Plotting your data

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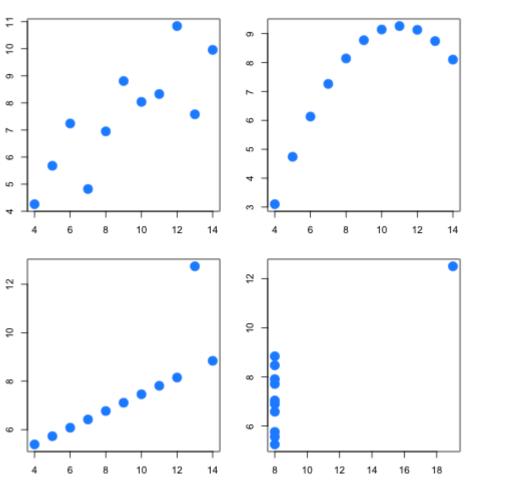


Robert Gentleman, Genentech: "make big data as small as possible as quick as is possible" to enable sharing #bigdatamed

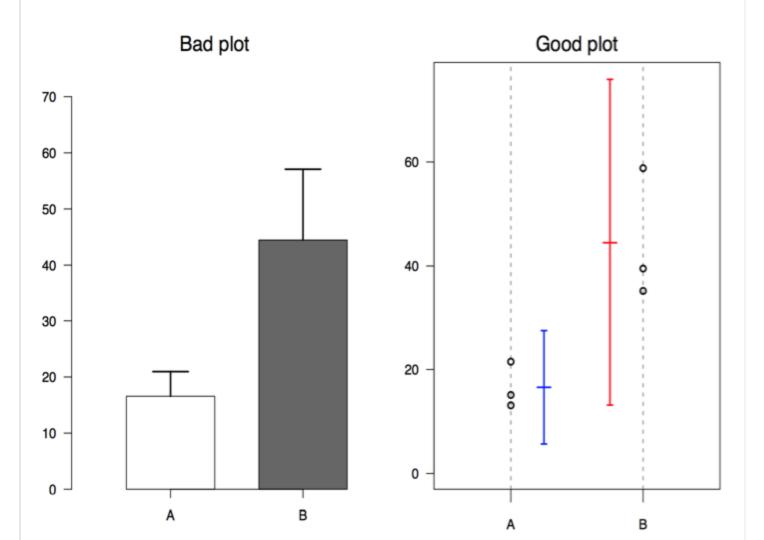


11:34 AM - 21 May 2014

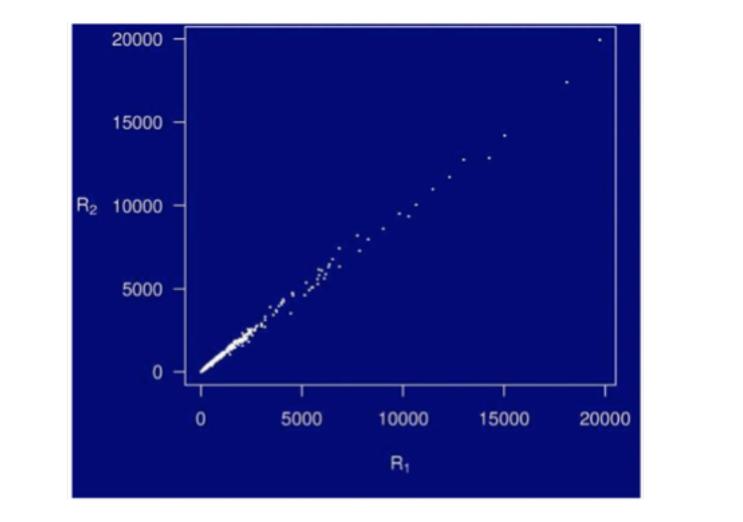
These data sets have the same properties



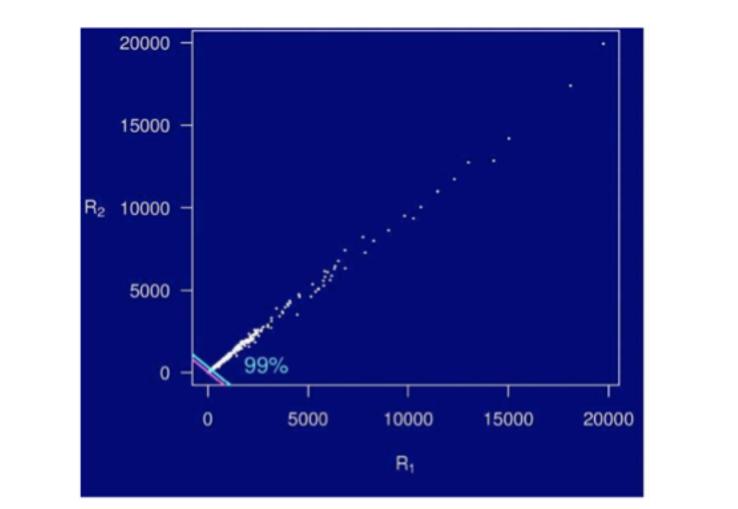
Interactivity allows for more discovery



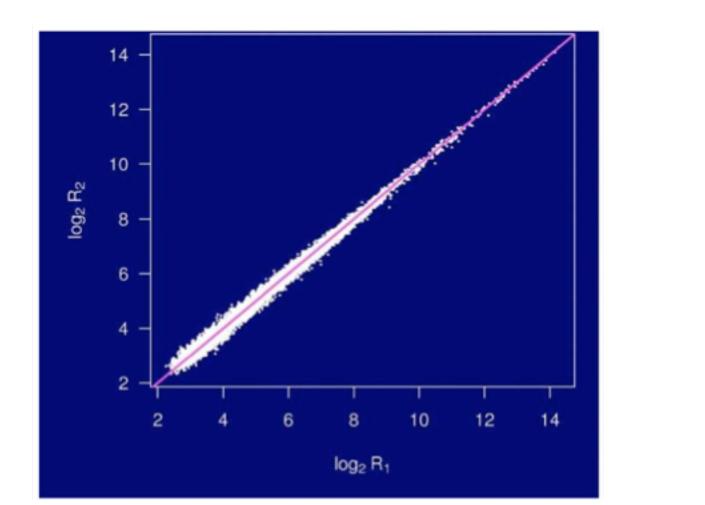
Plotting replicates



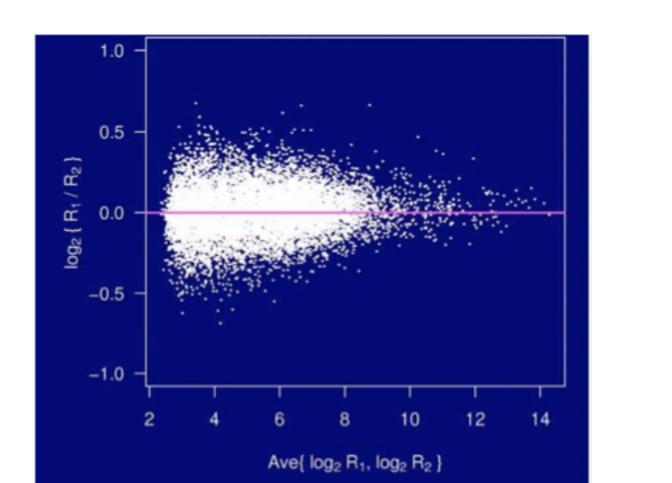
Be careful of scale



Log transform is useful



Bland Altman plots for replicates



Beware ridiculograms!

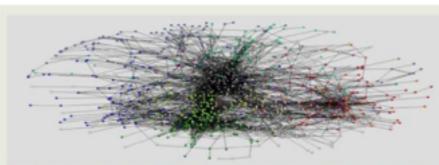
Collections

The MSigDB gene sets are divided into five major collections:

- c1 positional gene sets for each human chromosome and each cytogenetic band.
- c2 curated gene sets from online pathway databases, publications in PubMed, and knowledge of domain experts.
- c3 motif gene sets based on conserved cisregulatory motifs from a comparative analysis of the human, mouse, rat and dog genomes.
- c4 computational gene sets defined by expression neighborhoods centered on 380 cancer-associated genes.
- C5 GO gene sets consist of genes annotated by the same GO terms.

Citing the MSigDB

To cite your use of the Molecular Signatures Database (MSigDB), please reference Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550) and also the source for the gene set as listed on the gene set page.



Ridiculogram: meaningless albeit visually impressive image of a network

Thursday, July 17, 2008

When visuals gone wrong ...

If you are in biosciences related work many times you have seen a fabulous but meaning-less image in the sci papers, typical error to represent data with wrong visuals perceptions, M. E. J. Newman named "Ridiculograms" (you can see the related video in Youtube).

A ridiculogram can be defined as:

- Visual sturning
- · Scientifically worthless
- · Published in Nature or Science