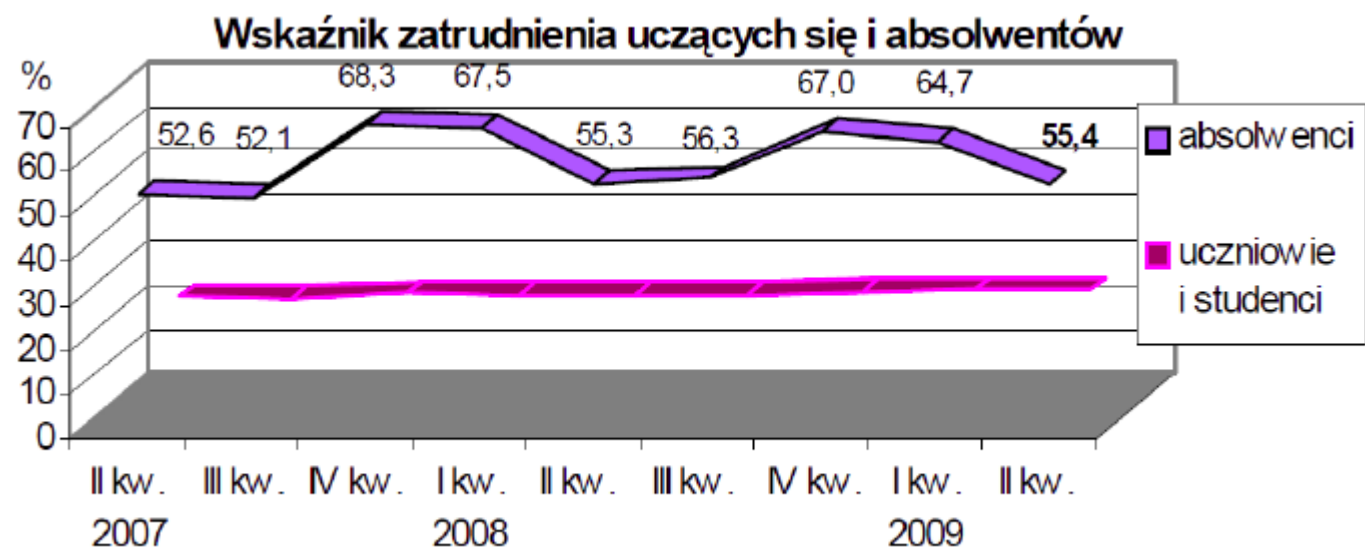


		Second Base					
		U	C	A	G		
First Base	U	UUU } Phe	UCU } Ser	UAU } Tyr	UGU } Cys	U	Third Base
		UUC } Phe	UCC } Ser	UAC } Tyr	UGC } Cys	C	
		UUA } Leu	UCA } Ser	UAA } STOP	UGA — STOP	A	
		UUG } Leu	UCG } Ser	UAG } STOP	UGG — Trp	G	
	C	CUU } Leu	CCU } Pro	CAU } His	CGU } Arg	U	
		CUC } Leu	CCC } Pro	CAC } His	CGC } Arg	C	
		CUA } Leu	CCA } Pro	CAA } Gln	CGA } Arg	A	
		CUG } Leu	CCG } Pro	CAG } Gln	CGG } Arg	G	
	A	AUU } Ile	ACU } Thr	AAU } Asn	AGU } Ser	U	
		AUC } Ile	ACC } Thr	AAC } Asn	AGC } Ser	C	
		AUA } Ile	ACA } Thr	AAA } Lys	AGA } Arg	A	
		AUG — Met or Start	ACG } Thr	AAG } Lys	AGG } Arg	G	
	G	GUU } Val	GCU } Ala	GAU } Asp	GGU } Gly	U	
		GUC } Val	GCC } Ala	GAC } Asp	GGC } Gly	C	
		GUA } Val	GCA } Ala	GAA } Glu	GGA } Gly	A	
		GUG } Val	GCG } Ala	GAG } Glu	GGG } Gly	G	

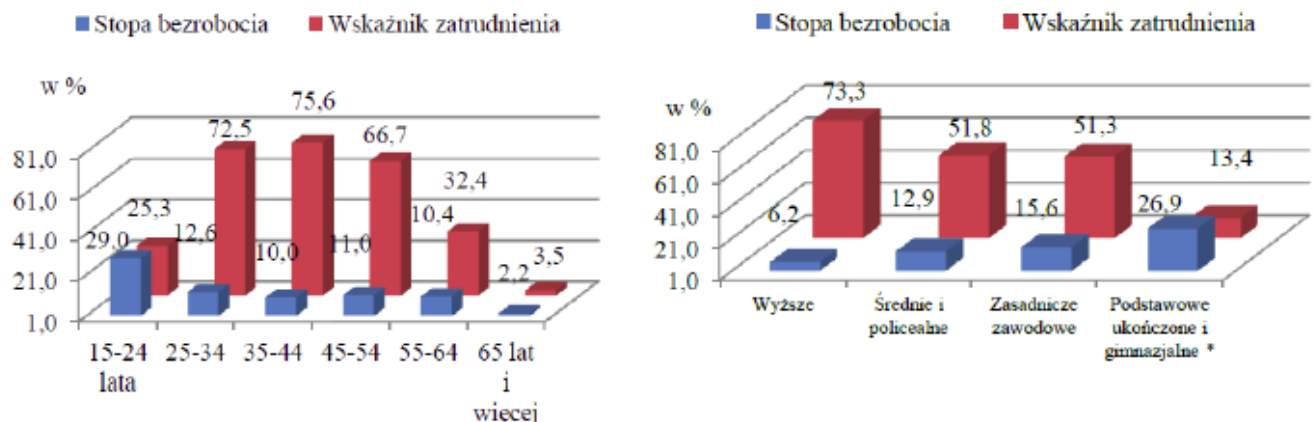








Wykres 7. Wskaźnik zatrudnienia oraz stopa bezrobocia według grup wieku i poziomu wykształcenia w 2011 r.



* łącznie z wykształceniem podstawowym nieukończonym i bez wykształcenia szkolnego

COMMENT

Genome Biology

Open Access



Gene name errors are widespread in the scientific literature

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

Abstract

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

frequently reused. Our aim here is to raise awareness of the problem.

We downloaded and screened supplementary files 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 tsv file was screened for the presence of gene symbols. 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*, *Drosophila melanogaster*, *Danio rerio*, *Escherichia coli*, *Gallus*

The problem of Excel software (Microsoft Corp., Redmond,

Gene symbols:

SEPT2 (Septin 2) --> '2-Sep'

MARCH1 [Membrane-Associated Ring Finger (C3HC4) 1] --> '1-Mar'

RIKEN identifiers:

'2310009E13' --> '2.31E+13'

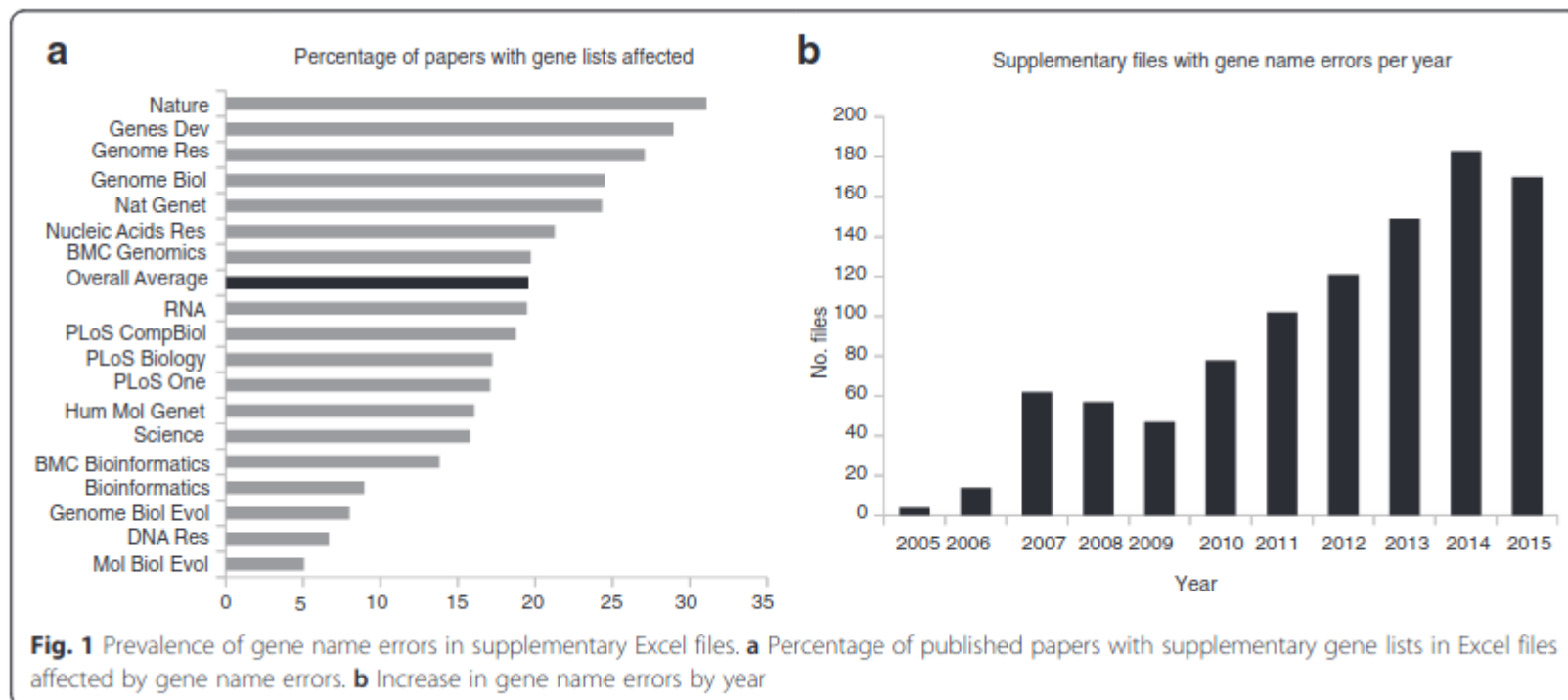
Gene symbols:

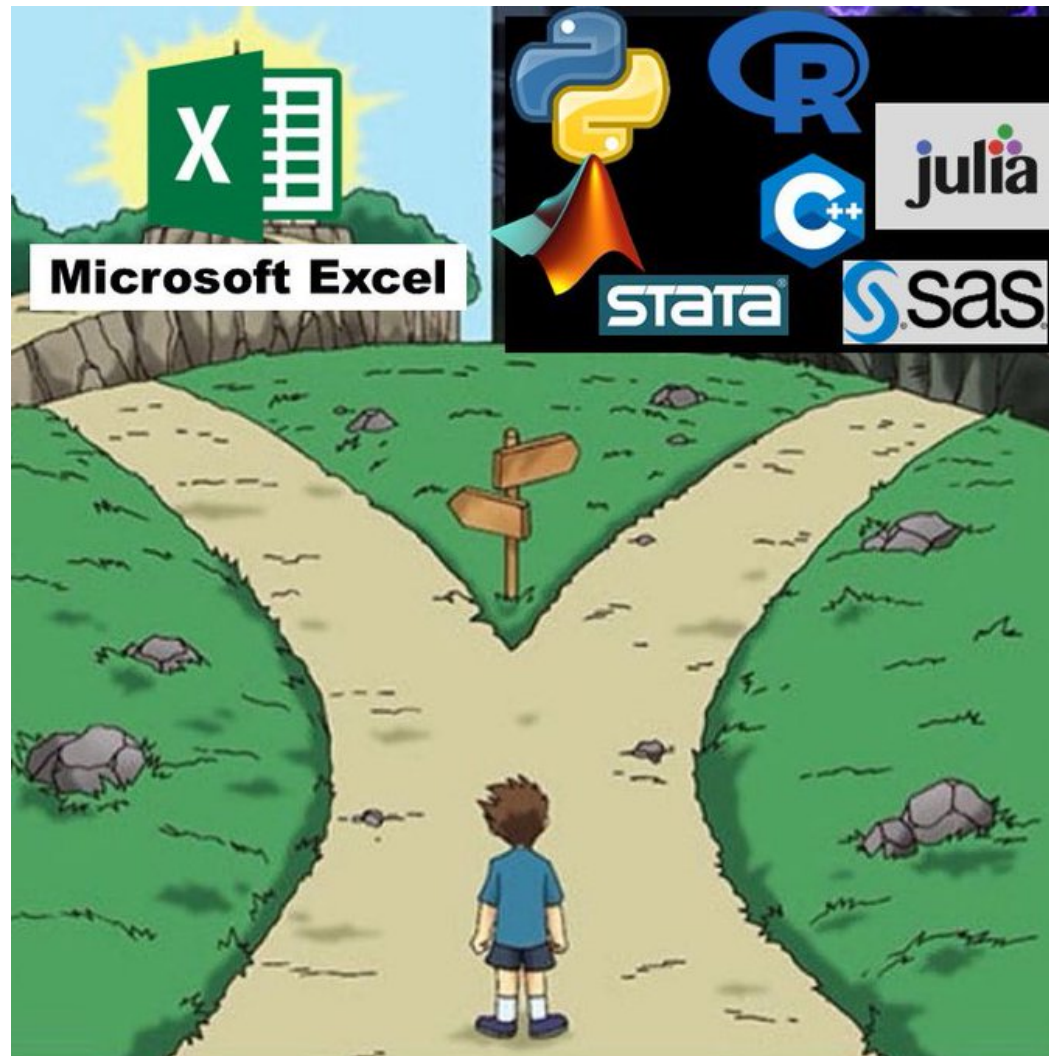
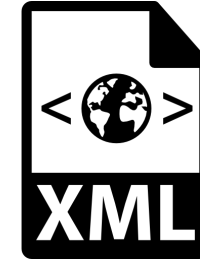
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This is not python programming course and it means that you should **know** how to program or you must learn the basics within short time



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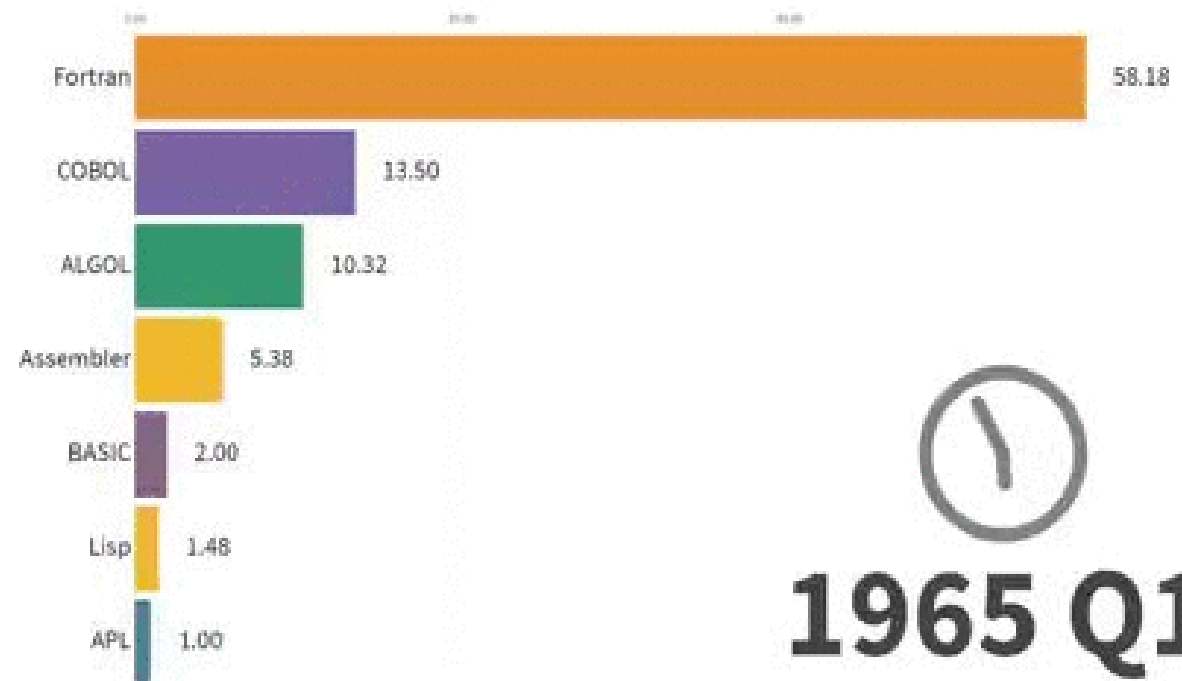
1. Dive Into Python 3 (also in Polish, check on wikibooks)
2. Python Data Analysis, Ivan Idris, 2014
3. Python for Data Analysis, Wes MacKinney, 2013



Guido van Rossum

Python was conceived in the late 1980s

- scripting language (no compilation)
- uses whitespace indentation, rather than curly brackets or keywords, to delimit blocks
- we use **python3** instead **python2**





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We will use a number of python libraries useful for data analysis and visualization such as:

jupyter, spyder, numpy, scipy, numba, pandas, dask, bokeh, holoviews, datashader, matplotlib, scikit-learn, seaborn, plotly and many others

We will use also external tools such as image-magick



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We will use also external tools such as **image-magick**

PYTHON 2.X



PYTHON 3.X

← **LEGACY**

It is still entrenched in the software at certain companies

FUTURE →

It will take over Python 2 by the end of 2019



LIBRARY

Many older libraries built for Python 2 are not forwards compatible

0100
0001

ASCII

Strings are stored as ASCII by default



7/2=3

It rounds your calculation down to the nearest whole number



print "WELCOME TO GEEKSFORGEEKS"

It rounds your calculation down to the nearest whole number

LIBRARY



Many of today's developers are creating libraries strictly for use with Python 3

UNICODE

0000
0000
0100
0001

Text Strings are Unicode by default

7/2=3.5



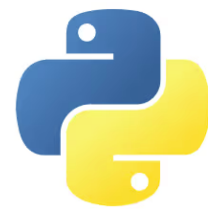
This expression will result in the expected result

print("WELCOME TO GEEKSFORGEEKS")



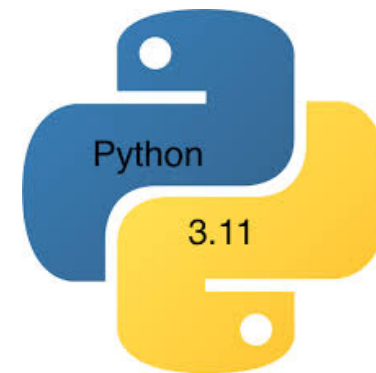
This expression will result in the expected result

Python 3.14 (in development)
Python 3.13 (stable)
Python 3.12 (stable)
Python 3.11 (security-fixes)
Python 3.10 (security-fixes)
Python 3.9 (security-fixes)
Python 3.8 (EOL)
Python 3.7 (EOL)
Python 3.6 (EOL)
Python 3.5 (EOL)
Python 3.4 (EOL)
Python 3.3 (EOL)
Python 3.2 (EOL)
Python 3.1 (EOL)
Python 3.0 (EOL)
Python 2.7 (EOL)
Python 2.6 (EOL)



~~3.6~~

3.9



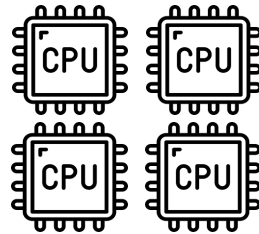
<https://docs.python.org/3.13/>

<https://docs.python.org/3.12/whatsnew/3.12.html>

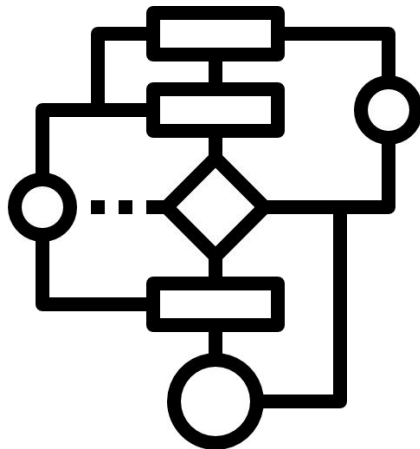
<https://docs.python.org/3.11/whatsnew/3.10.html#removed>



CPU vs GPU speed



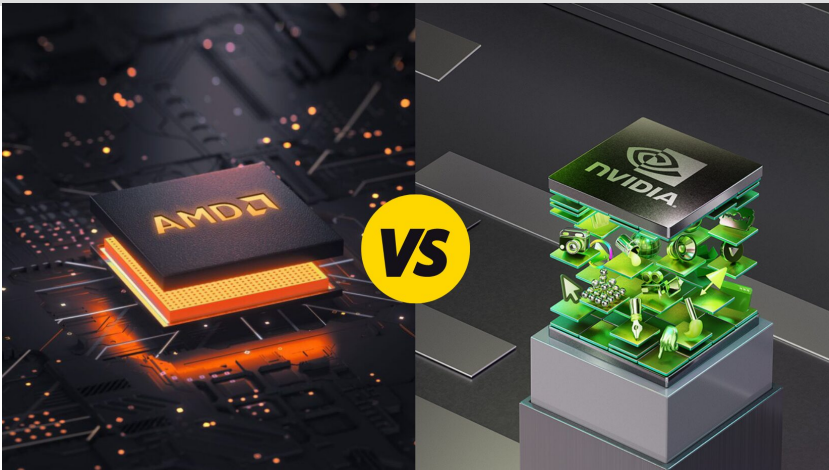
100 CPUs = 1 GPU





ROCm vs CUDA

<https://thescimus.com/blog/rocm-vs-cuda-a-practical-comparison-for-ai-developers/>



[Części PC](#) > [Karty graficzne](#) > [Serwer GPU](#) > [NVIDIA Hopper](#) > [NVIDIA HGX H100 640GB - 935-24287-0001-000](#)

NVIDIA HGX H100 640GB - 935-24287-0001-000



Graphics Engine: Hopper Memory size: 640 GB Number of tensor cores: 535 Theoretical performance: 268 TFLOP

Wszystkie u GPU architektury NVIDIA Ampere, NVIDIA Grace Hopper, NVIDIA Ada Lovelace i NVIDIA Blackwell podlegają **NCNR (Non-Cancellable, Non-Returnable) wynoszącemu 52 tygodnie**. Ponadto produkt podlega sankcjom dla niektórych krajów i konieczne jest udokumentowanie końcowego klienta.

Możemy dostarczyć te karty GPU bezpośrednio i z indywidualną ceną B2B. **Skontaktuj się z nami i zapytaj o cenę.**

Kod towaru	214.166385
Part number	935-24287-0001-000
Supermicro Part No.	GPU-NVHGX-H100-LC-88-EX2
Producent	NVIDIA
Dostępność	Na zamówienie
Gwarancja	36 miesięcy
Waga	2 kg
Cena zawiera wszystkie obowiązujące opłaty	

1 171 773 PLN bez VAT
1 441 281 PLN z VAT

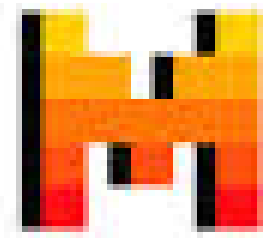
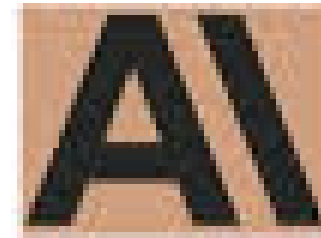
1 szt.

+

-

Dodaj do koszyka

Zapytanie o ilość



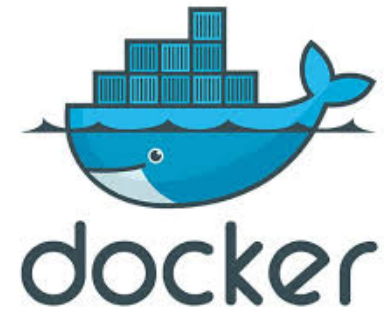
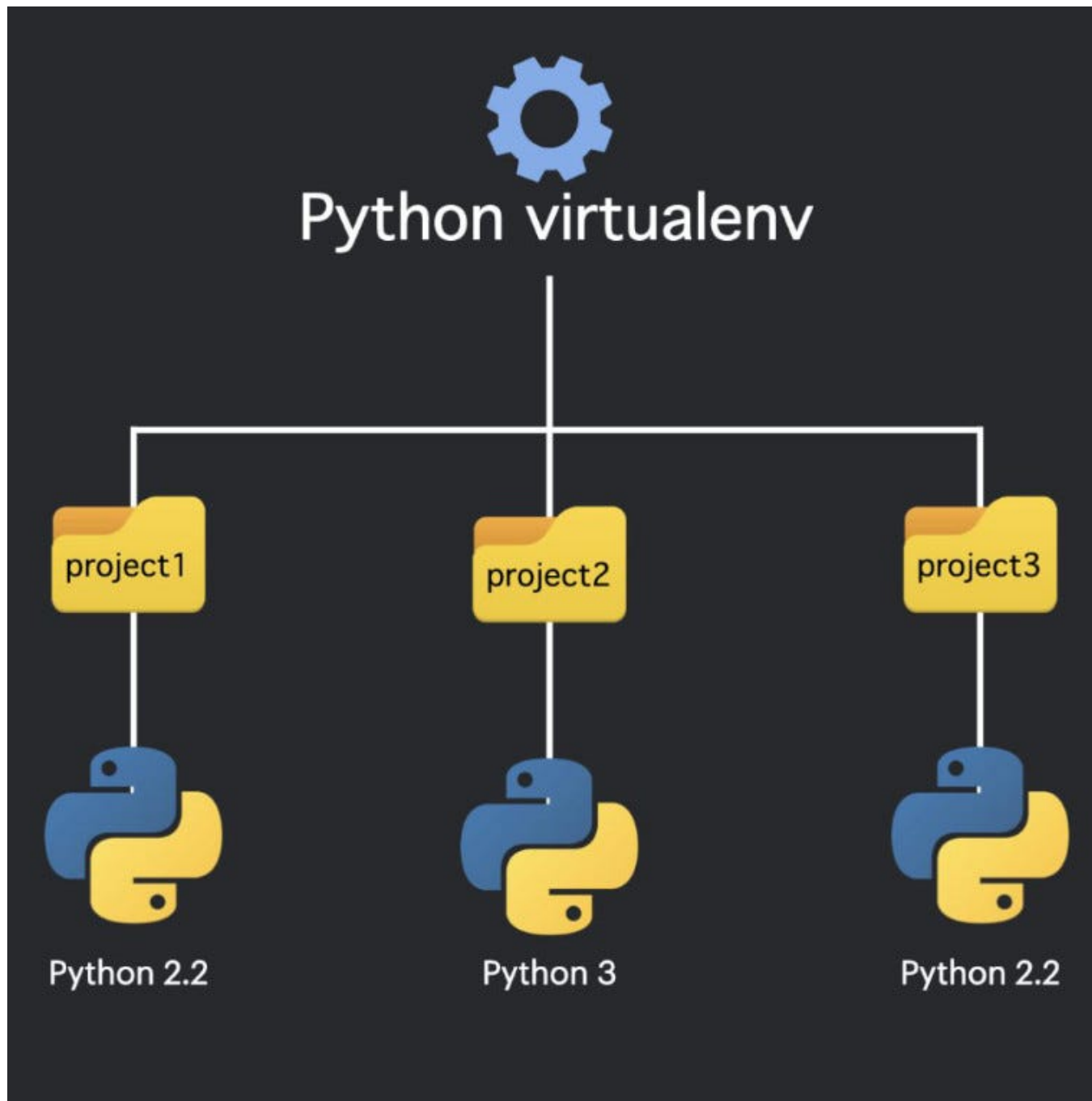


A massive computing investment

To construct this supercomputer, xAI will rely on tens of thousands of **NVIDIA H100 GPUs**. The project is expected to cost billions of dollars, making it a significant investment in the future of artificial intelligence. Musk has previously mentioned that the third version of Grok will need at least **100,000 of these high-powered chips**. This is a substantial increase from the 20,000 GPUs currently used for training Grok 2.0.

The Information also reported that Musk told investors the planned GPU cluster would be at least four times larger than anything used by xAI's competitors today. This ambitious scale is intended to provide a substantial edge in the AI industry.







We will use (and compare) different formats such as general ones (csv, xml, json, etc.) and domain specific

This means that you will need to write custom parsers* as well.



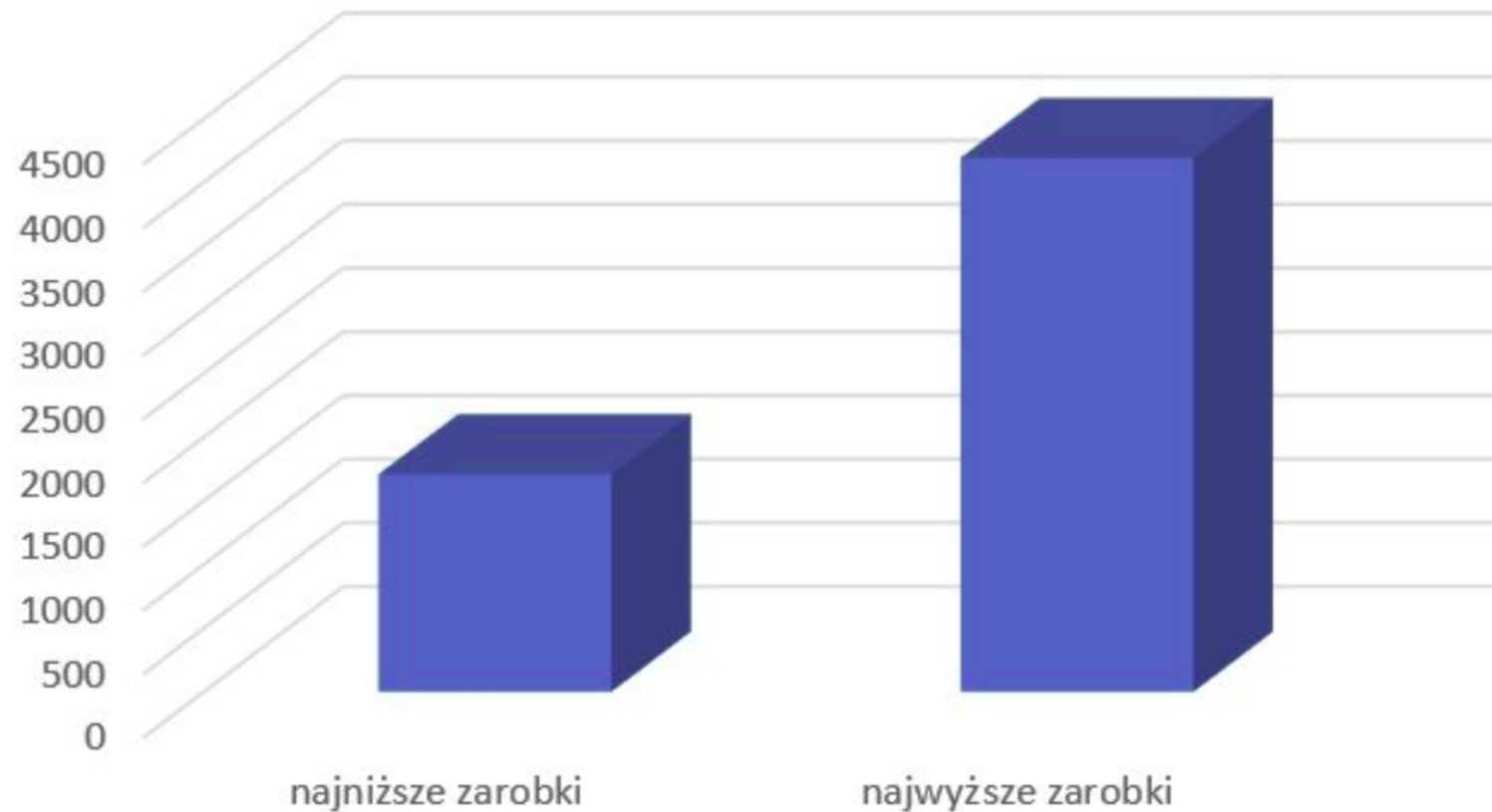
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* during labs frequently you will be asked to implement simple functionalities even if some libraries are available

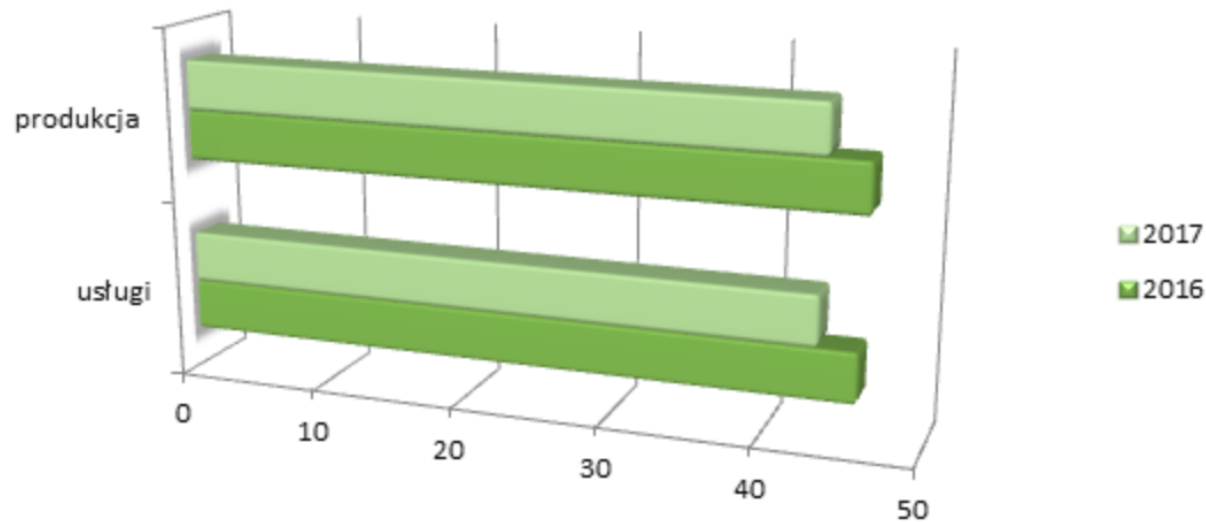
BAD PLOTS

Wykres 2. Zróźnicowanie dochodów najniższych i najwyższych wśród ankieterów



Źródło: badania własne

Wykres 2. Absencja ogólna (w tym urlopy) w przedsiębiorstwach produkcyjnych i usługowych (w dniach)

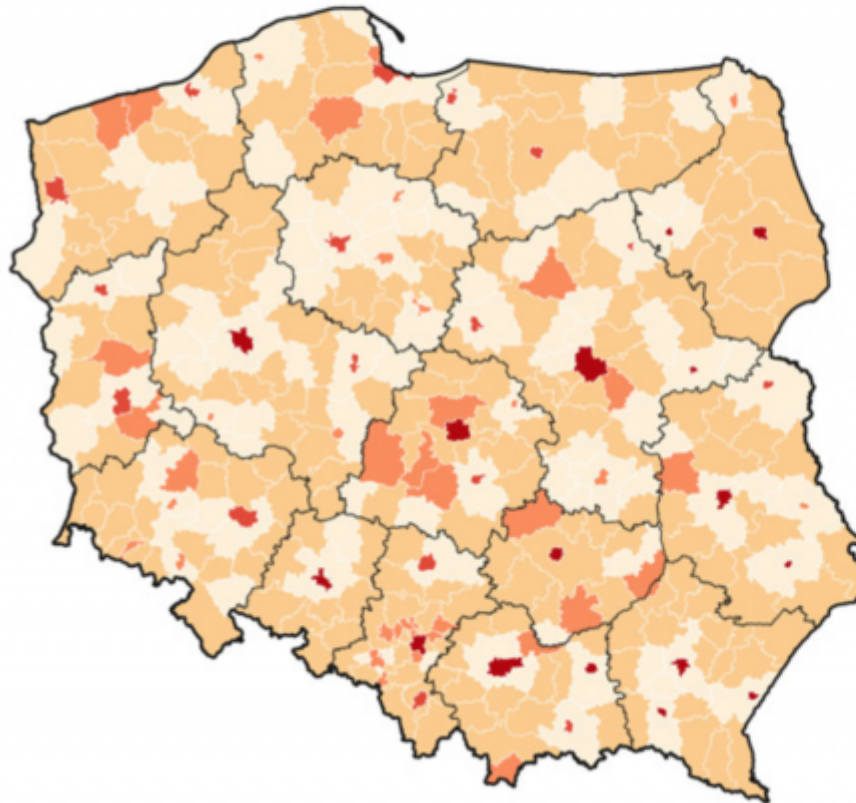


Źródło: Raport WskaźnikiHR 2017 i 2018

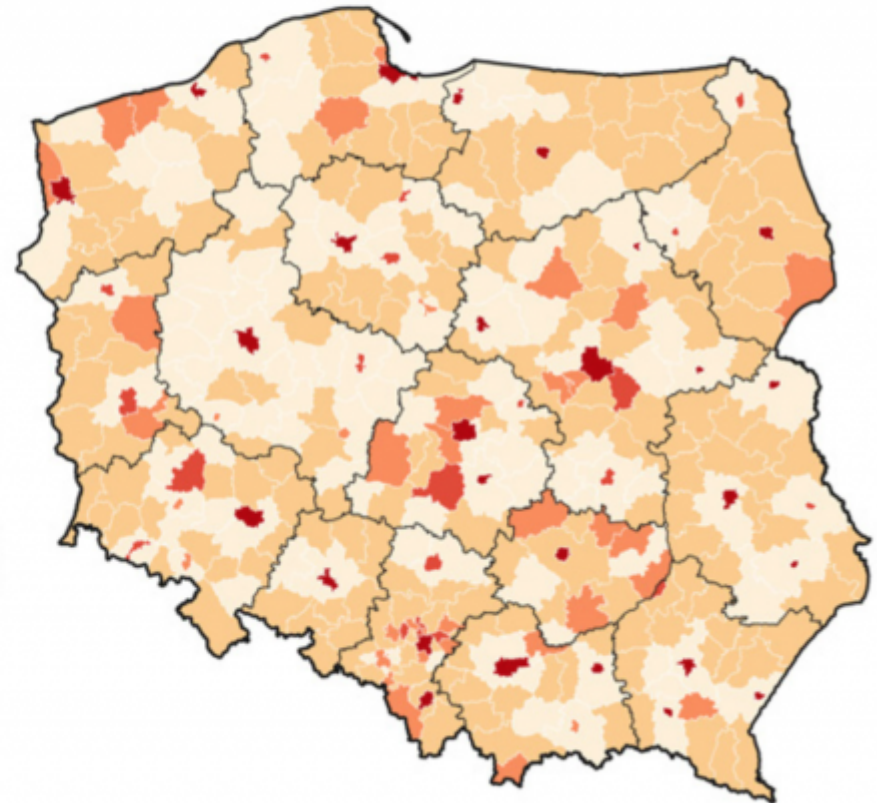
Liczba lekarzy na 1000 mieszkańców wg głównego miejsca zatrudnienia



2006



2015



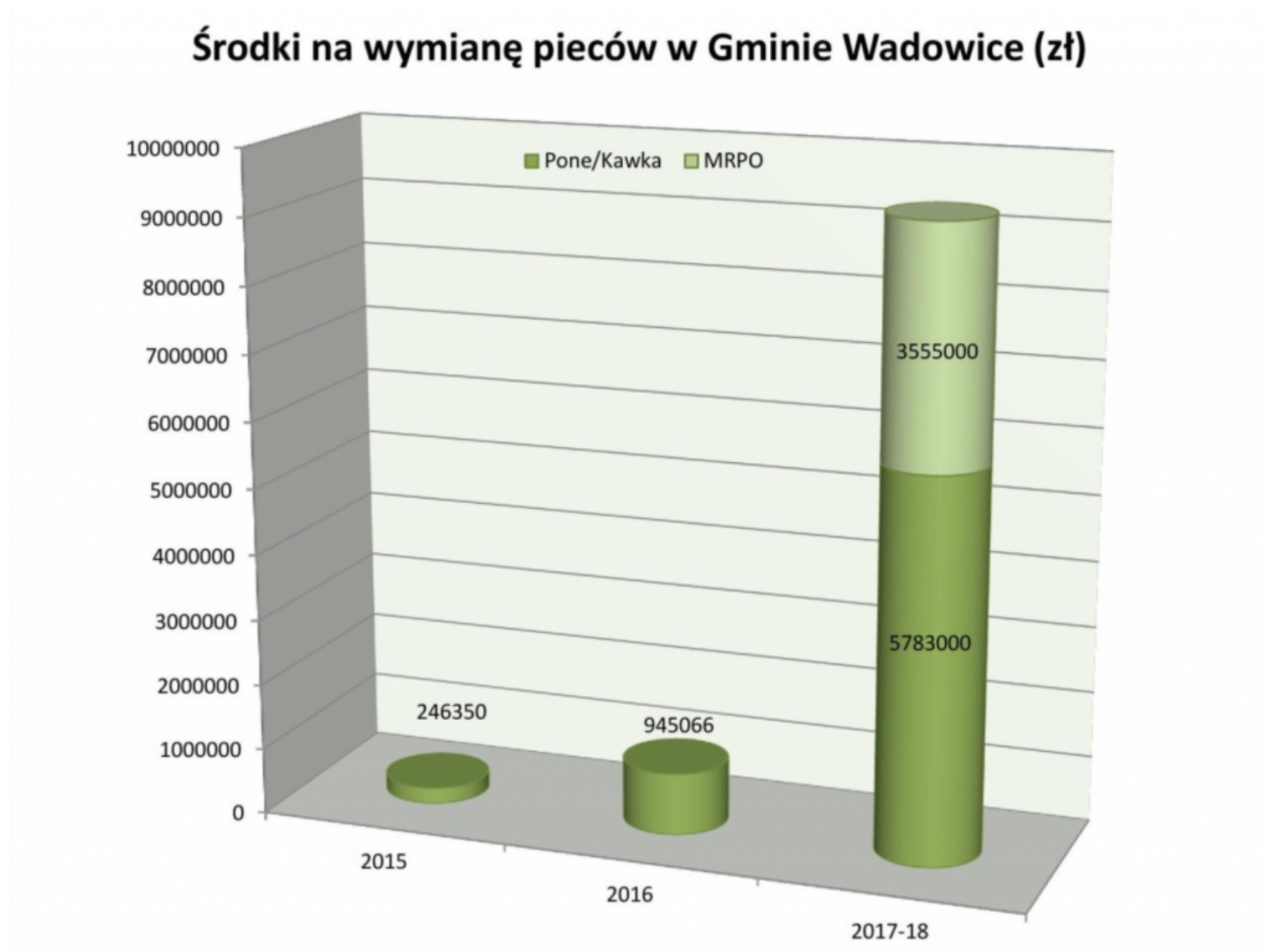
Źródło: Bank Danych Lokalnych Infografika: Szymon Piłczyk

KTÓRE Z WYDARZEŃ MIJAJĄCEGO ROKU MOŻNA, PANA(I) ZDANIEM UZNAĆ ZA NAJWAŻNIEJSZE DLA POLSKI

Dane w proc. Pytanie miało charakter otwarty



Na siódmym miejscu znalazł się konflikt wokół Trybunału Konstytucyjnego (2,1 proc.), na jedenastym protesty KOD i czarne marsze (1 proc.).

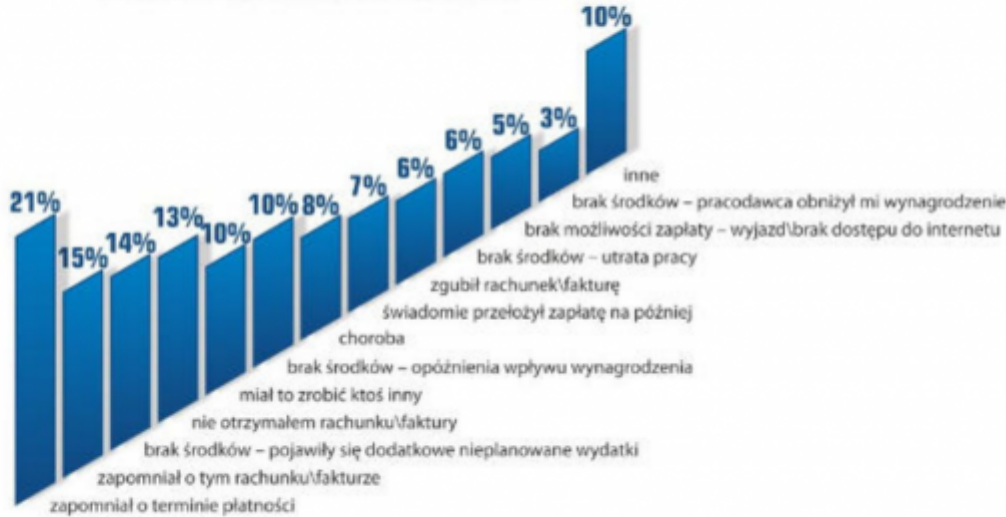




CO ROBISZ, ABY PAMIĘTAĆ
O ZAPŁACENIU RACHUNKU?

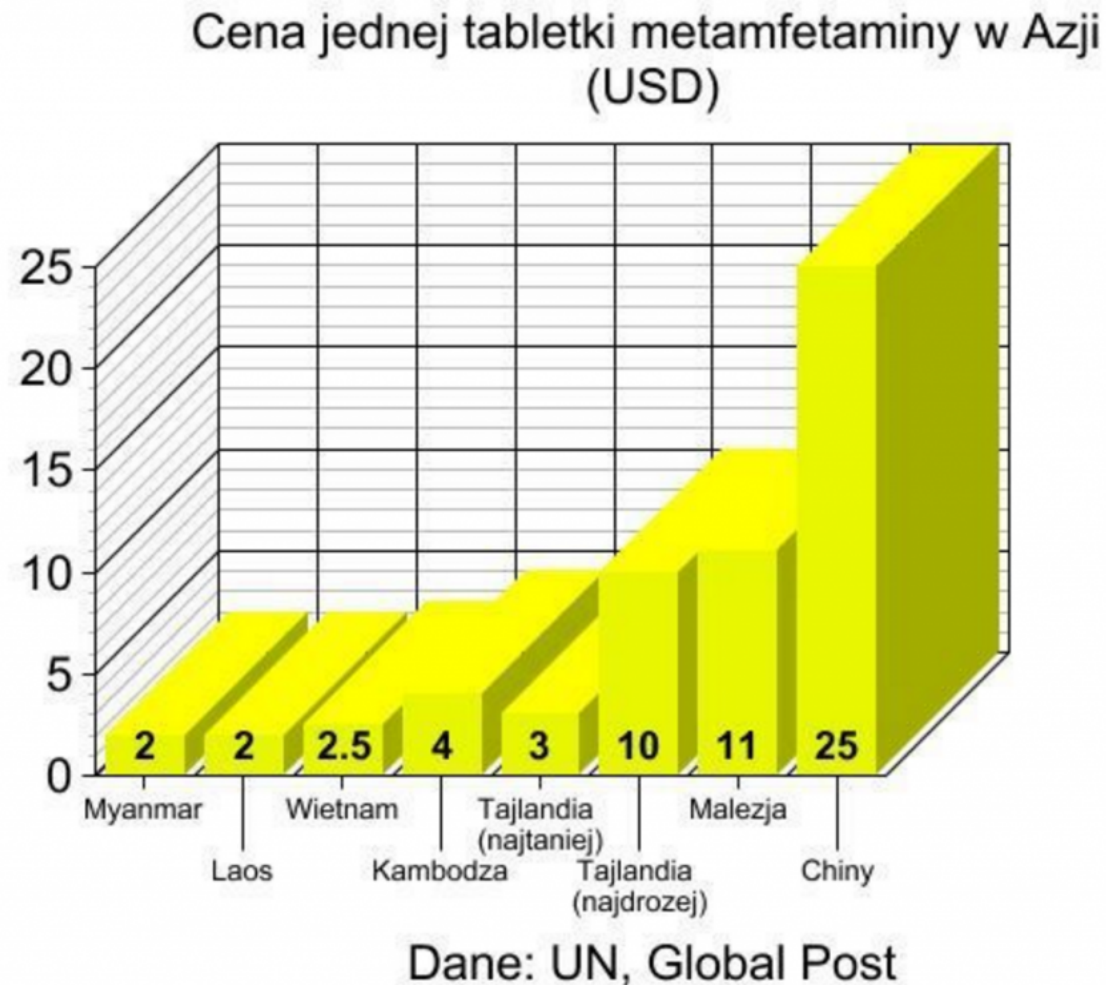


POWODY NIE PŁACENIA RACHUNKU



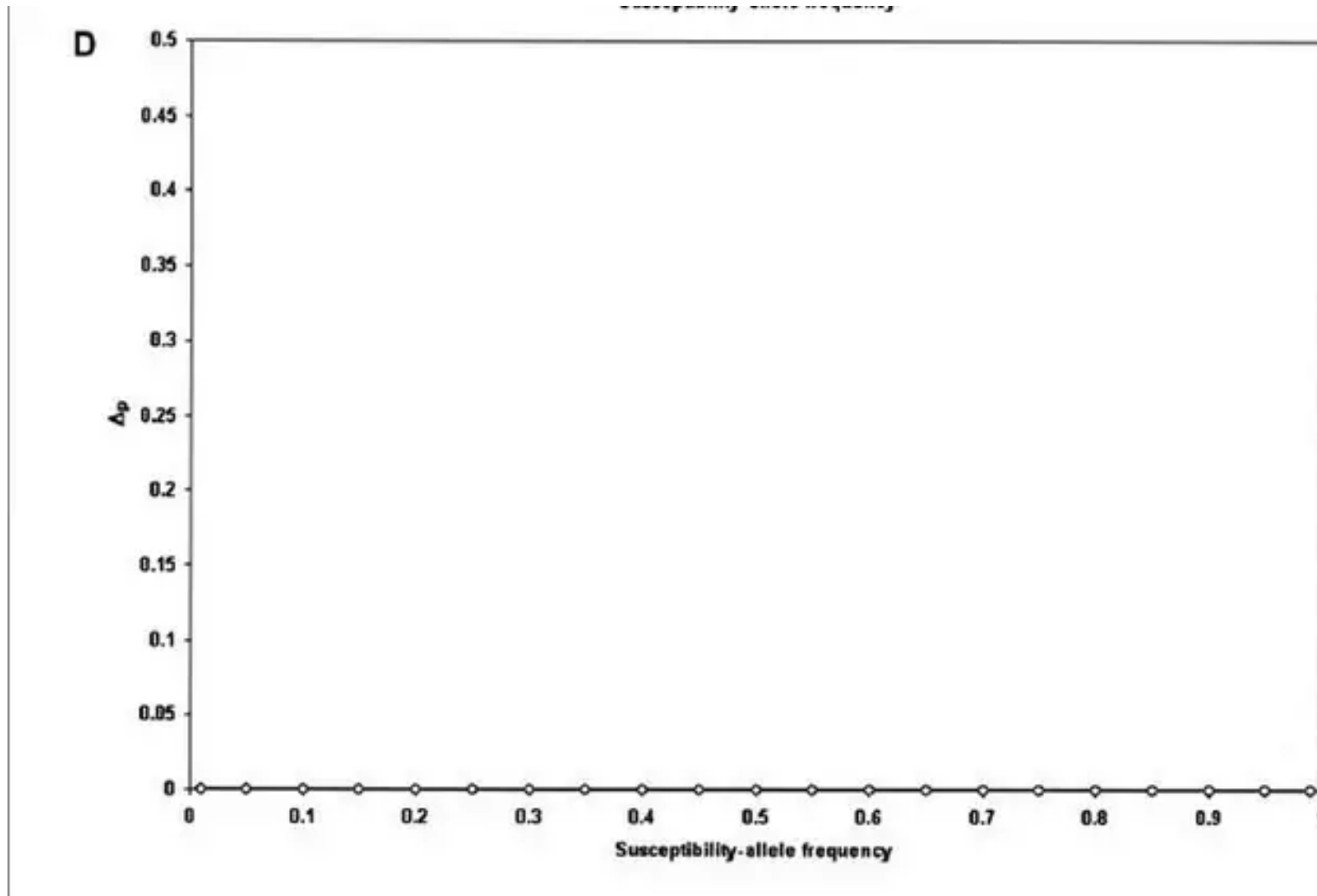
N=772

Źródło: Badanie MillwardBrown wykonane na zlecenie BIG InfoMonitor S.A.



Cena w dolarach za jedną tabletkę metamfetaminy w wybranych krajach Azji (wykres graficzny); wg danych: UN, Global Post. / Fot. Paweł Jankowski/Global Post
Zdjęcie 2 z 2

ZAMKNIJ ✕



Wittke-Thompson JK, Pluzhnikov A, Cox NJ (2005) Rational inferences about departures from Hardy-Weinberg equilibrium. American Journal of Human Genetics 76:967-986, Figure 1

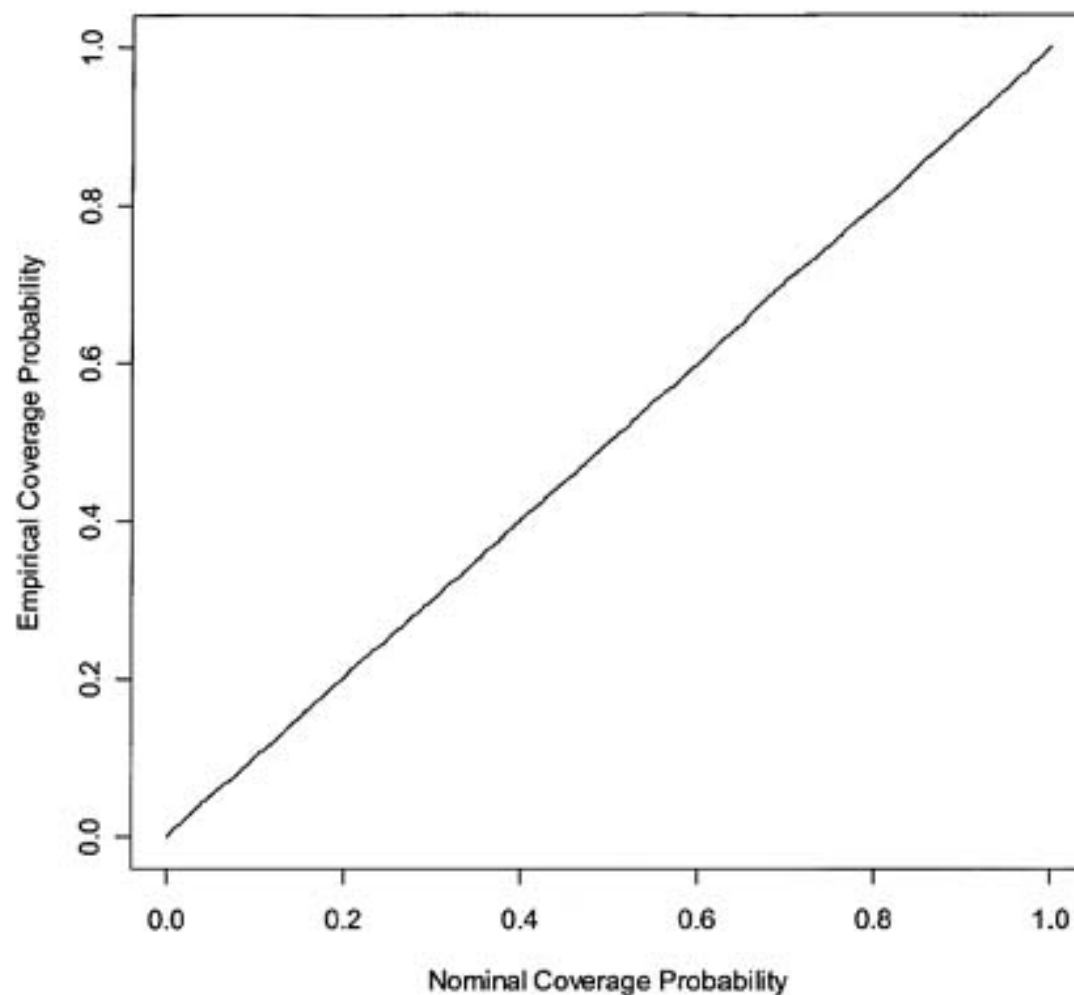


Figure 1 Empirical coverage of CIs for the relative-risk parameter β of haplotype 01100. Results are based on 10,000 simulated data sets with the same haplotype frequencies as the FUSION data. Haplotype 01100 has a multiplicative effect on disease risk, with $\beta = 0.35$.

Epstein MP, Satten GA (2003) Inference on haplotype effects in case-control studies using unphased genotype data. *American Journal of Human Genetics* 73:1316-1329, Figure 1



COMMUTING TO WORK

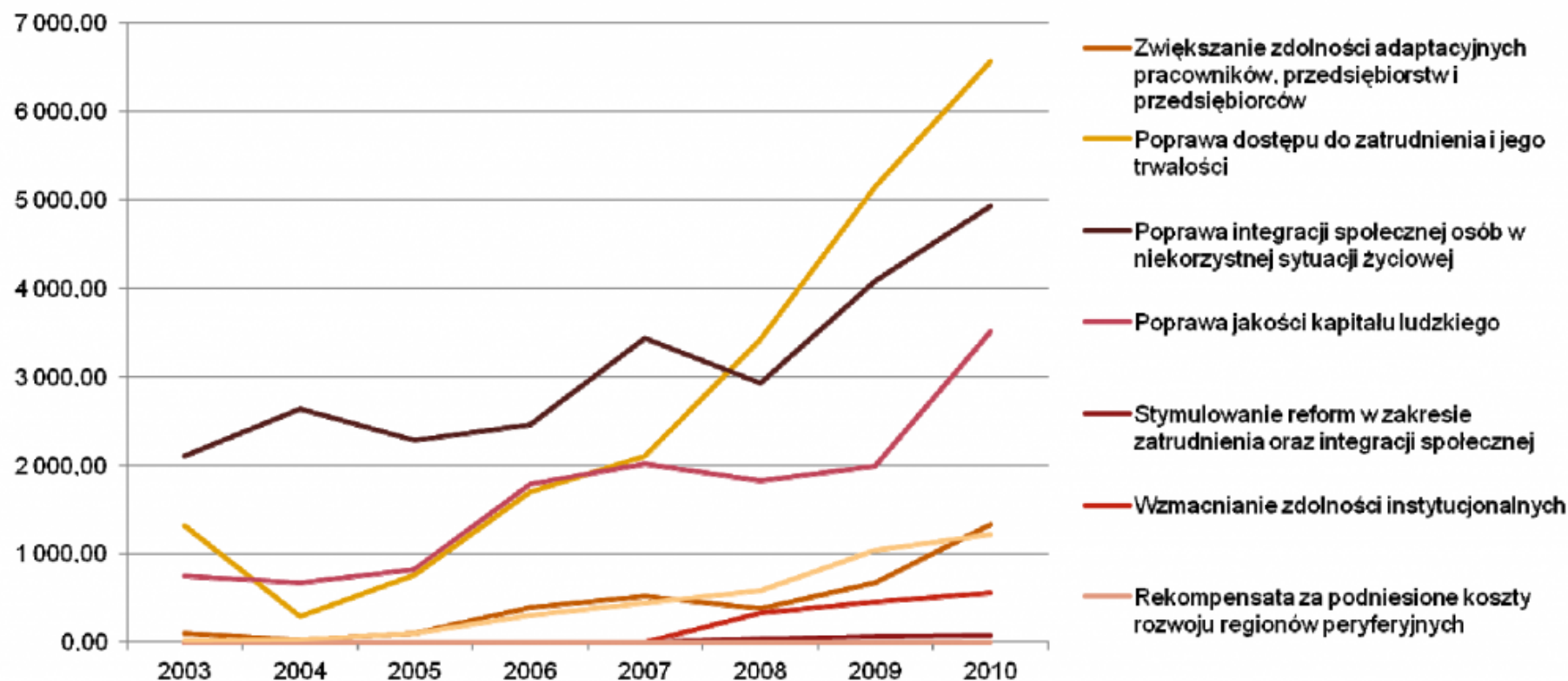
CHICAGO / LOS ANGELES / NEW YORK CITY / ATLANTA
SAN FRANCISCO / HOUSTON / WASHINGTON / SEATTLE



Martha Kang McGill, Data source: Census Bureau's American Community Survey 2008

Rozwój Zasobów Ludzkich – ogół wydatków w latach 2003-2010 w mln zł

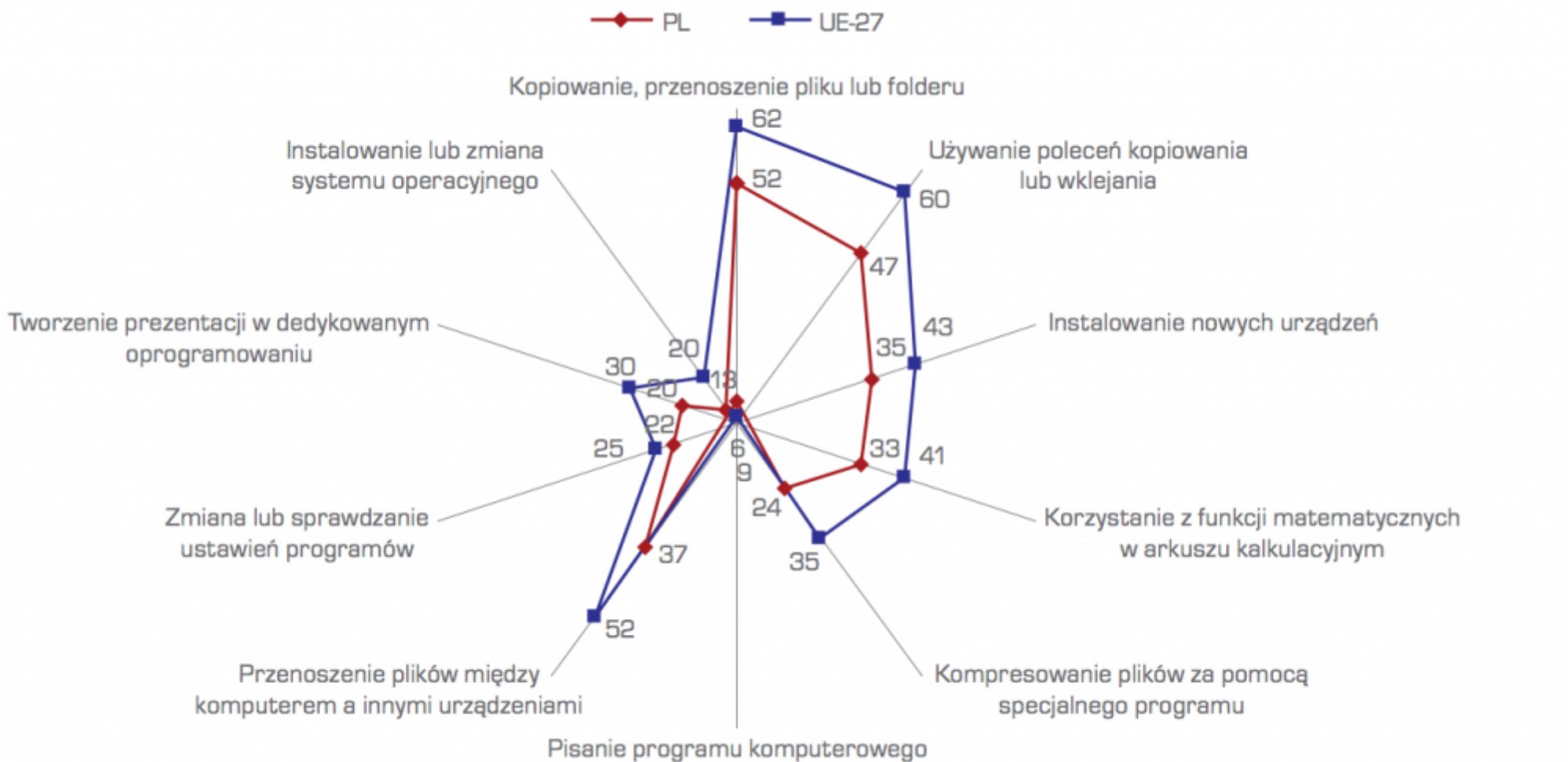
• Poziom wydatków w tej kategorii był w tych latach determinowany głównie przez wydatki w trzech obszarach tematycznych: Poprawa dostępu do zatrudnienia i jego trwałości (5,16%), Poprawa integracji społecznej osób w niekorzystnej sytuacji życiowej (6,02%), a także Poprawa jakości kapitału ludzkiego (3,24%).



PwC

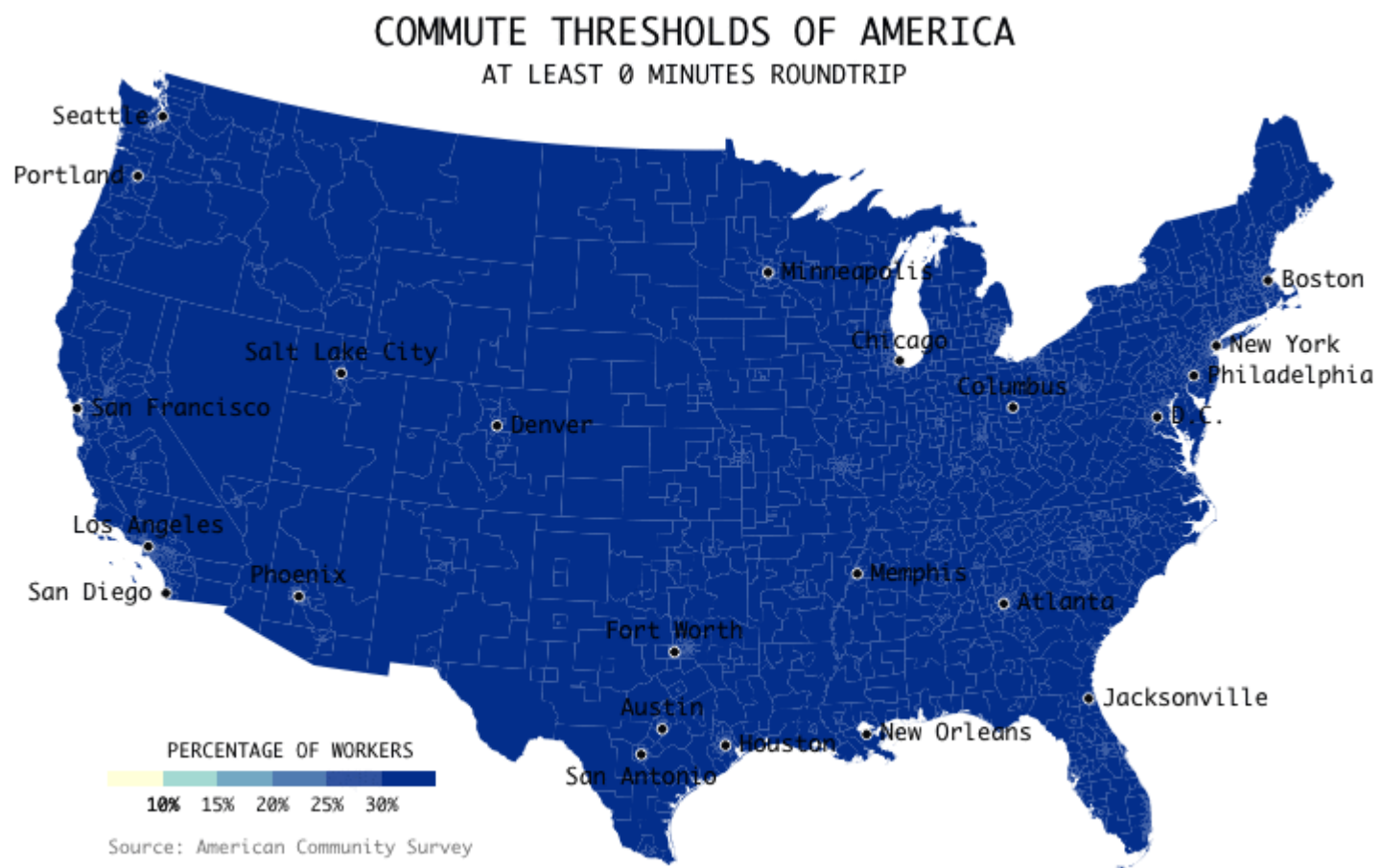
marzec 2012
13

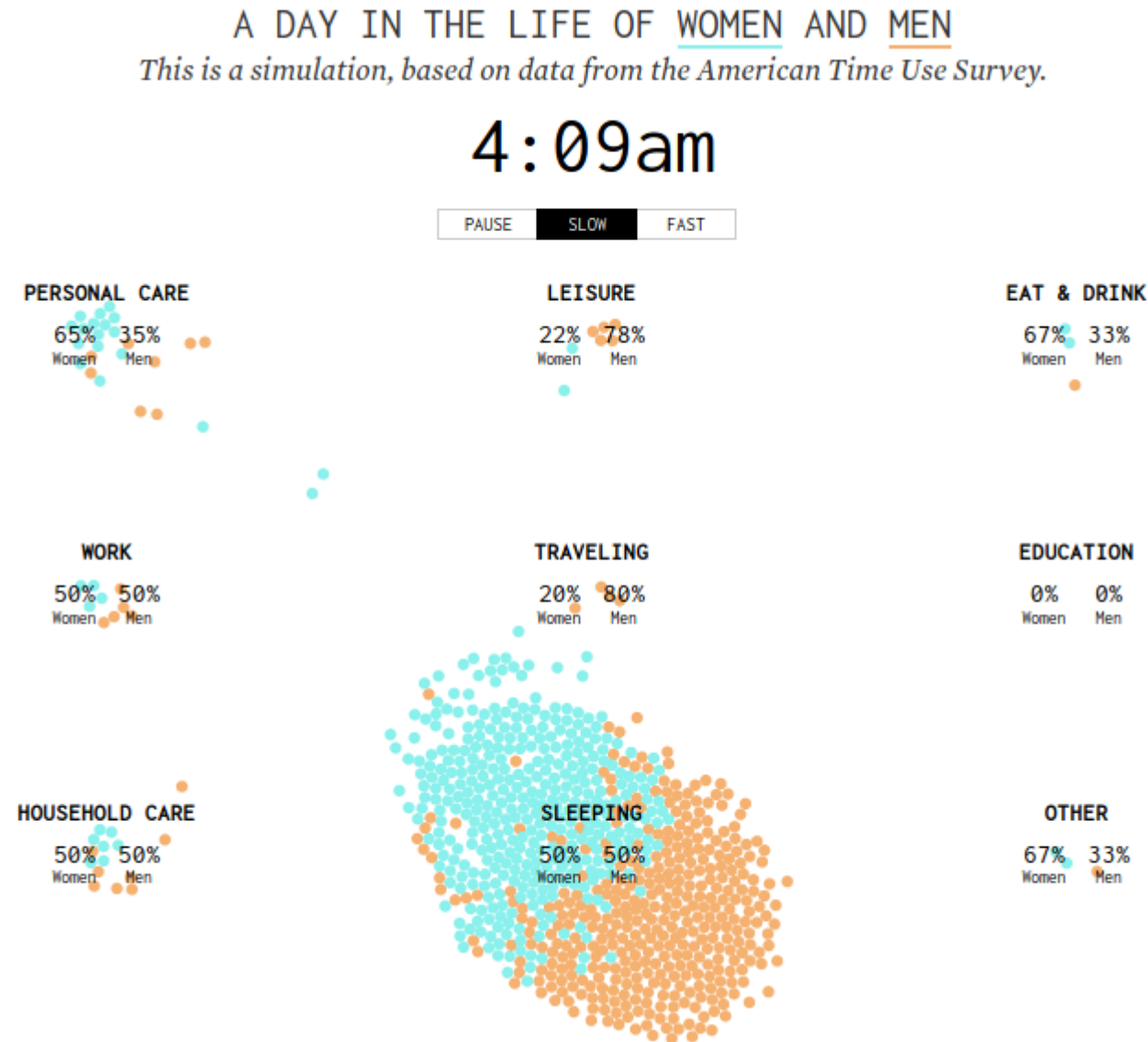
Wykres 8. Osoby wykonujące określone czynności związane z obsługą komputera w 2012 r. – Polska a średnia unijna [w %]



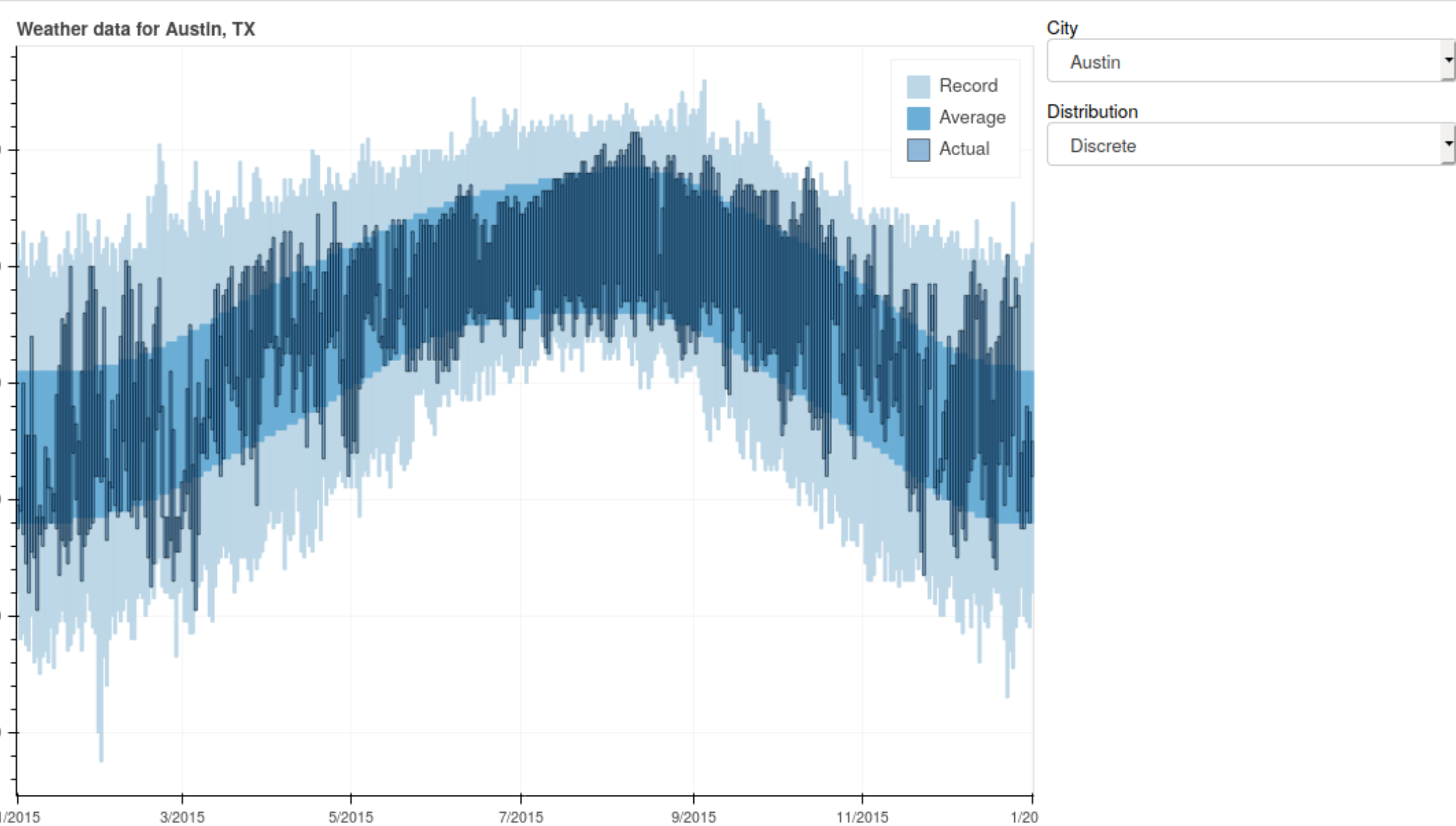
Opracowanie własne na podstawie danych Eurostatu.

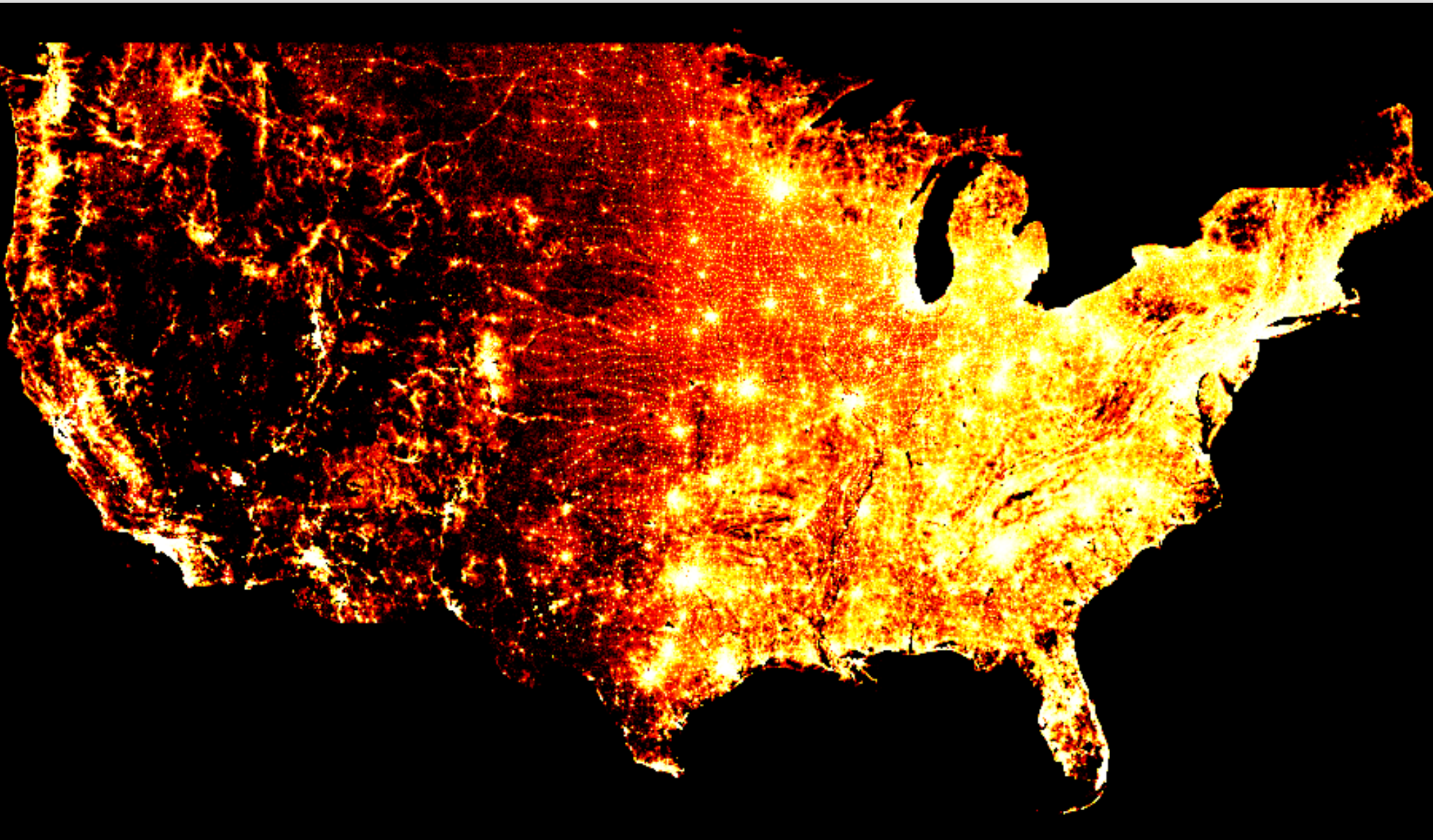
HOW ABOUT NICE PLOTS ?





<https://flowingdata.com/2019/03/06/women-men-timeuse/>



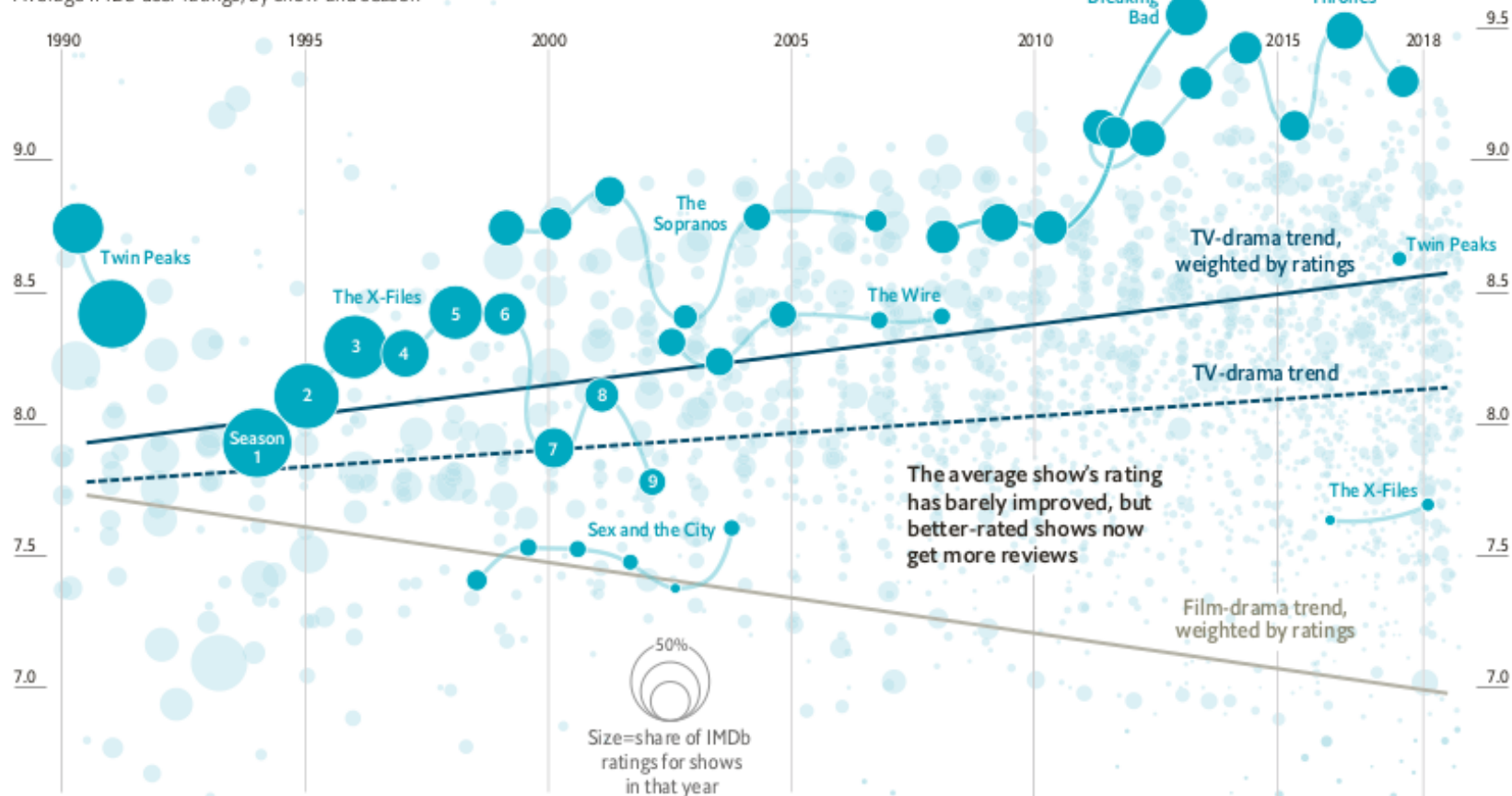


300M points
1 point = 1 person

<https://datashader.org/>

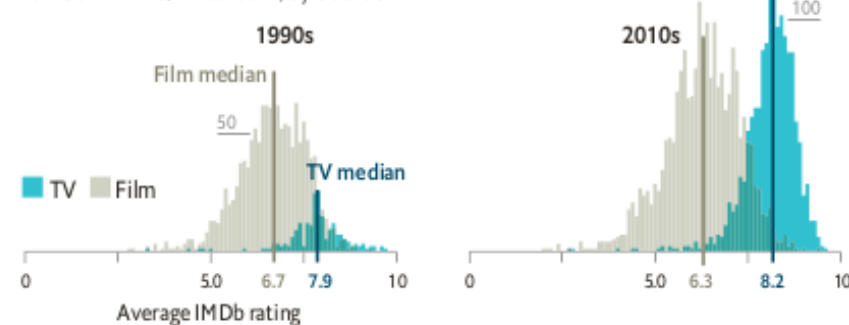
TV dramas shown in America

Average IMDb user ratings, by show and season*



Distribution of ratings

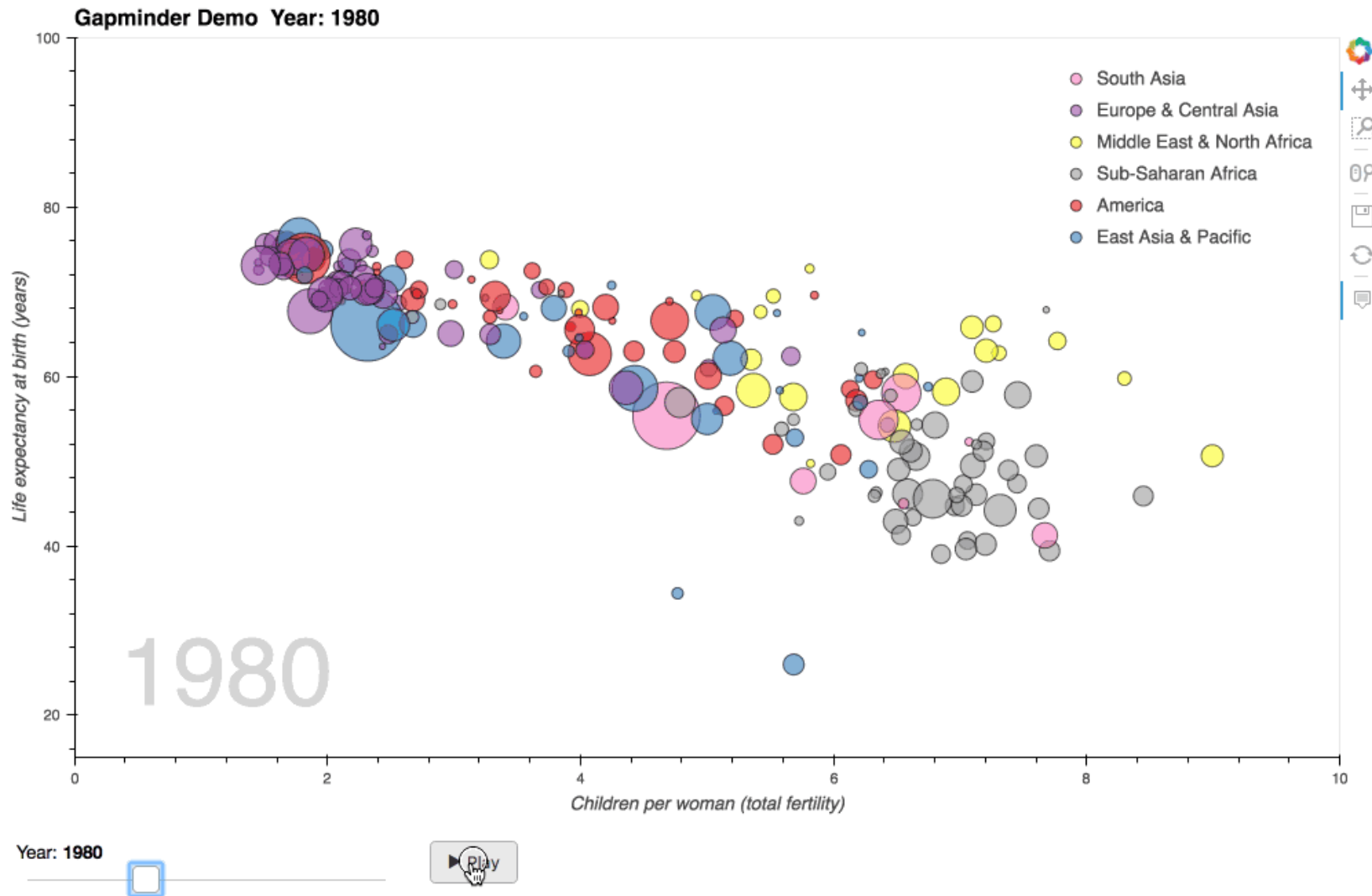
Number of films/TV seasons, by decade



Far more TV is made now than in the 1990s. There are more highly rated shows, but just as many that disappoint reviewers

*Seasons with at least 100 ratings on average

Sources: IMDb; OMDb; The Economist



Hans Rosling
1948-2017

Hans Rosling
1948-2017



https://www.ted.com/talks/hans_rosling_the_best_stats_you_ve_ever_seen#t-72754

Thank you for your time
and
See you at the next lecture

Any other
questions & comments

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