

(Mis)information visualization

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Committee on Evolutionary Biology
University of Chicago

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Outline

Good data visualization

Academic

Media

Excel

Things to remember

Outline

Good data visualization

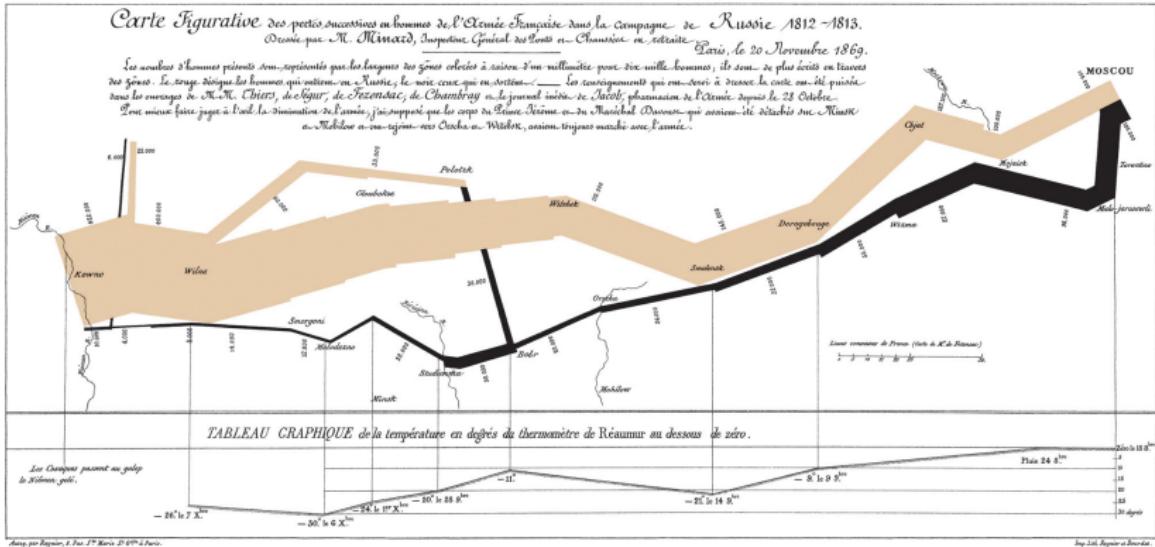
Academic

Media

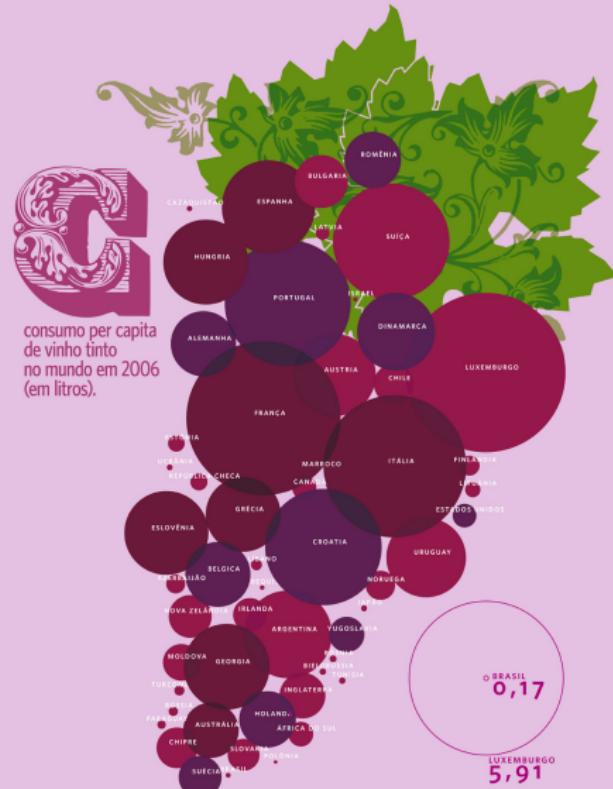
Excel

Things to remember

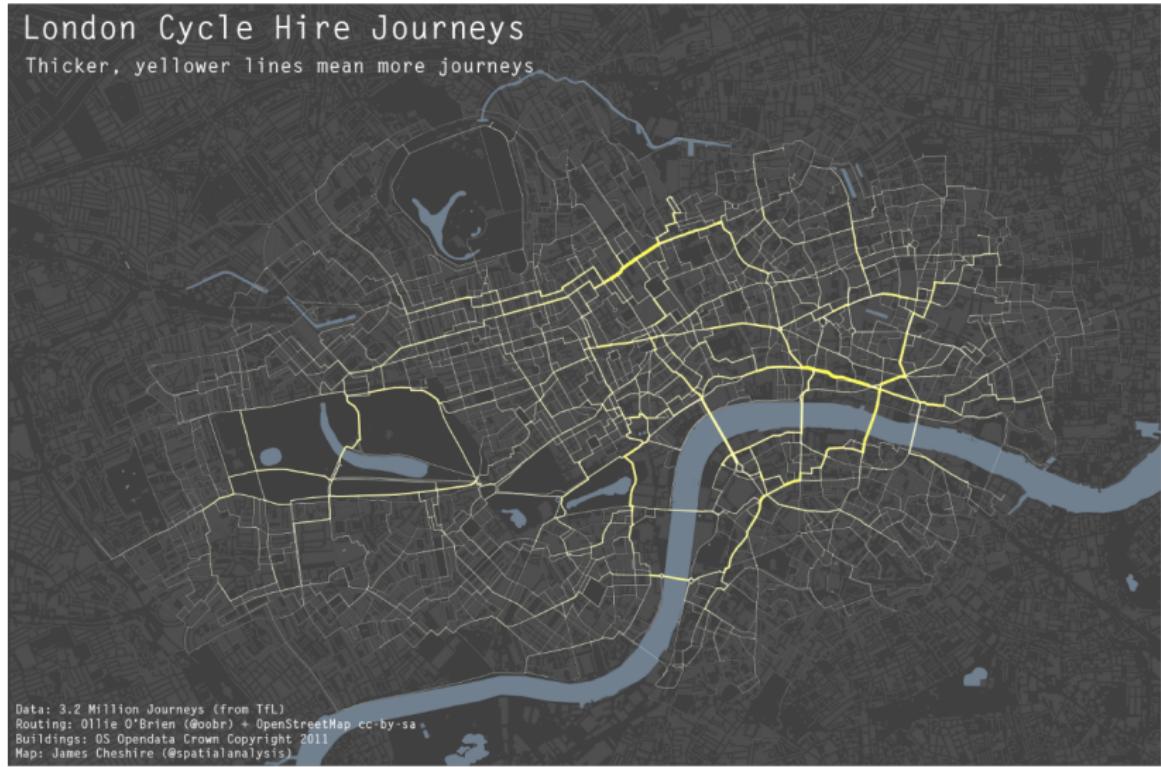
Minard's depiction of Napoleon's invasion of Russia



Beautiful



Tells a story



Gives advice



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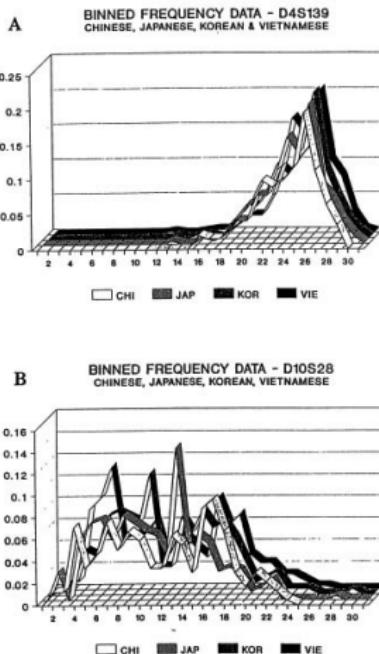


FIG. 4. Fixed bin distribution (histogram) for two loci and four Asian subpopulations (used with permission from John Hartmann): the boundaries of the 30 bins (vertical axis) are determined by the FBI; these bins are not of equal length. Sample sizes (numbers of individuals) for Chinese, Japanese, Korean and Vietnamese are 103, 125, 93 and 215 for D4S139 and 120, 137, 100 and 193 for D10S28. The horizontal axis is the bin number; bins are not of equal length.

These say what exactly?

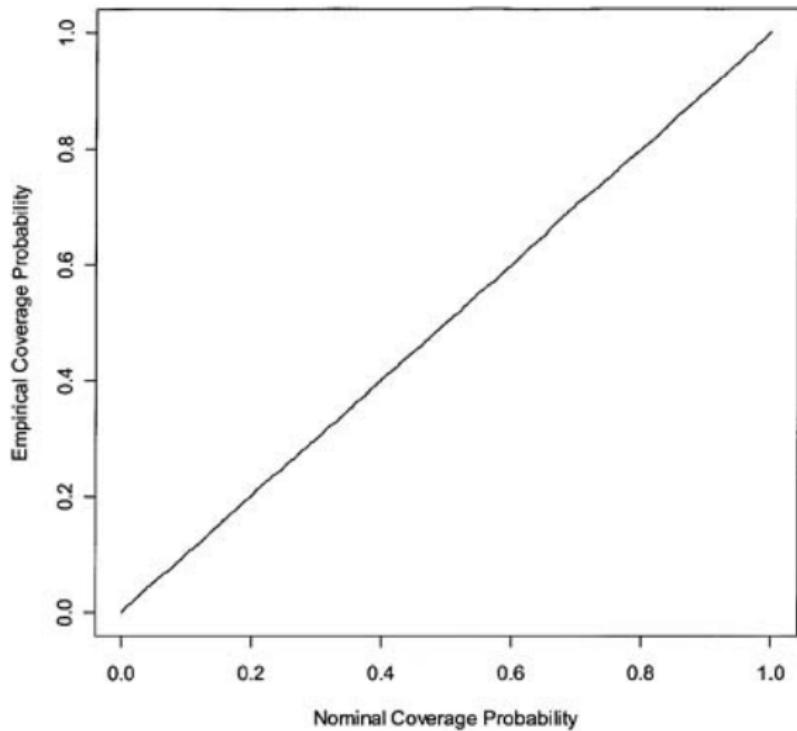
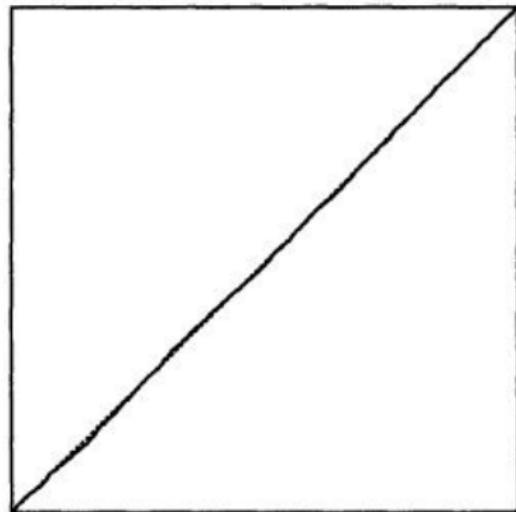
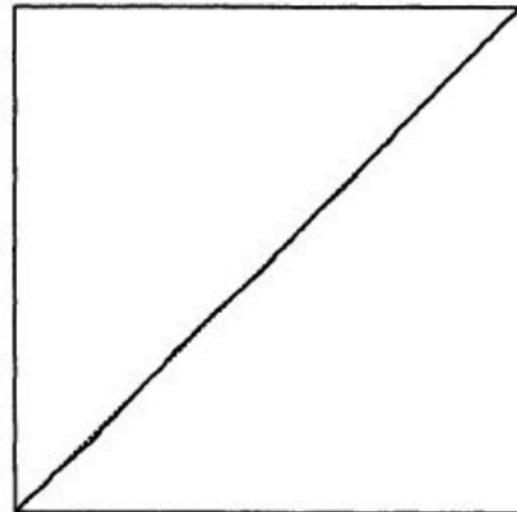


Figure 1 Empirical coverage of CIs for the relative-risk parameter β of haplotype 01100. Results are based on 10,000 simulated data sets with the same haplotype frequencies as the FUSION data. Haplotype 01100 has a multiplicative effect on disease risk, with $\beta = 0.35$.

Surely that was a unique phenomenon...



(a)



(b)

Figure 1. SRQ Plots of T_i/T_n (Vertical Axes) Against i/n (Horizontal Axes) for the Gibbs Sampler (a) and an Alternating Gibbs/Independence Sampler (b) for the Pump Failure Data Based on Runs of Length 5,000. Lines through the origin with unit slope are shown dashed; axis ranges are from 0 to 1 for all axes.

What is worse than one pie chart?

Distribution of All TFBS Regions

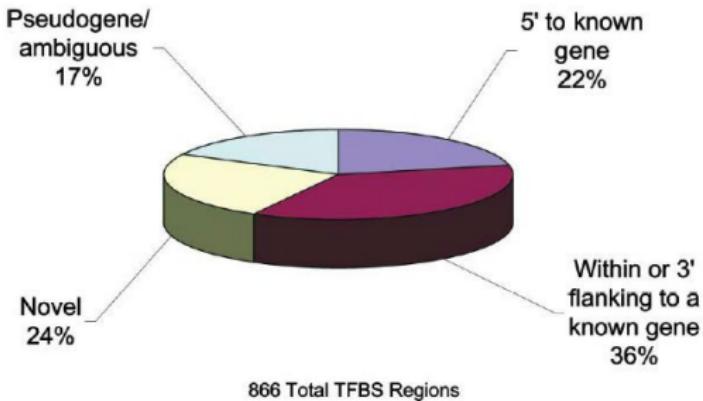


Figure 1. Classification of TFBS Regions

TFBS regions for Sp1, cMyc, and p53 were classified based upon proximity to annotations (RefSeq, Sanger hand-curated annotations, GenBank full-length mRNAs, and Ensembl predicted genes). The proximity was calculated from the center of each TFBS region. TFBS regions were classified as follows: within 5 kb of the 5' most exon of a gene, within 5 kb of the 3' terminal exon, or within a gene, novel or outside of any annotation, and pseudogene/ambiguous (TFBS overlapping or flanking pseudogene annotations, limited to chromosome 22, or TFBS regions falling into more than one of the above categories).

Can it even get worse?

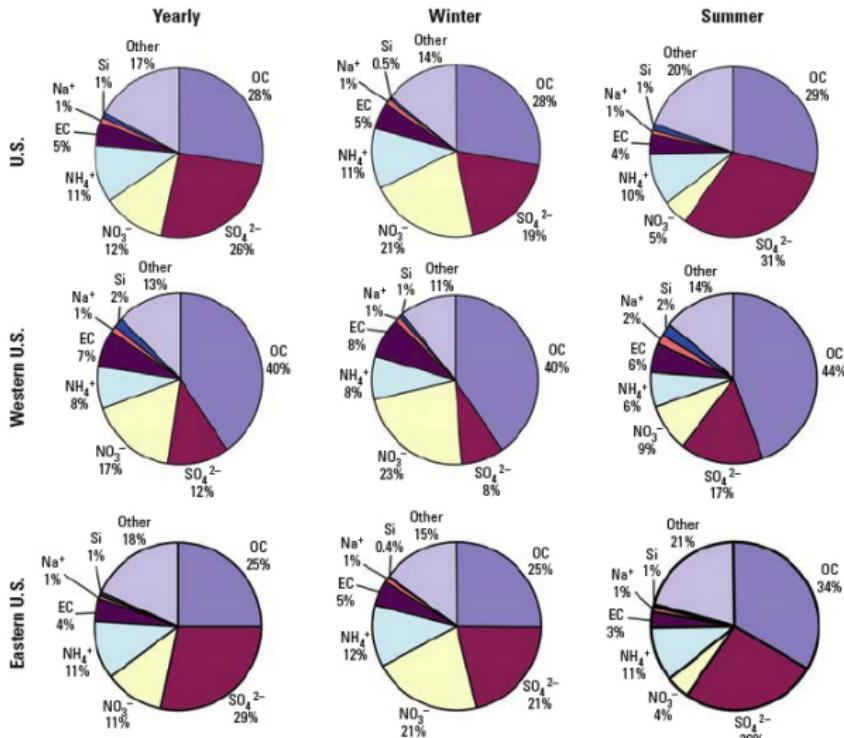
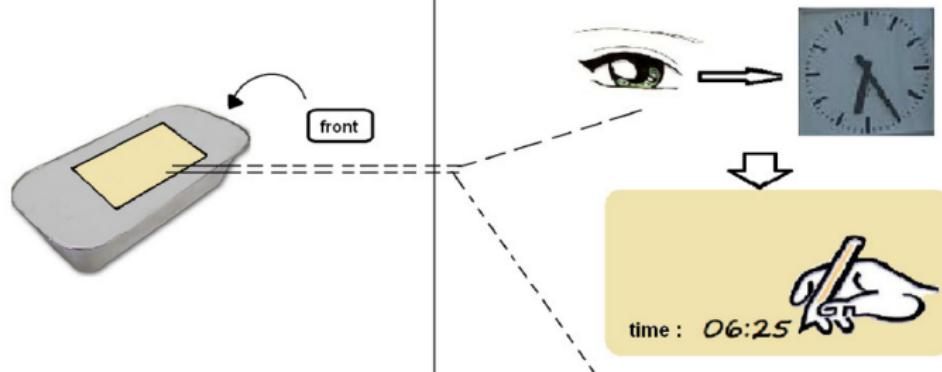
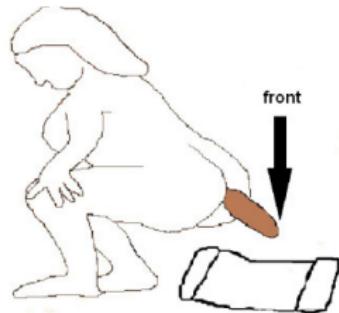


Figure 3. Percent of PM_{2.5} composition by component for yearly, winter, and summer averages, by region.

Pardon me as I vomit



wtf is this

nerd shit

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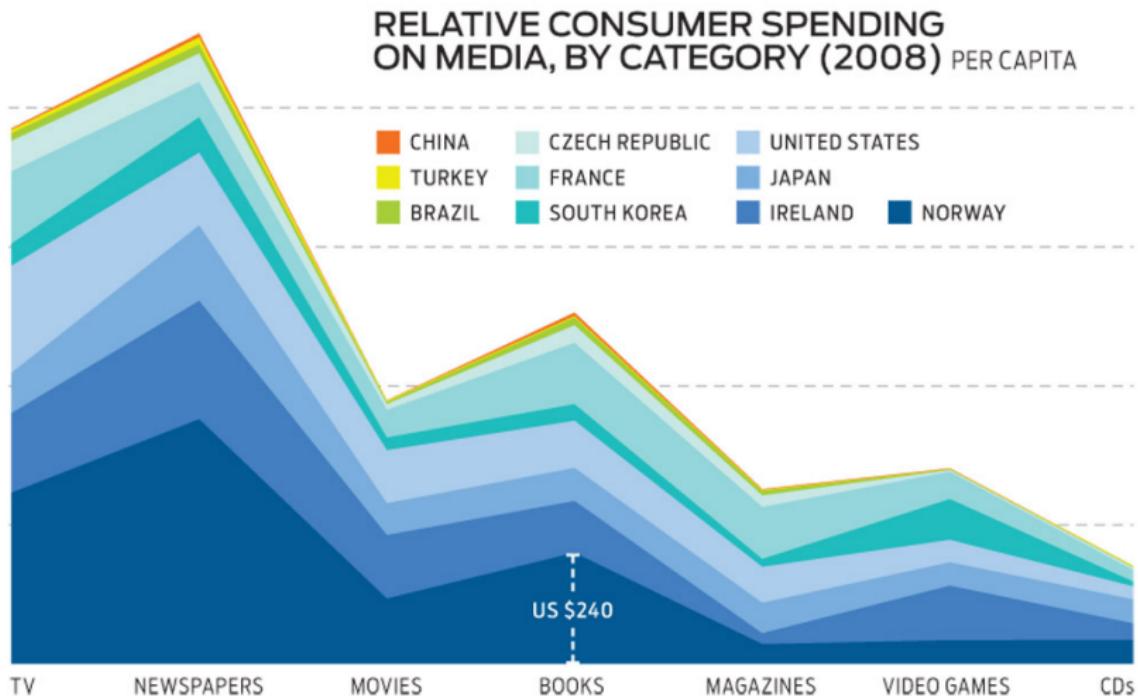
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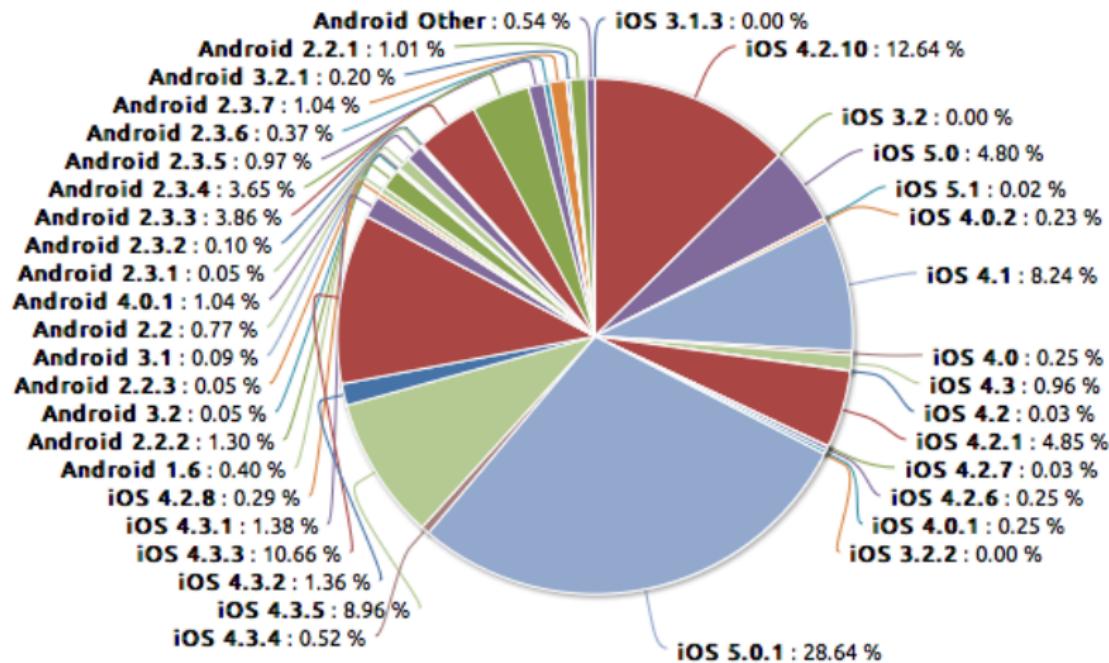
Things to remember

Wrong choice



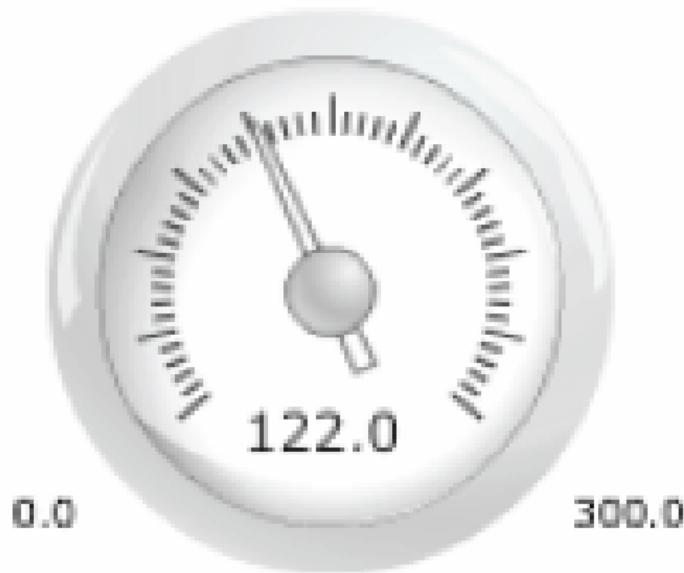
My sides

Crashes by OS Version Normalized (12/1 - 12/15)

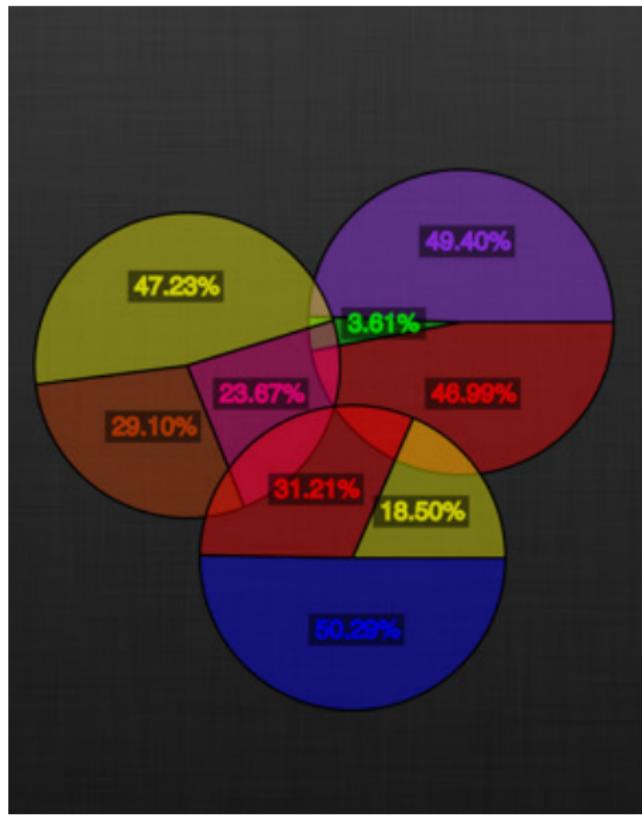


Does this even mean anything?

Current Bike Production Rate



Why can't I hold all these graphical sins?



What is this I don't even

Sotheby's / Christie's

Worldwide Sales Market Share Analysis

1985

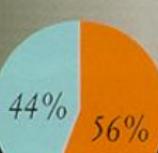
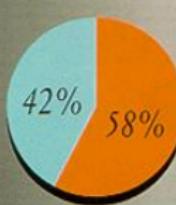
1986

1987

1988

1989

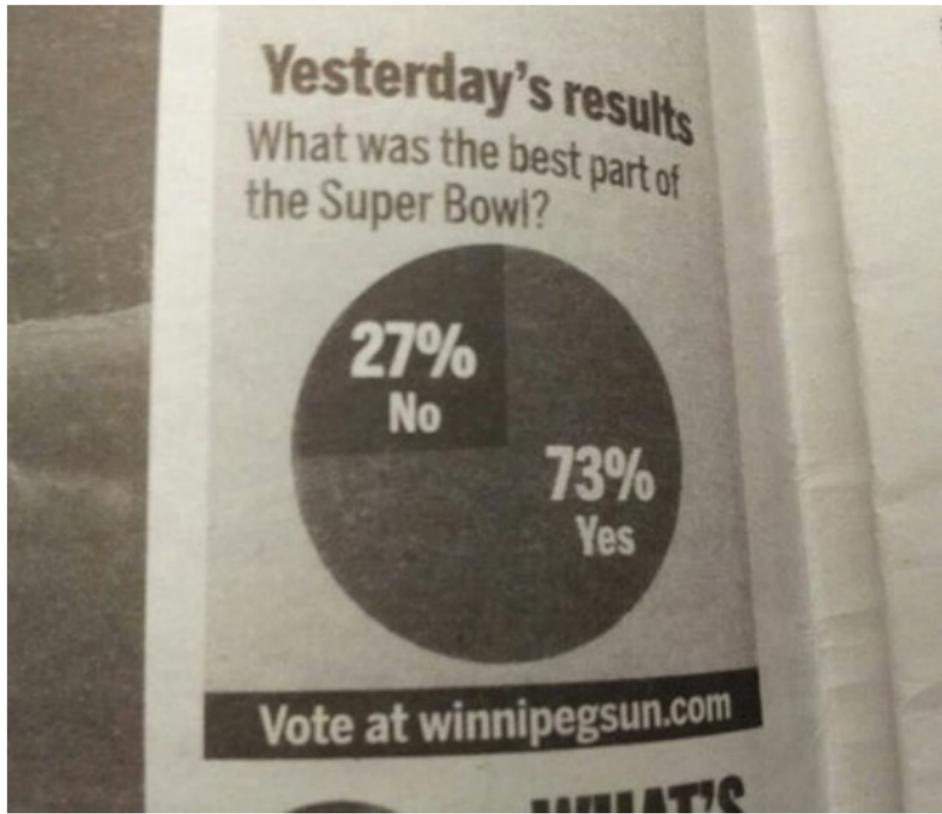
1990



SOTHEBY'S
CHRISTIE'S

Market Share Analysis With Buyer's Premium

Oh god how did this get here I am not good with questions



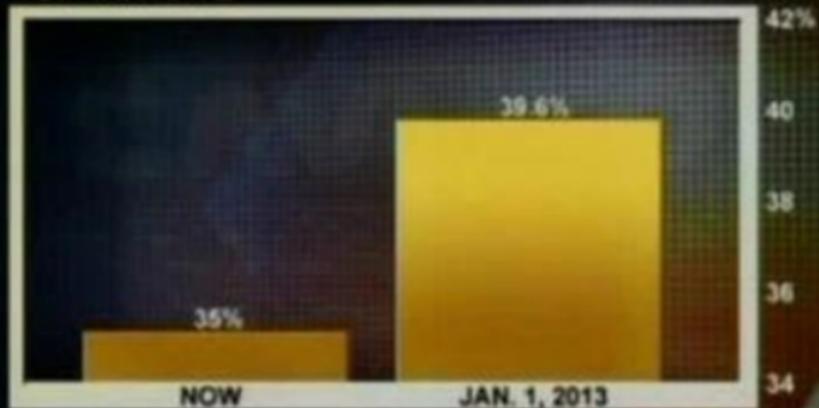
Fox is an easy target



A really easy target...

IF BUSH TAX CUTS EXPIRE

TOP TAX RATE



8:01 p. ET

FOX
BUSINESS

TOP STORIES

TECHNOLOGY

CONSUMER

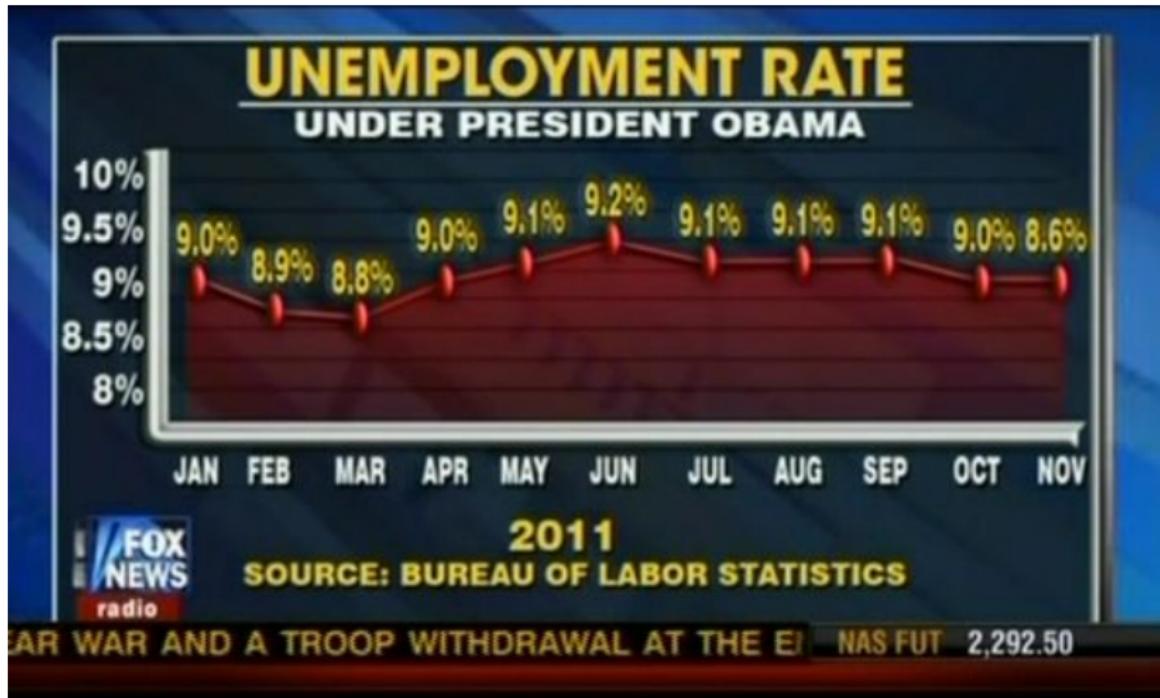
WITH THE JUSTICE DEPARTMENT AND ACQUIRES FULL T

DOW 13008.68 ▼ 64.33

S&P 1379.32 ▼ 5.98

NASDAQ 2939.52 ▼ 6.32

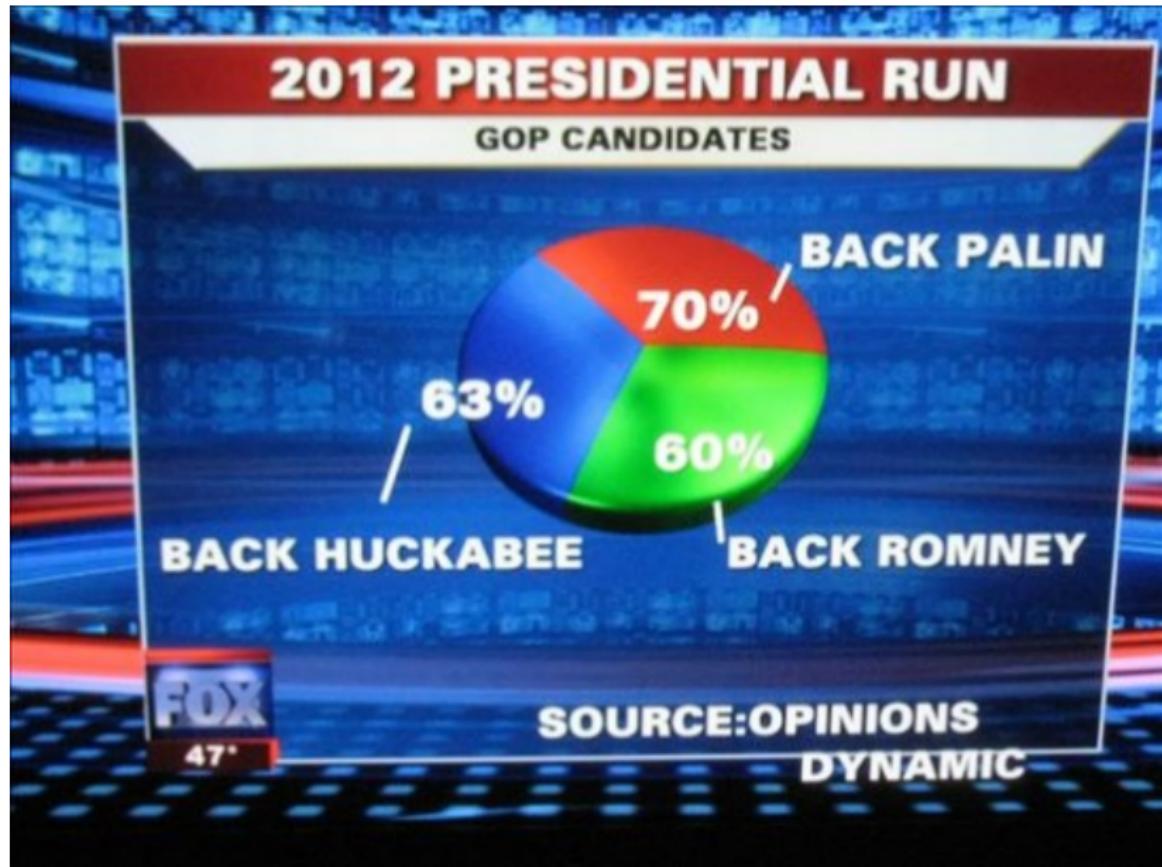
Too easy even



[Screams internally]



They can't even get the worst graph "right"...



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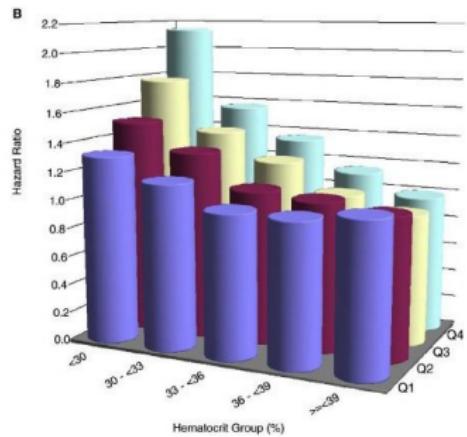
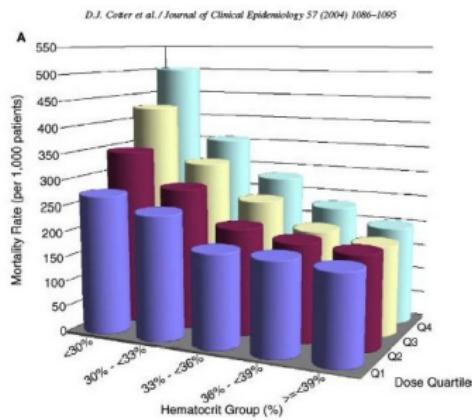
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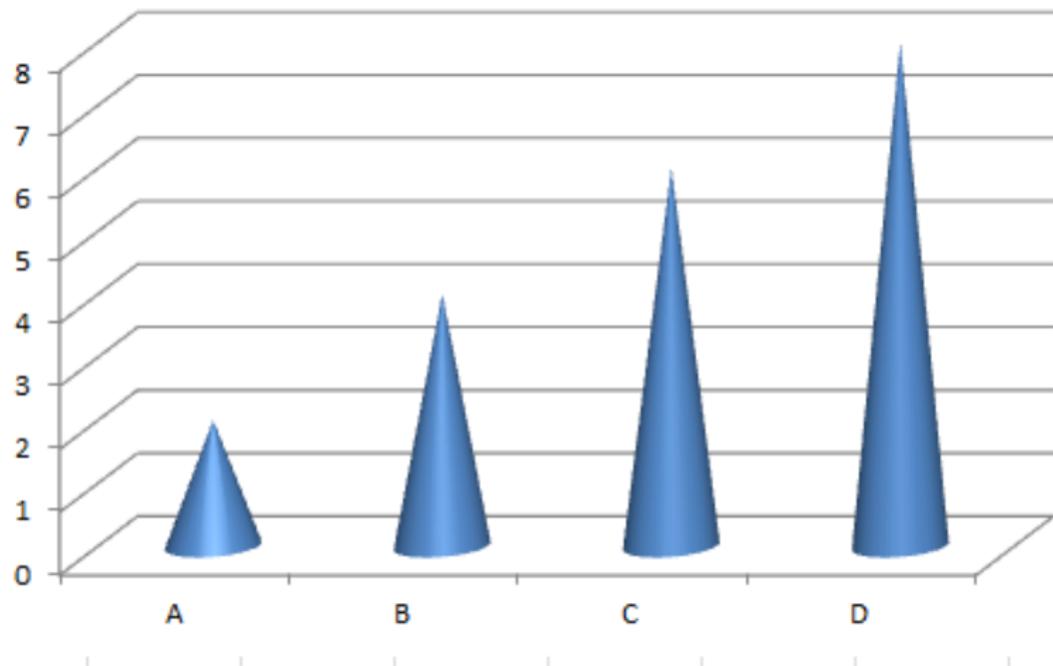
Excel

Things to remember

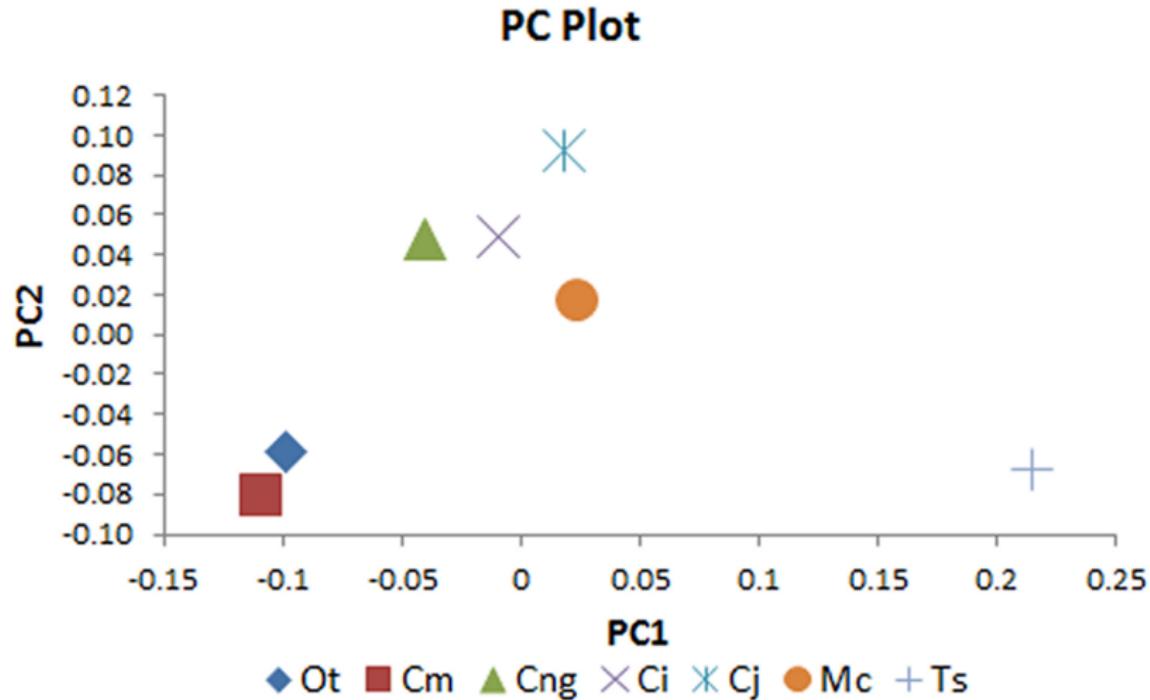
3D is best D



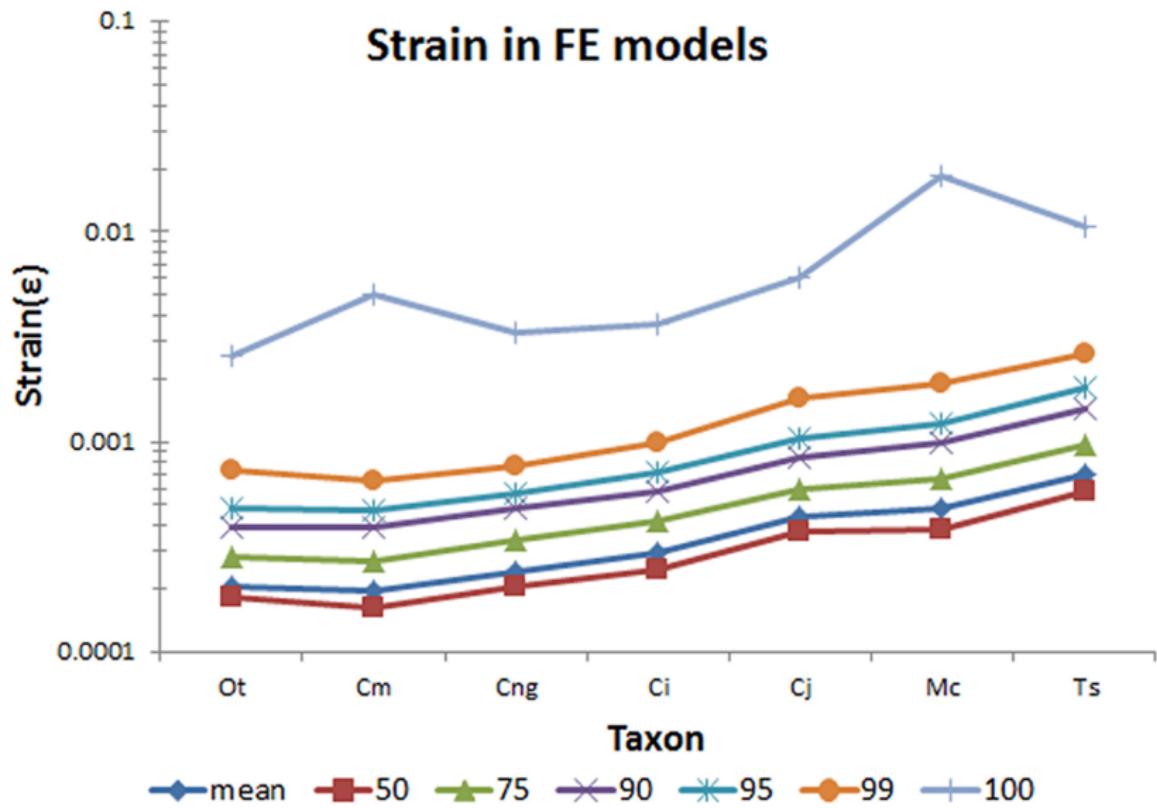
Absolute best D



I'm embarrassed



Really embarrassed



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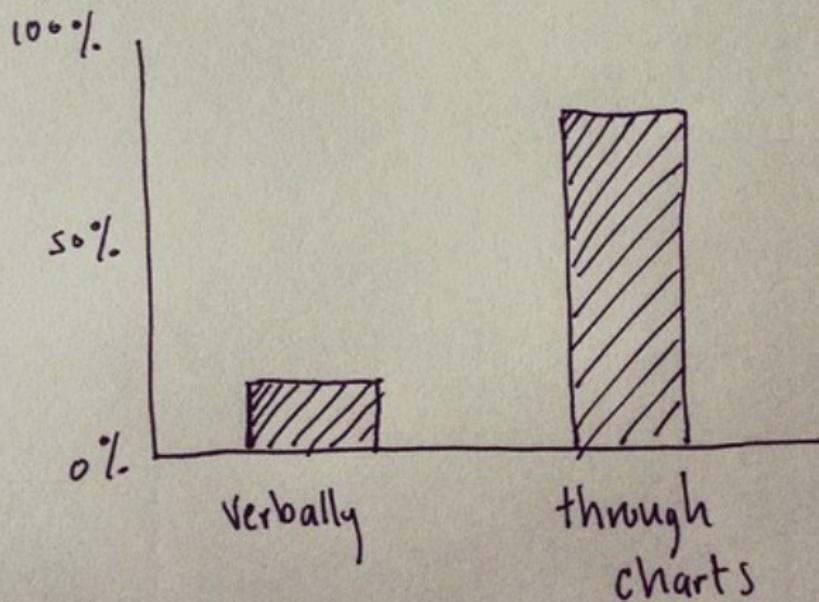
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success I have in
expressing myself



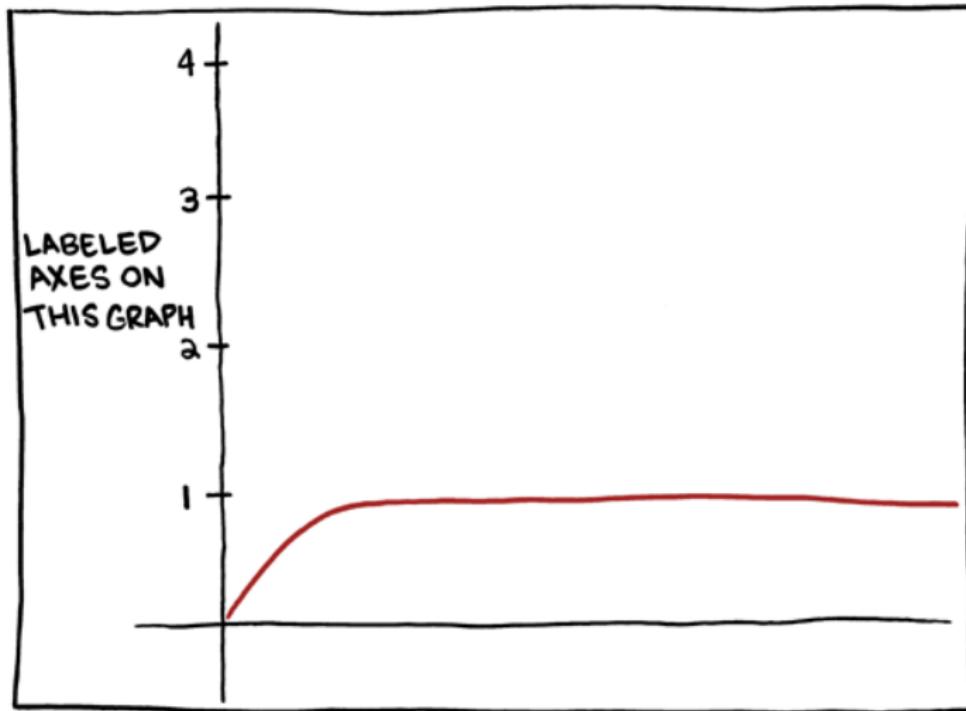
EFFECTS OF COFFEE BINGE OVER TIME

■ PRODUCTIVITY ■ ANXIETY



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Facts and Cite your Sources
TODAY!**

I'm 12 and what is this?

