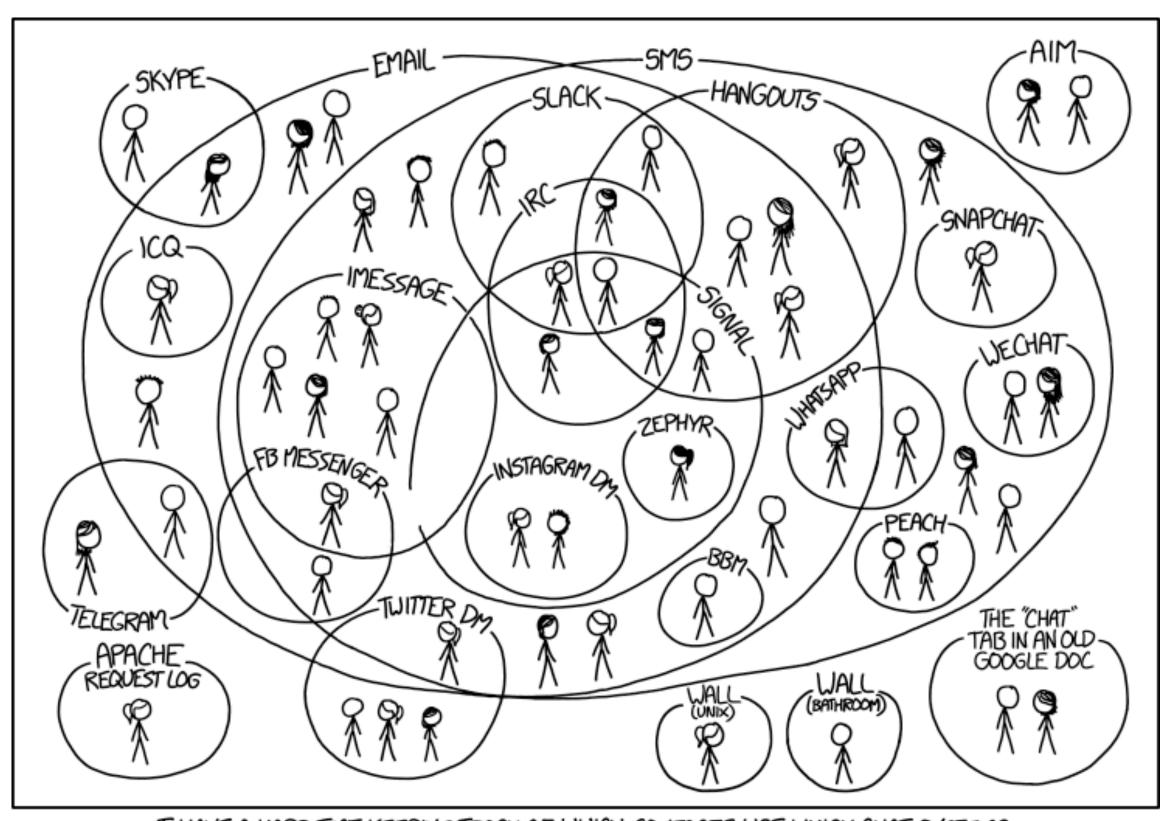
CS-5630 / CS-6630 Visualization for Data Science Set Visualization

Alexander Lex alex@sci.utah.edu





I HAVE A HARD TIME KEEPING TRACK OF WHICH CONTACTS USE WHICH CHAT SYSTEMS.

Design Workshop

item1 : A

item2 : A

item3 : A, B

item4 : A, C

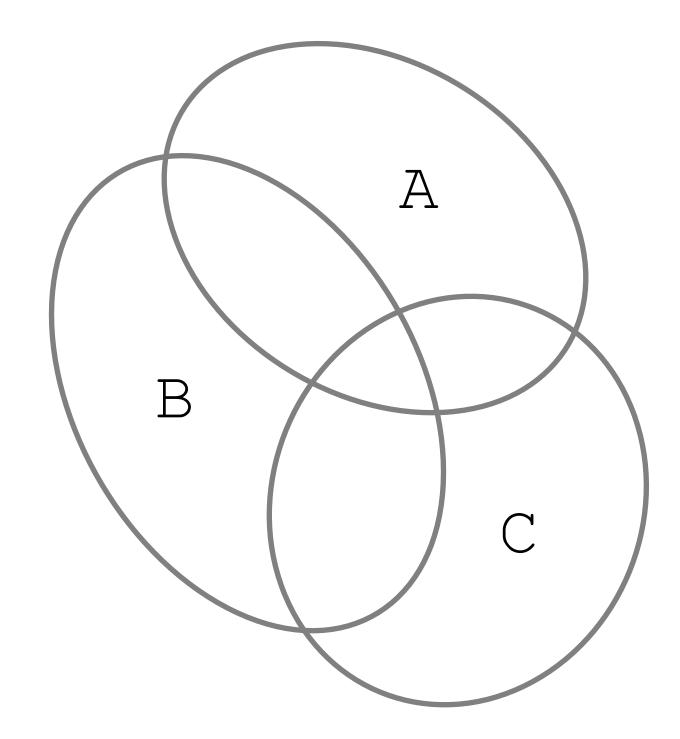
item5 : A, B, C

item6 : B

item7 : B, C

item8 : C

• • •



Venn diagram

LETTER

The banana (Musa acuminata) genome and the evolution of monocotyledonous plants

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Bananas (Musa spp.), including dessert and cooking types, are giant perennial monocotyledonous herbs of the order Zingiberales, a sister group to the well-studied Poales, which include cereals. Bananas are vital for food security in many tropical and subtropical countries and the most popular fruit in industrialized countries¹. The Musa domestication process started some 7,000 years ago in Southeast Asia. It involved hybridizations between diverse species and subspecies, fostered by human migrations², and selection of diploid and triploid seedless, parthenocarpic hybrids thereafter widely dispersed by vegetative propagation. Half of the current production relies on somaclones derived from a single triploid genotype (Cavendish)¹. Pests and diseases have gradually become adapted, representing an imminent danger for global banana production^{3,4}. Here we describe the draft sequence of the 523-megabase genome of a Musa acuminata doubled-haploid genotype, providing a crucial stepping-stone for genetic improvement of banana. We detected three rounds of whole-genome duplications in the Musa lineage, independently of those previously described in the Poales lineage and the one we detected in the Arecales lineage. This first monocotyledon high-continuity whole-genome sequence reported outside Poales represents an essential bridge for comparative genome analysis in plants. As such, it clarifies commelinidsequence errors. The assembly consisted of 24,425 contigs and 7,513 scaffolds with a total length of 472.2 Mb, which represented 90% of the estimated DH-Pahang genome size. Ninety per cent of the assembly was in 647 scaffolds, and the N50 (the scaffold size above which 50% of the total length of the sequence assembly can be found) was 1.3 Mb (Supplementary Text and Supplementary Tables 1–3). We anchored 70% of the assembly (332 Mb) along the 11 *Musa* linkage groups of the Pahang genetic map. This corresponded to 258 scaffolds and included 98.0% of the scaffolds larger than 1 Mb and 92% of the annotated genes (Supplementary Text, Supplementary Table 4 and Supplementary Fig. 1).

We identified 36,542 protein-coding gene models in the *Musa* genome (Supplementary Tables 1 and 5). A total of 235 microRNAs from 37 families were identified, including only one of the eight microRNA gene (*MIR*) families found so far solely in Poaceae⁸ (Supplementary Tables 6 and 7).

Viral sequences related to the banana streak virus (BSV) dsDNA plant pararetrovirus were found to be integrated in the Pahang genome, with 24 loci spanning 10 chromosomes (Supplementary Text and Supplementary Fig. 2). They belonged to a badnavirus phylogenetic group that differed from the endogenous BSV species (eBSV) found in *M. balbisiana*⁹ and most of them formed a new

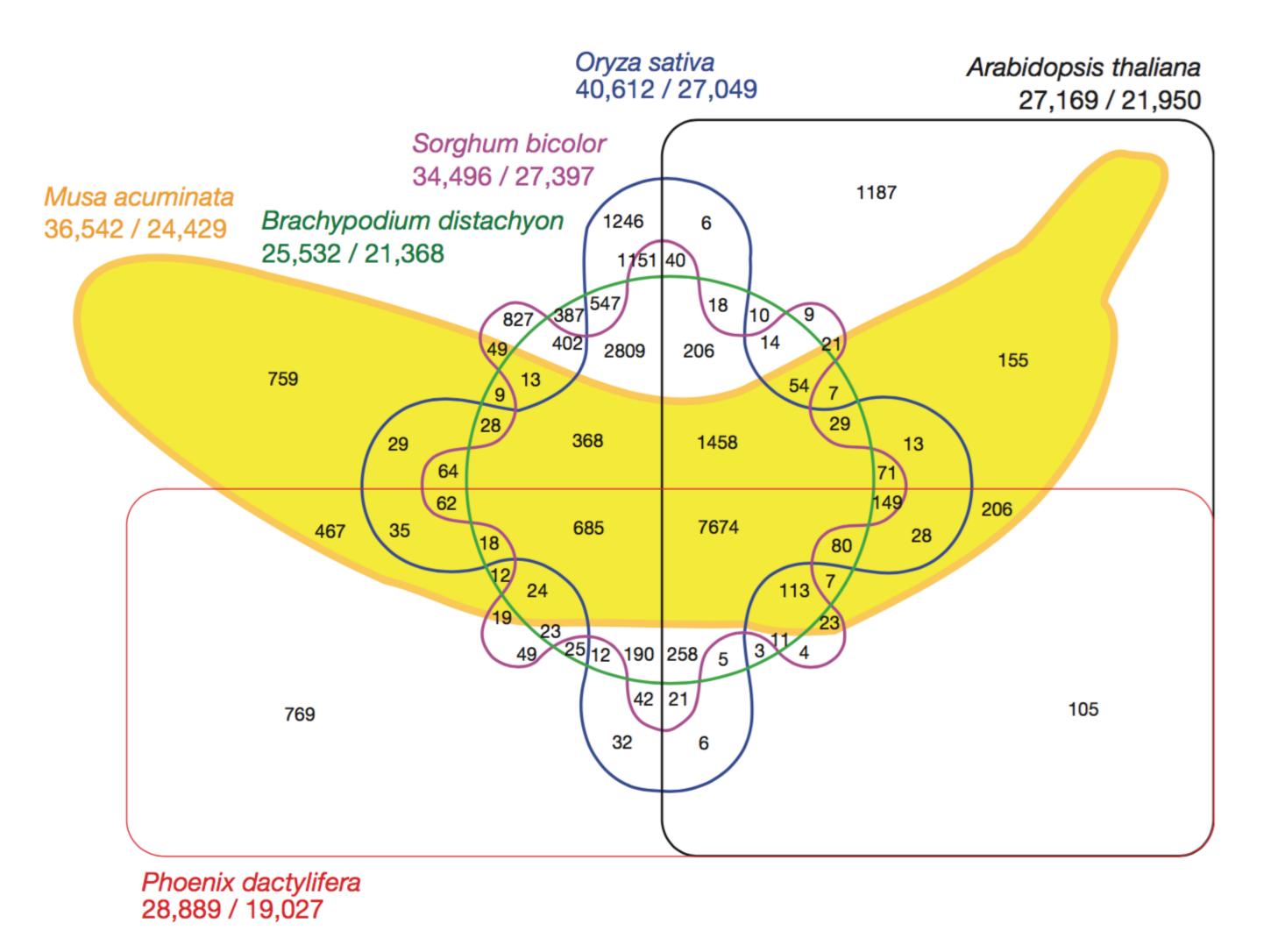
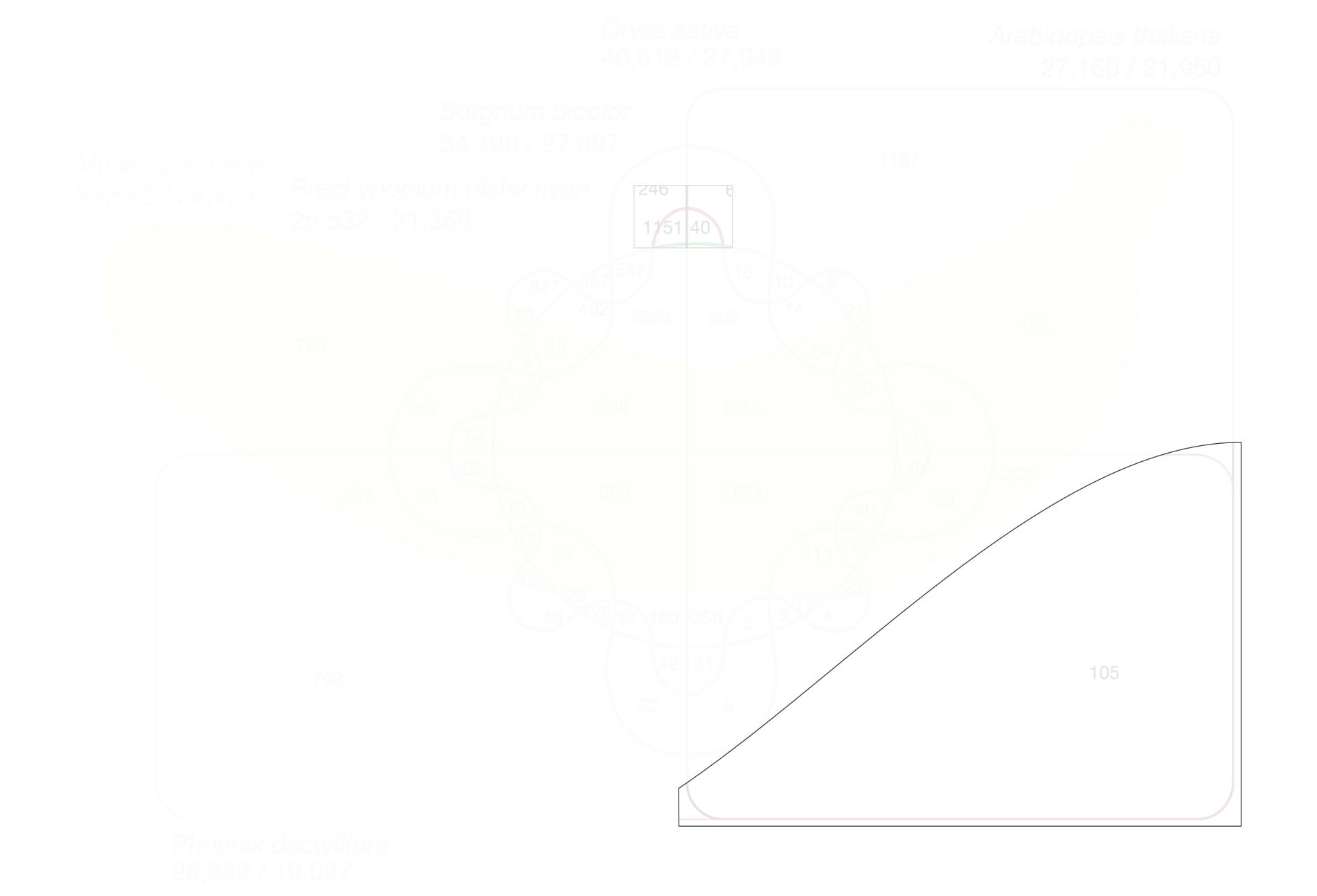
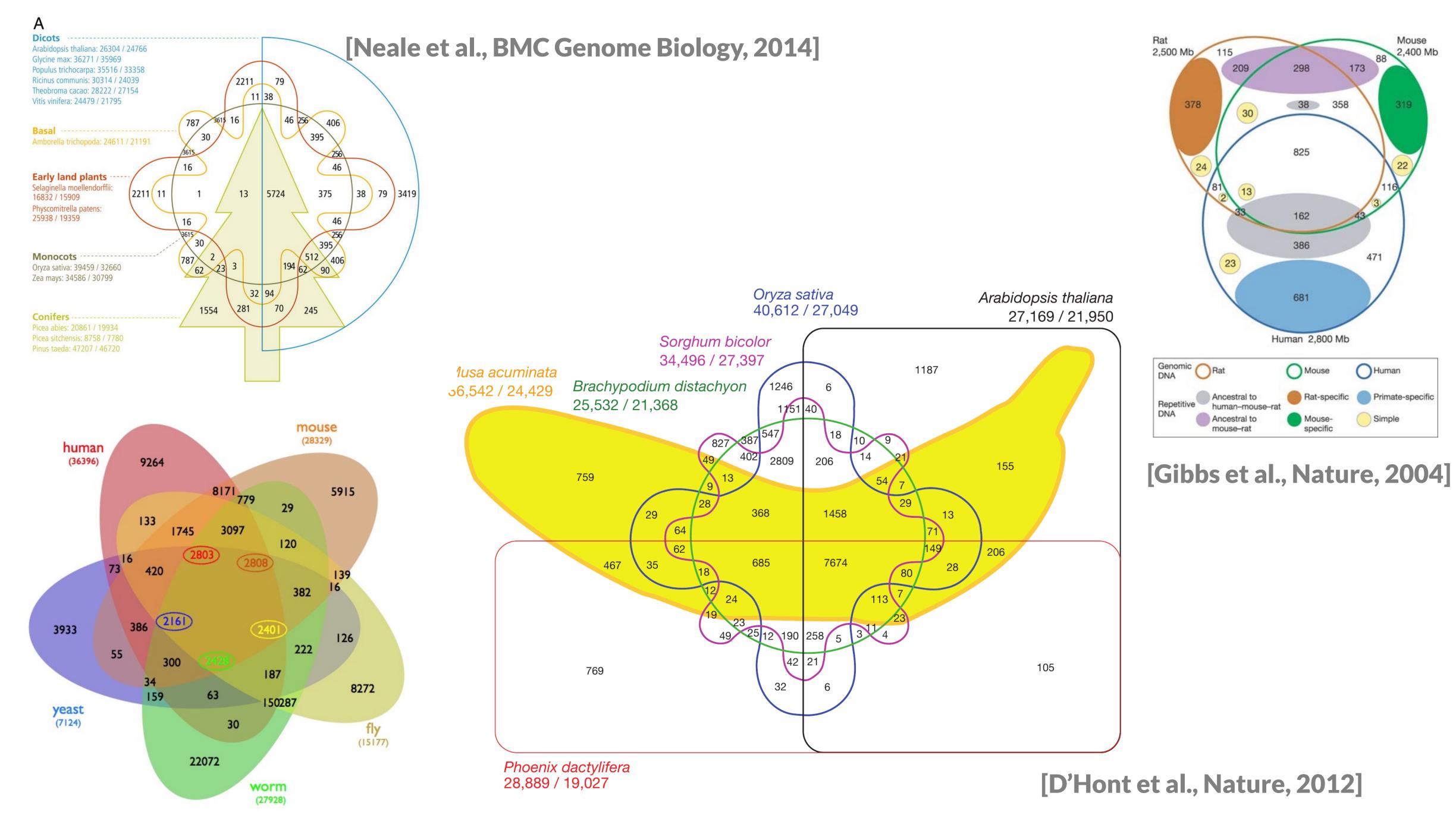


Figure 4 | Six-way Venn diagram showing the distribution of shared gene families (sequence clusters) among *M. acuminata*, *P. dactylifera*, *Arabidopsis thaliana*, *Oryza sativa*, *Sorghum bicolor* and *Brachypodium distachyon* genomes. Numbers of clusters are provided in the intersections. The total number of sequences for each species is provided under the species name (total number of sequences/total number of clustered sequences).





[Wiles et al., BMC Systems Biology]

Element ID Attribute(s) Sets Characteristics Name Age School, Female Lisa 8 School, Male 10 Bart Power Plant, Male Homer 40 Evil, Power Plant, Male Mr. Burns 90

What are some questions we'd like to ask?

Design Workshop

work in groups

get to know the data (5 mins)

create two (rapid!) prototypes (2x5 mins)

Write up your two favorites (5 mins)

Upload to "Bonus" Canvas Dropbox by EOD

Element ID	Sets	Attribute(s)	
Name	Characteristics	Age	
Lisa	School, Female	8	
Bart	School, Male	10	
Homer	Power Plant, Male	40	
Mr. Burns	Evil, Power Plant, Male	90	

- 1. What is the biggest intersection?
- 2. Which sets make up an intersection?
- 3. How big is an intersection?
- 4. Does it work for more than four sets?
- 5. Does attribute value correlate with intersection

Tip: Don't always try to show all individuals

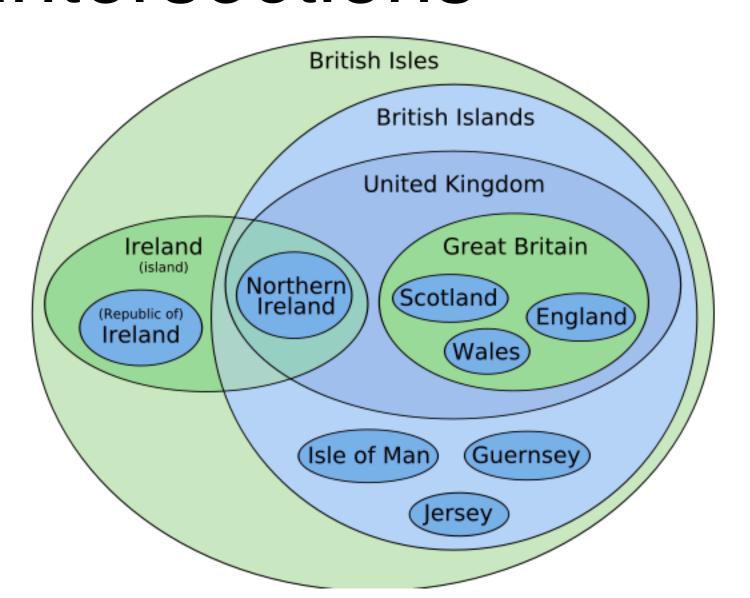
Uenn and Euler Diagrams

Venn vs Euler

Euler Diagram

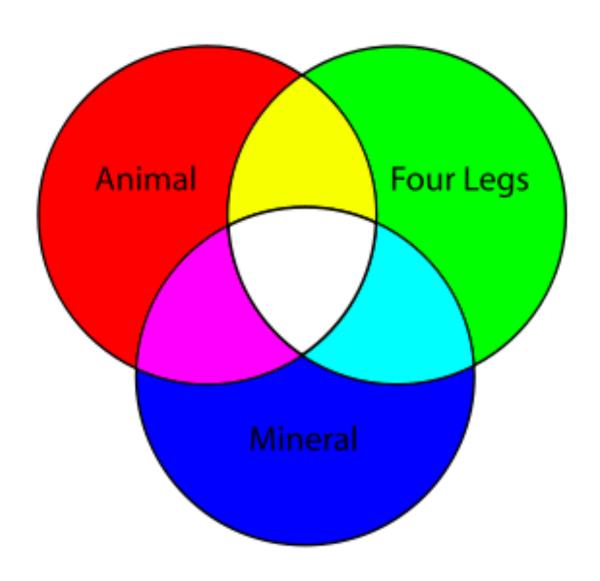
Shows logical relations

May omit empty intersections



Venn Diagram

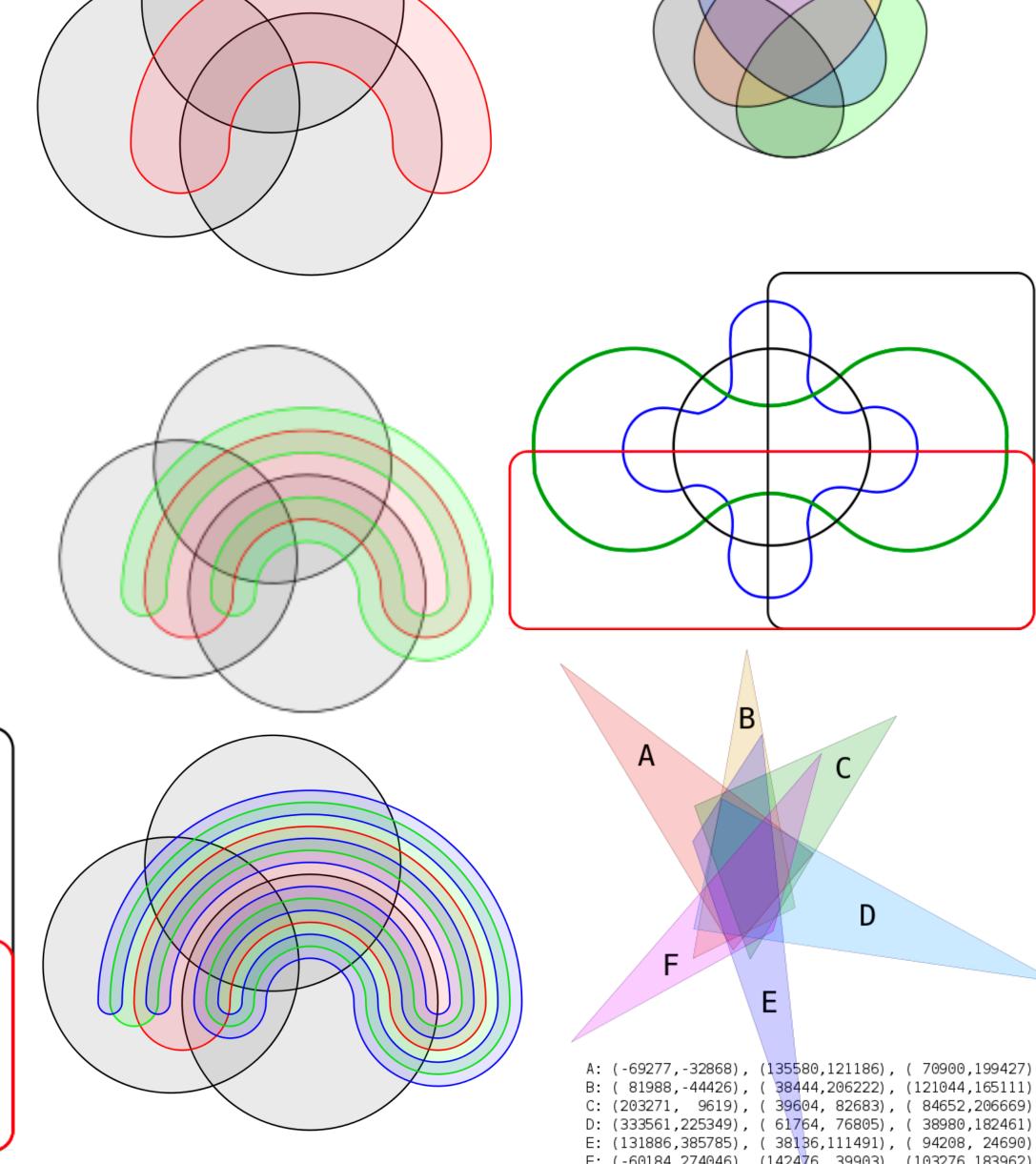
Shows all possible logical relations between sets (even if empty)

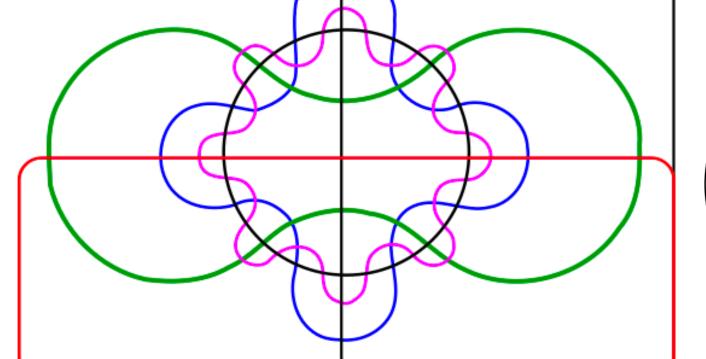


Venn Diagrams

Venn diagrams for many sets are hard

of intersections is 2ⁿ





Area-Proportional Euler Diagrams

Problem with Venn: size doesn't correspond to the data.

Creating area-proportional Euler diagrams is hard.

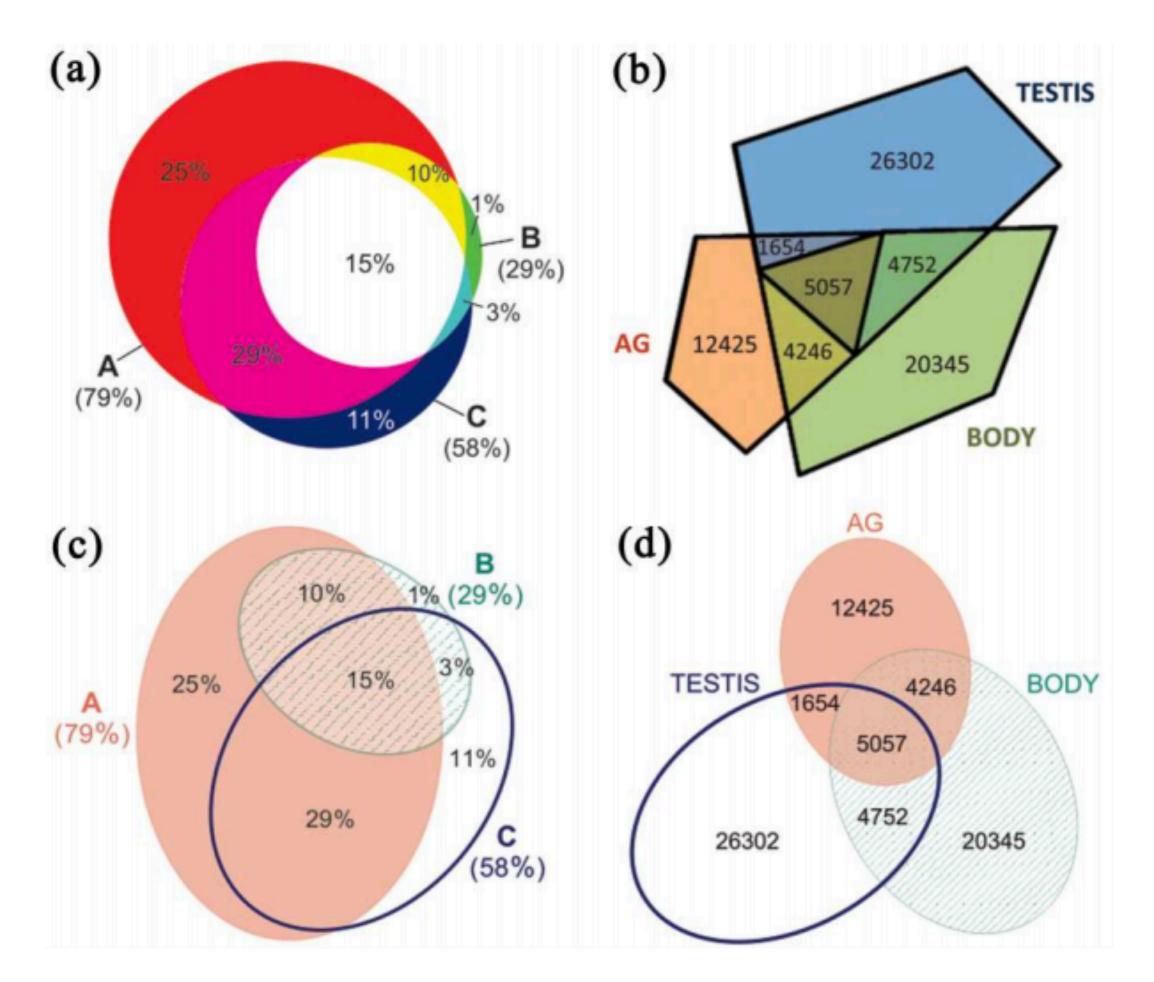
Layout criteria:

area proportional

simple curves (circles are best)

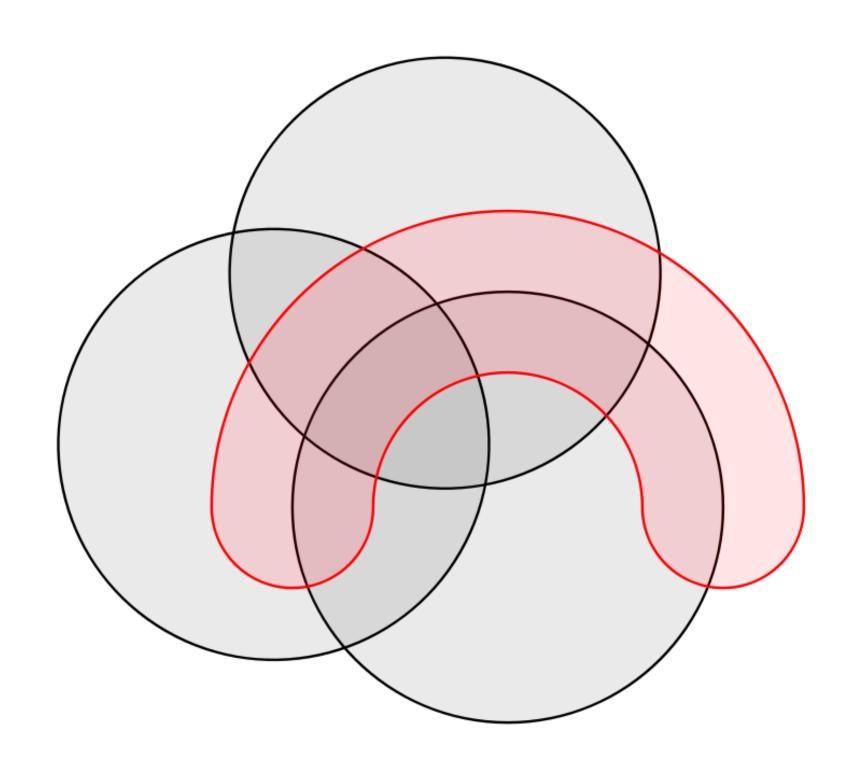
makes it easy to identify which sets are participating in intersection

Gestalt-principle: good continuation

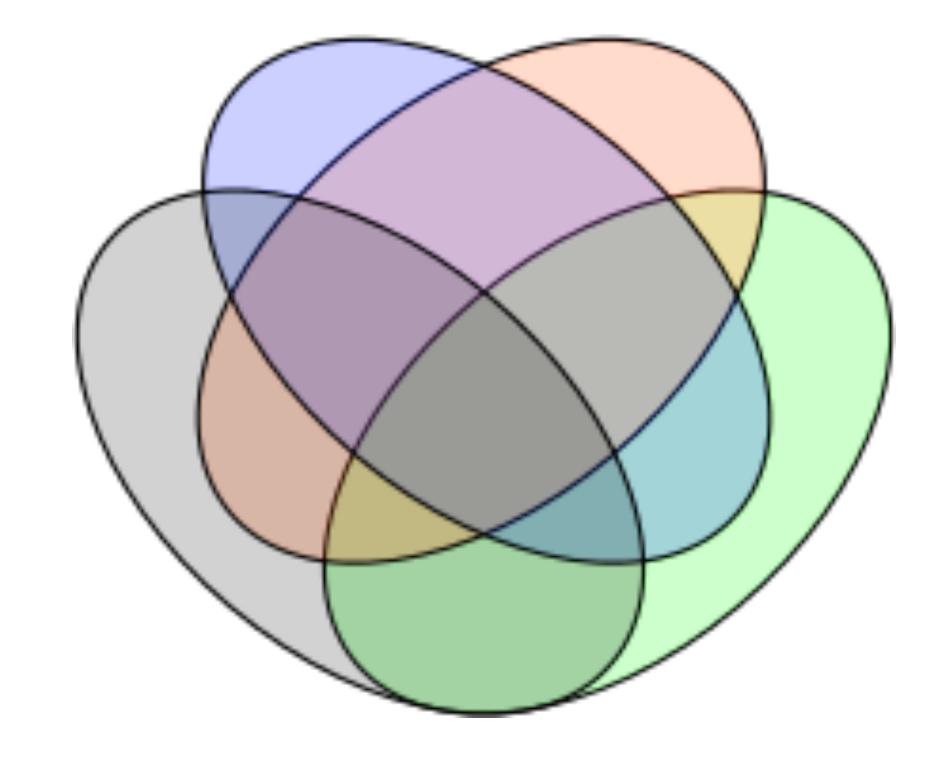


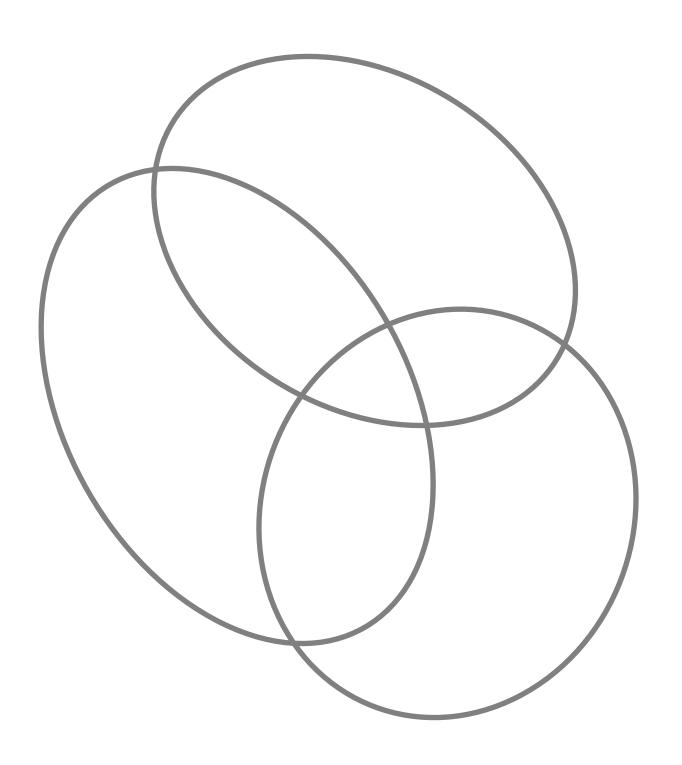
Compare Simple vs Complex Shape

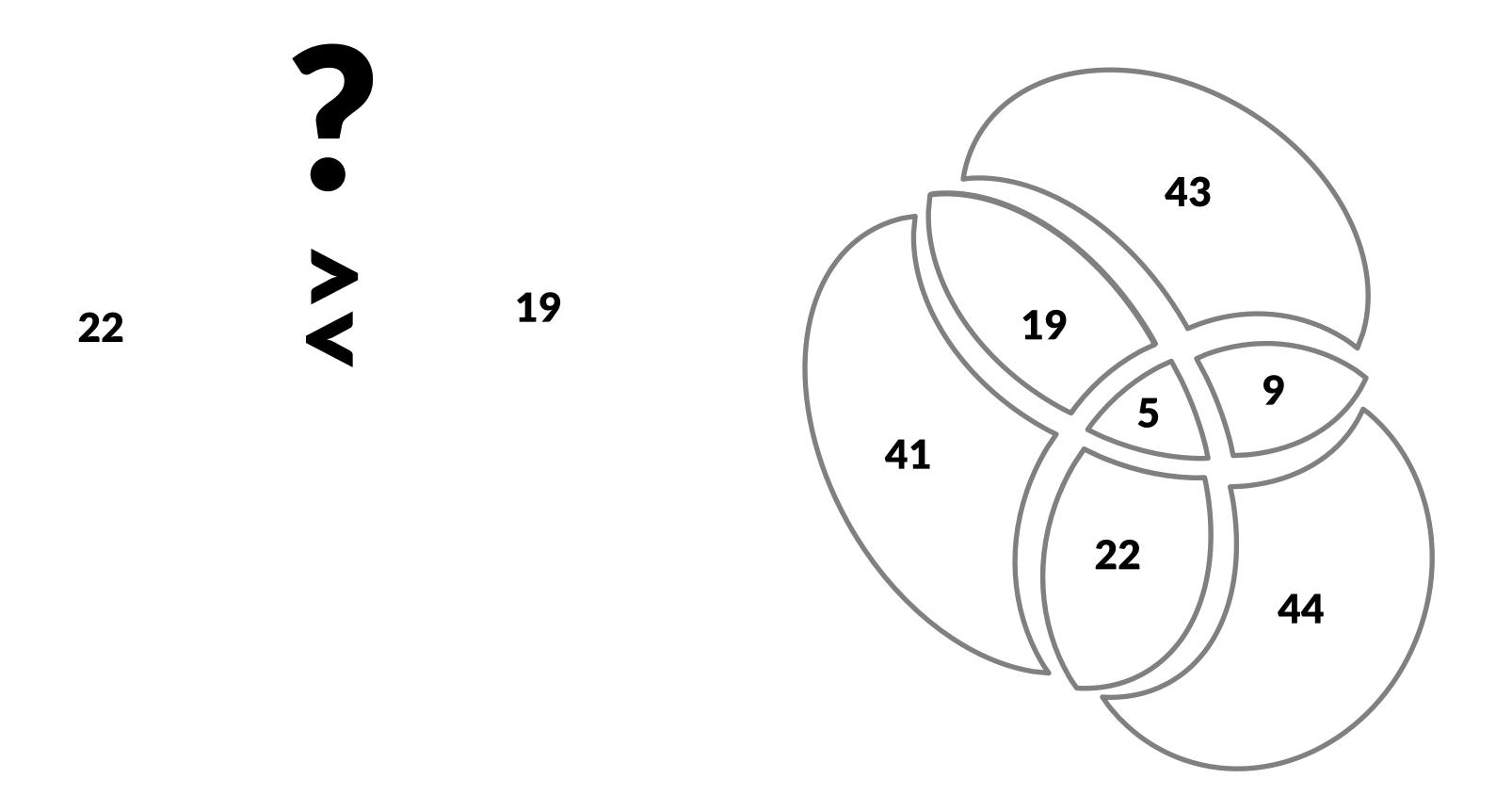
Complex



Simple







Venn-Euler Pros/Cons

Pros

Familiar

Intuitive

Work well for 2-4 sets

Cons

Doesn't work well for more

than 4 sets

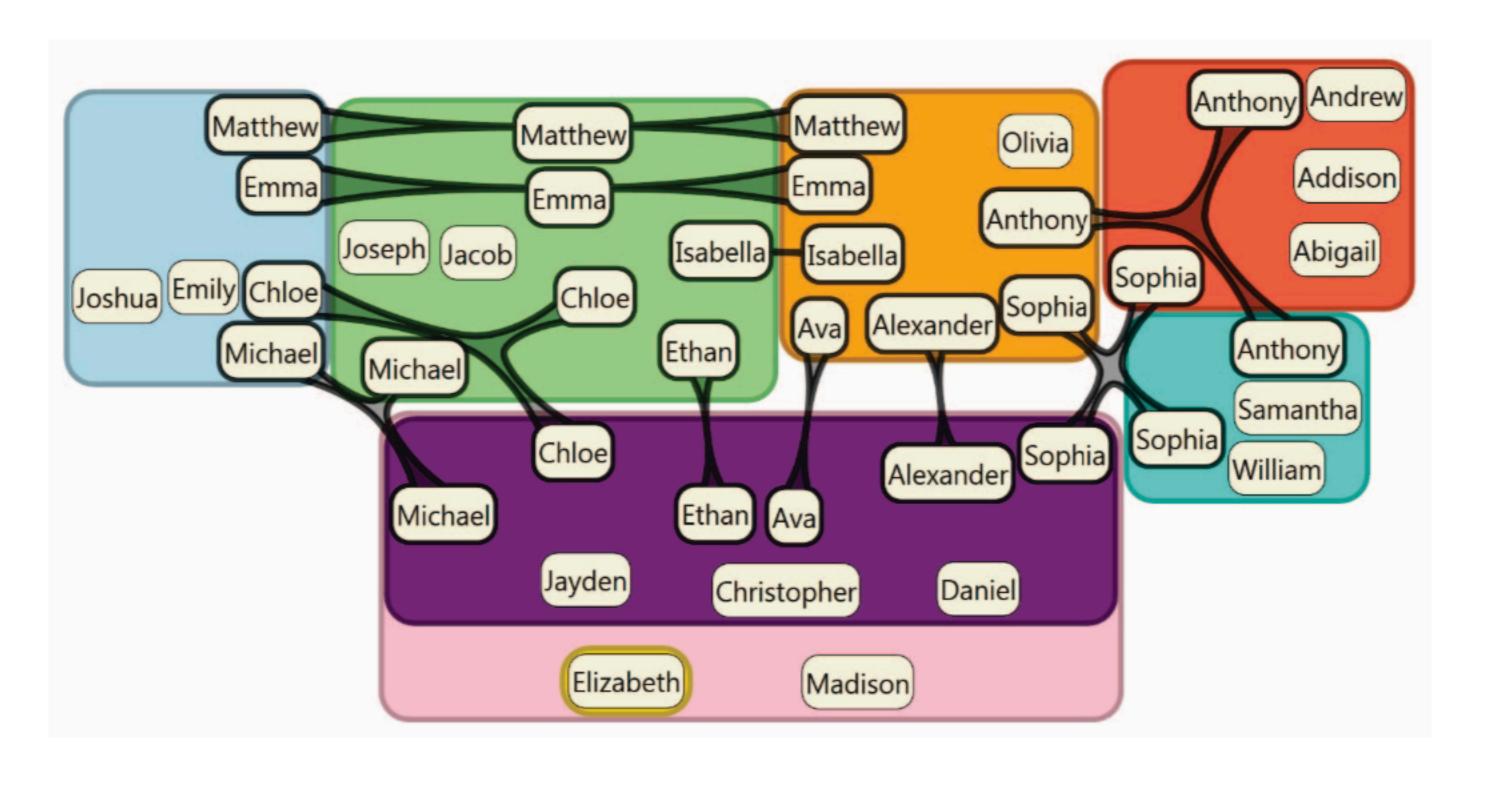
Area proportionality hard to do

Not well suited to show

attributes

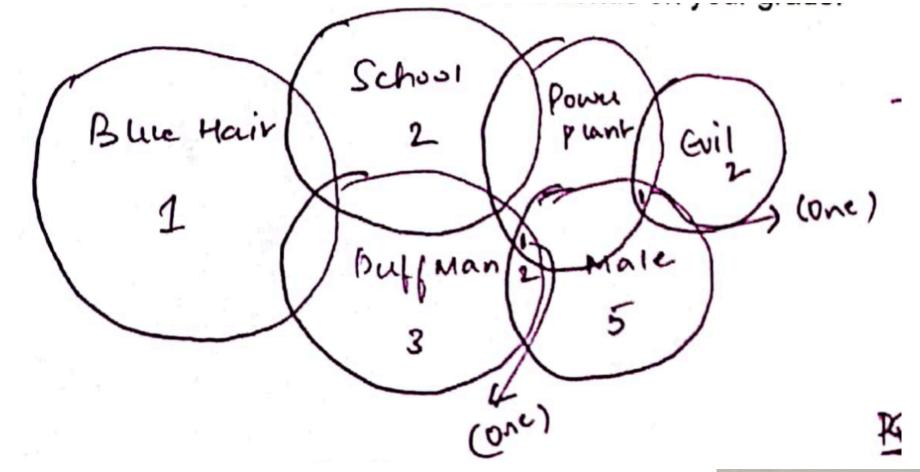
Relationships for specific Items

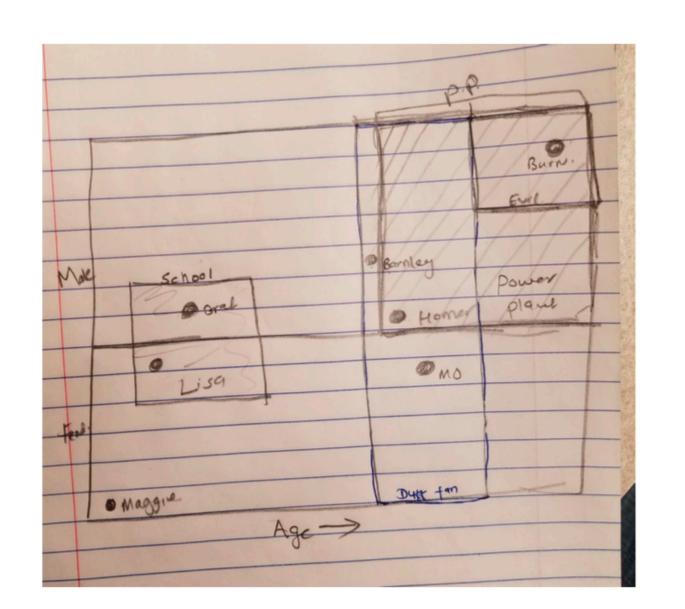


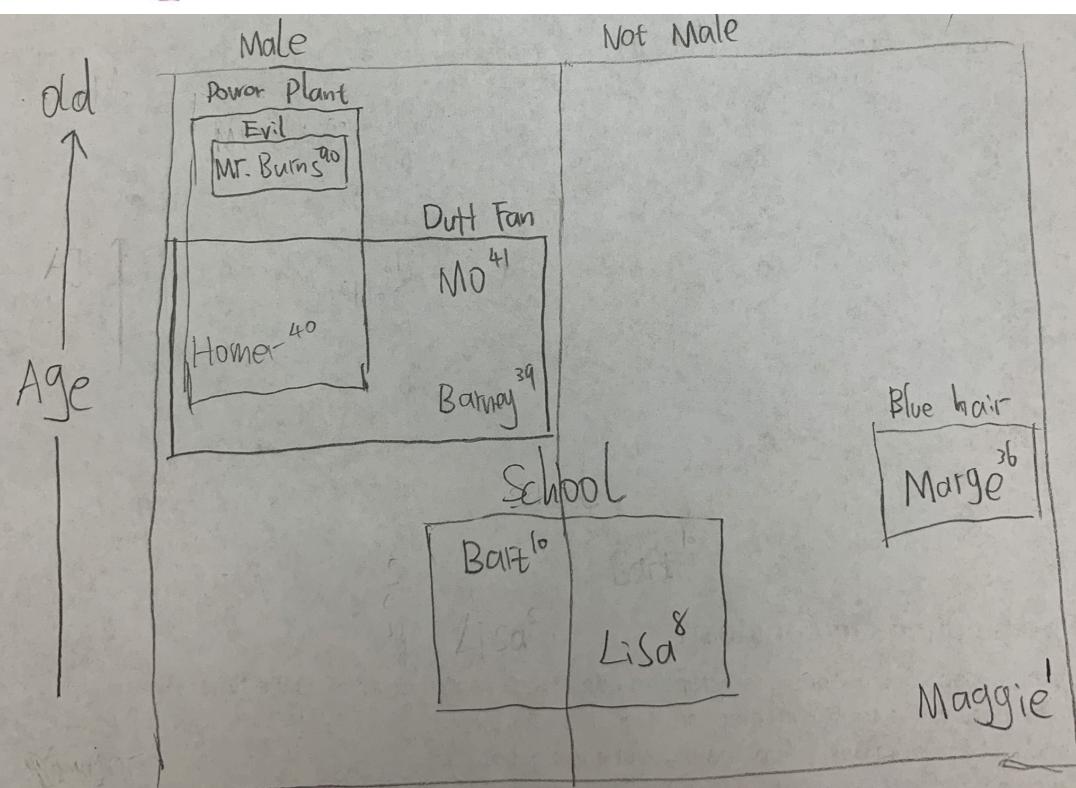


No Duplicate Nodes Complex Shapes Notice the Nesting

Duplicate Nodes
Simple Shapes





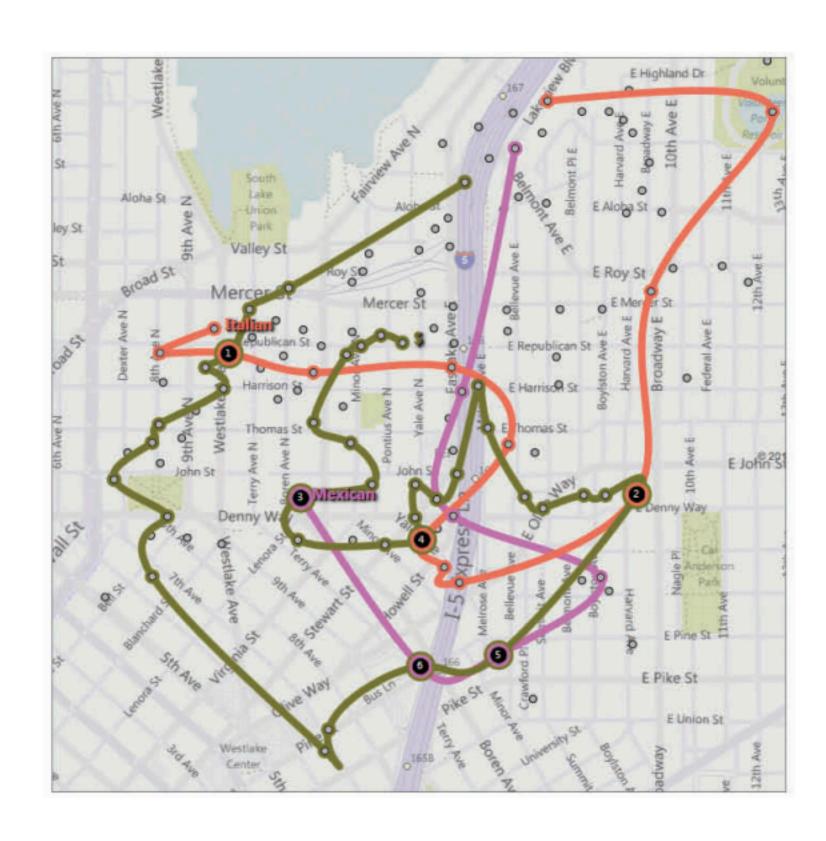


Sets on top of a fixed layout



Sets on top of a fixed layout

LineSets



Kelp Diagrams

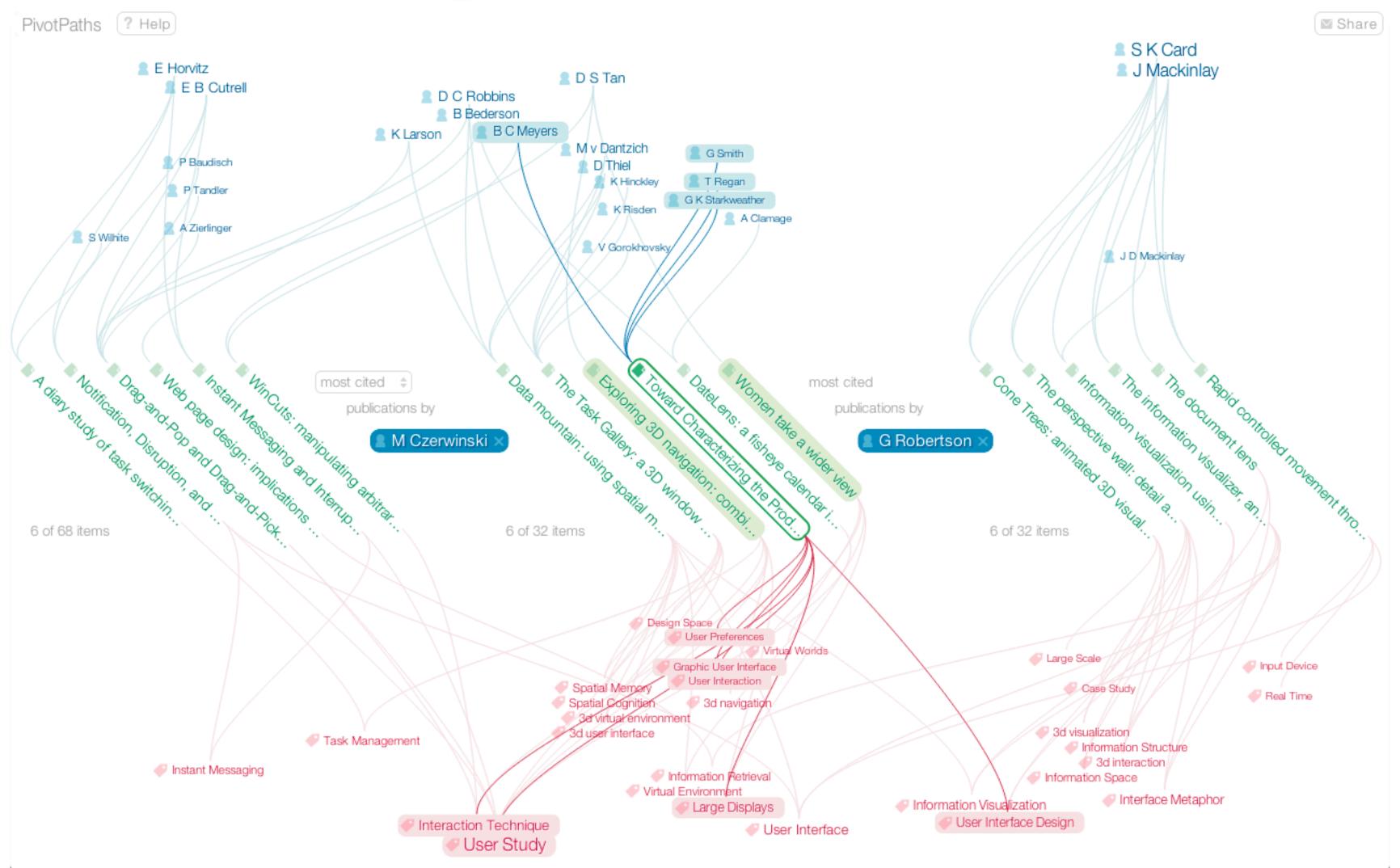


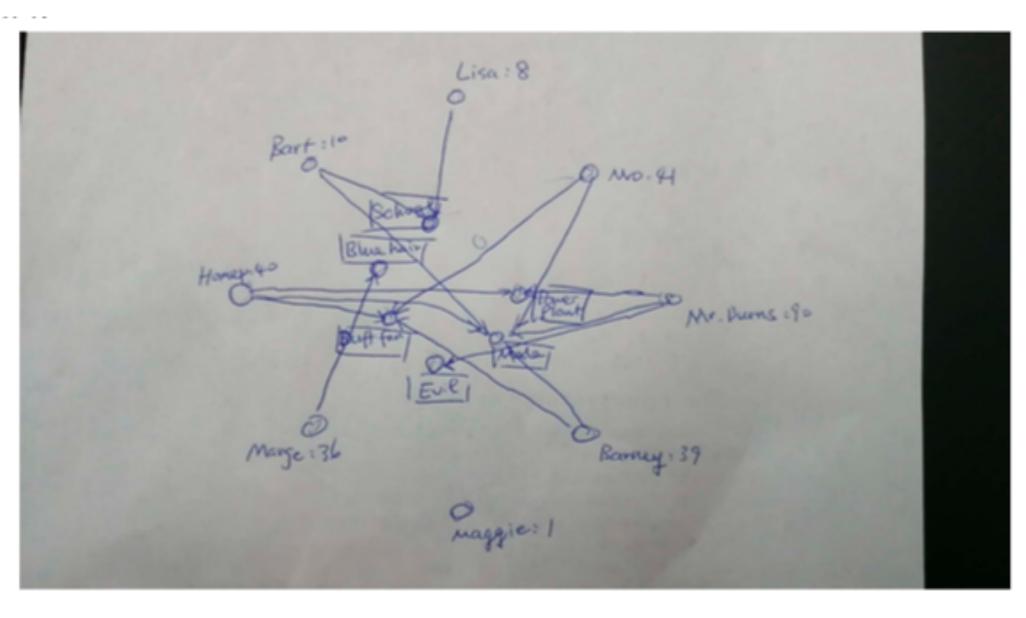
[Alper 2011] [Dinkla 2012]

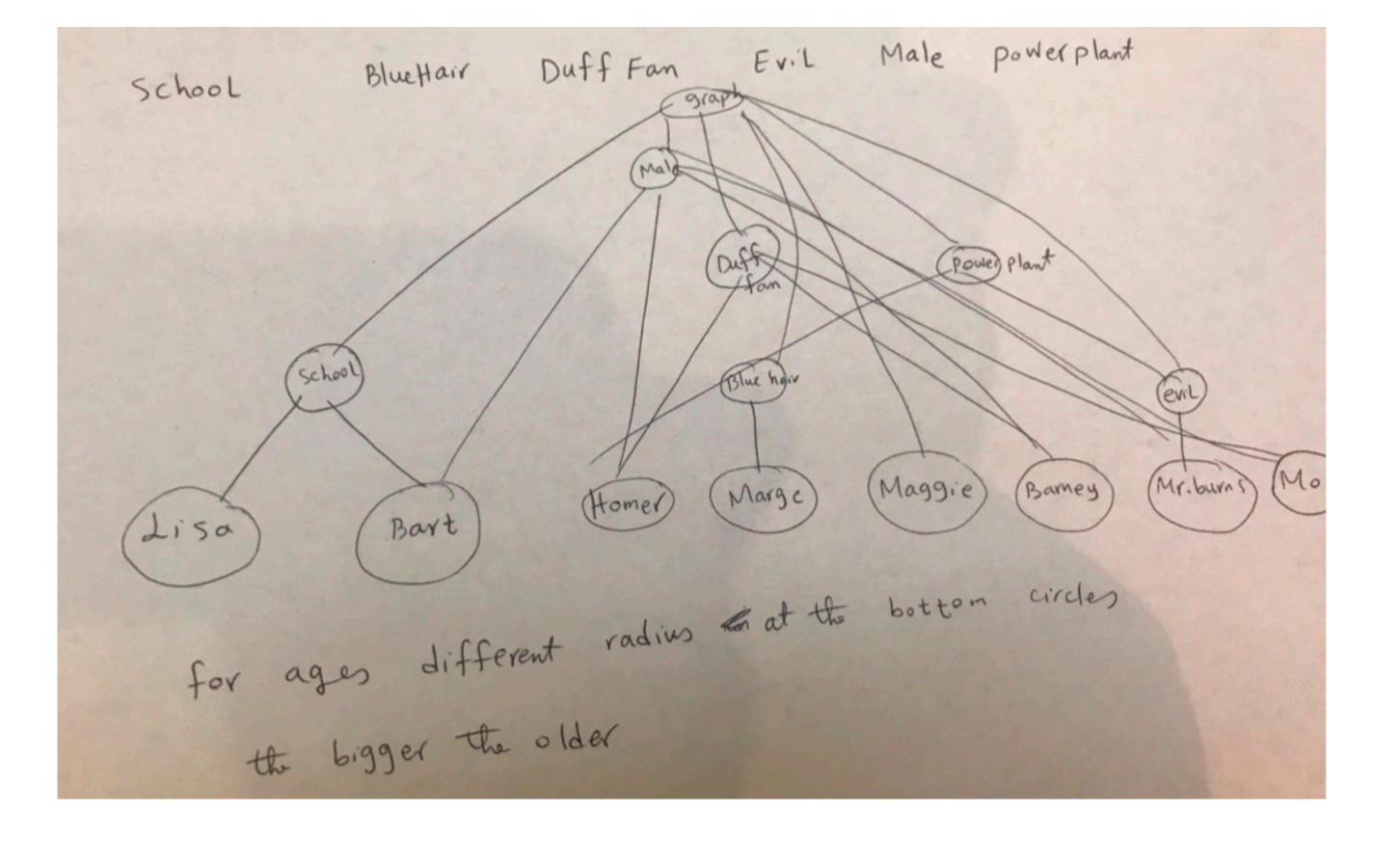
Node-Link Techniques

Treat sets as nodes

Connect to elements that are in set







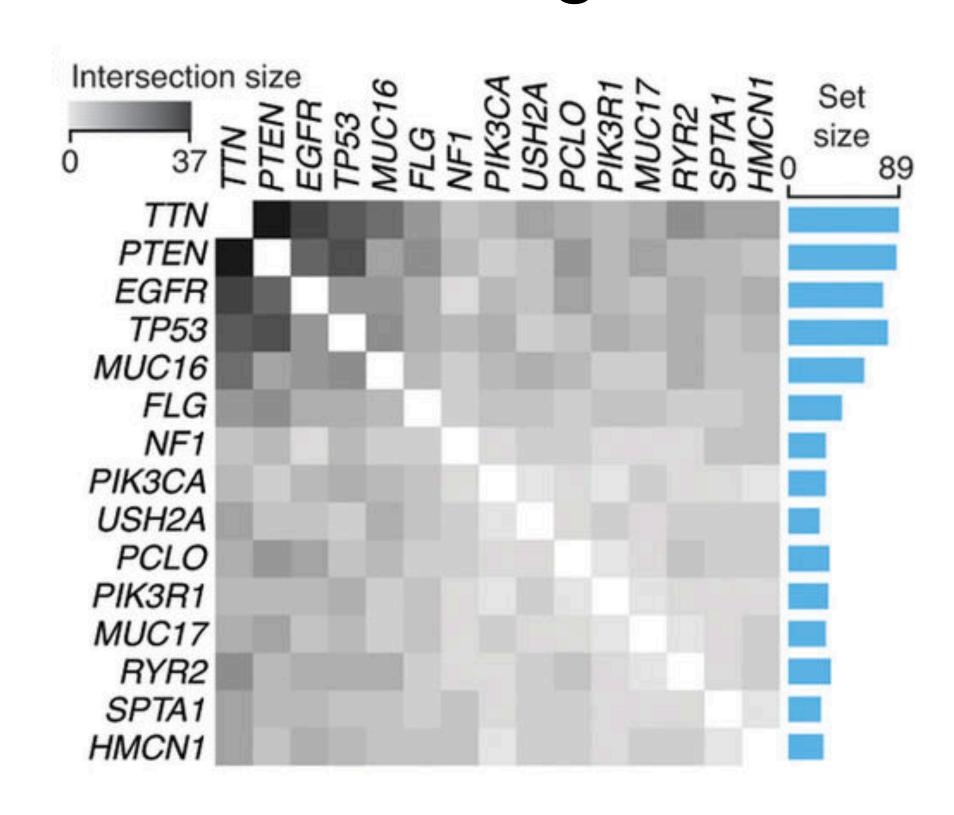
Showing Pairwise Overlap

Doesn't show higher-order overlaps

Very scalable

Can't show attributes

Co-Mutations of genes

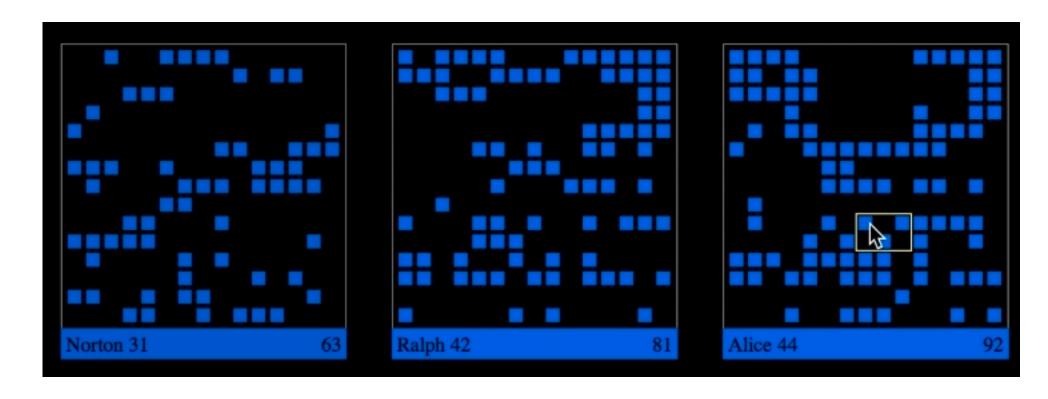


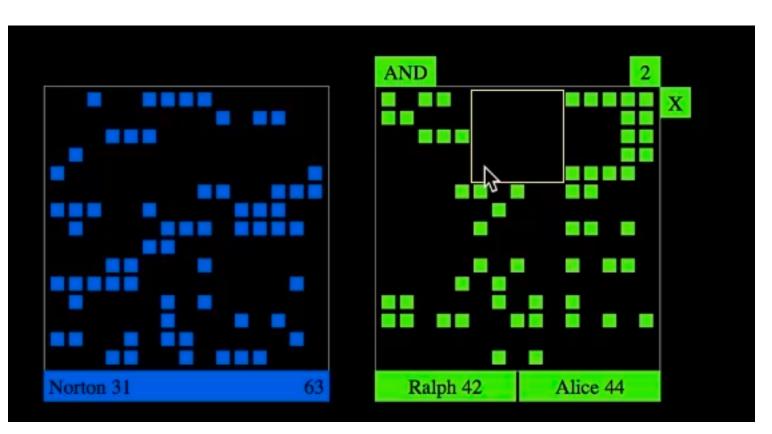
Set Matrices: OnSet

Set membership for each item shown in matrix

Comparisons can be made using AND or OR operations

Good for many sets and few items





Linear Diagrams

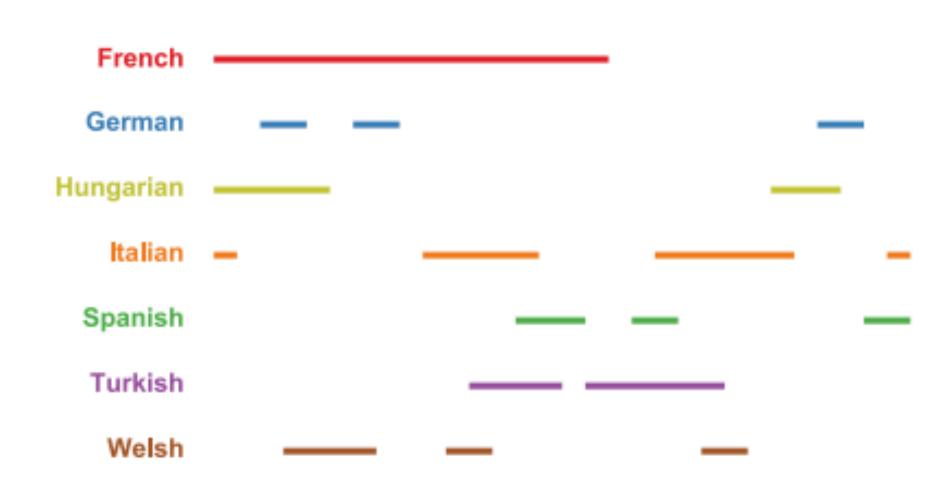


Fig. 1. Visualizing sets: linear diagrams.

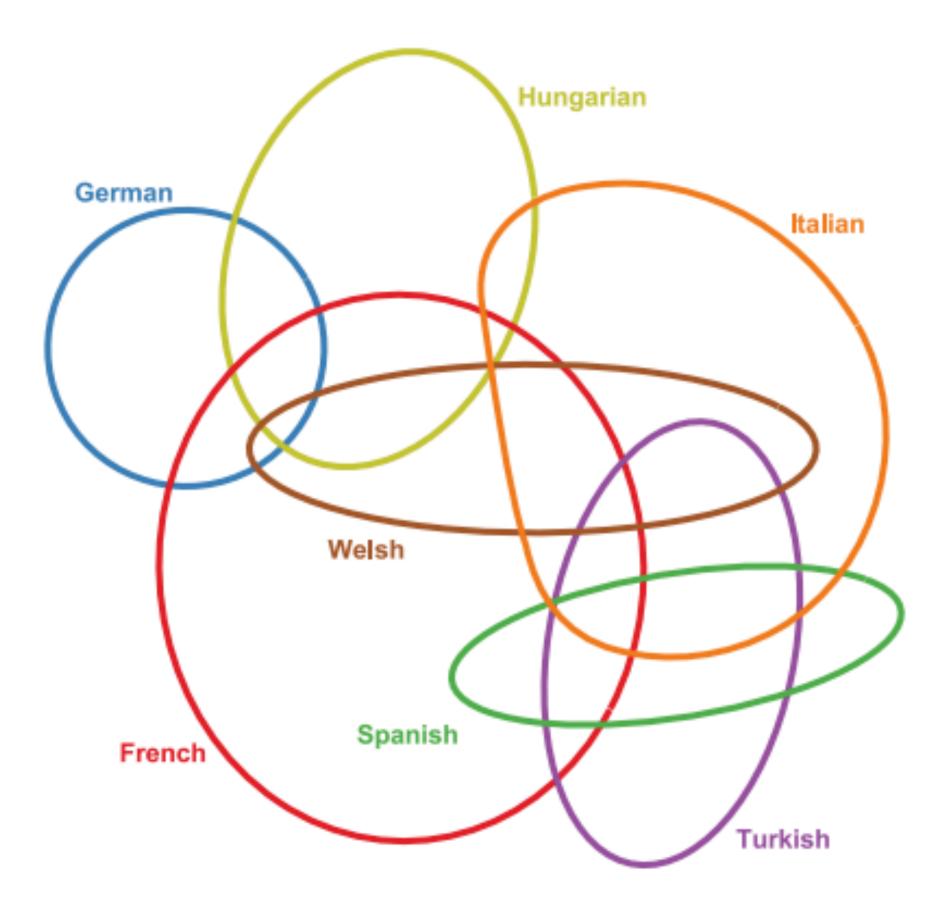
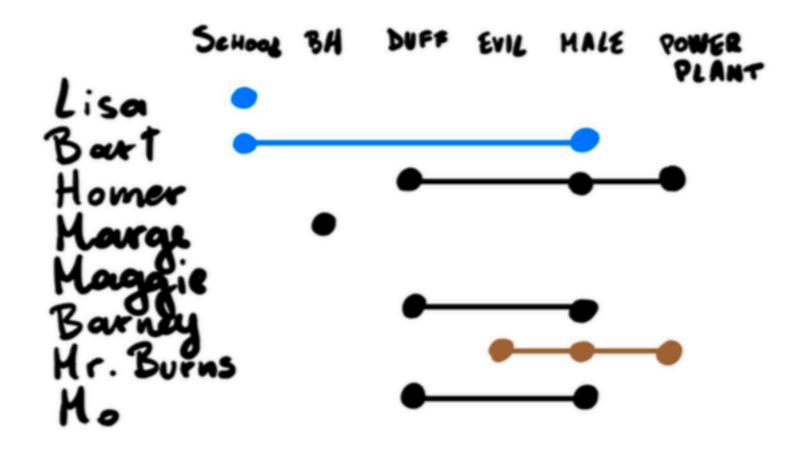
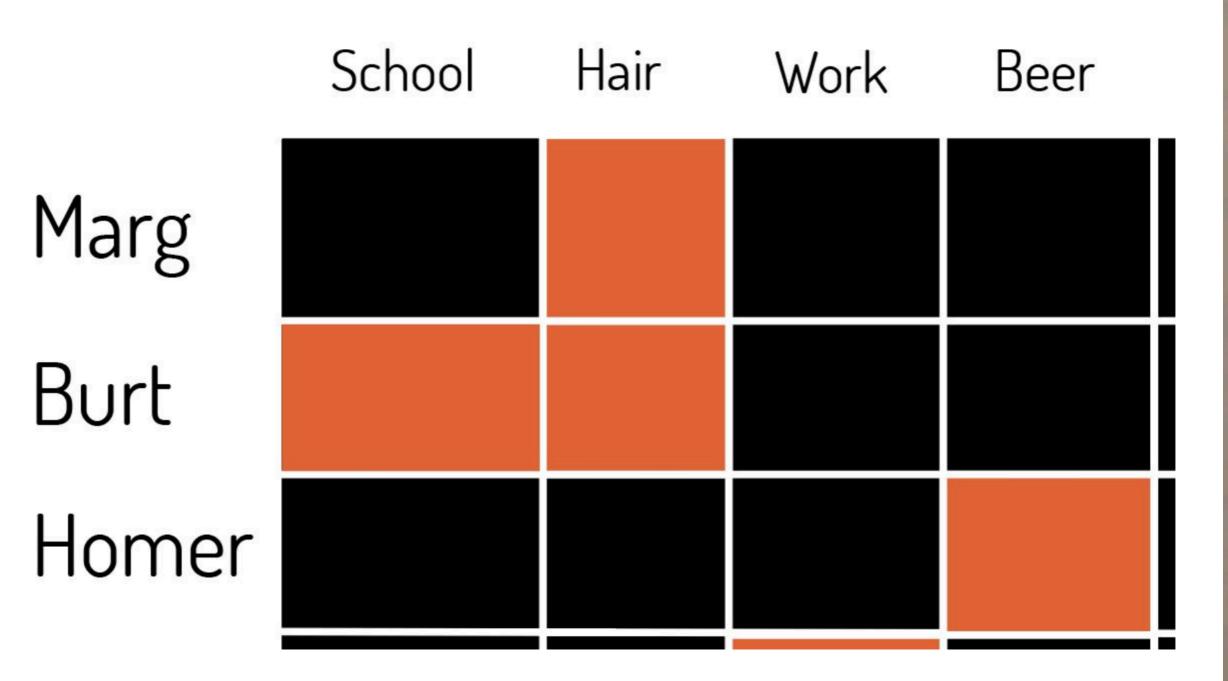


Fig. 2. Visualizing sets: Euler diagrams.





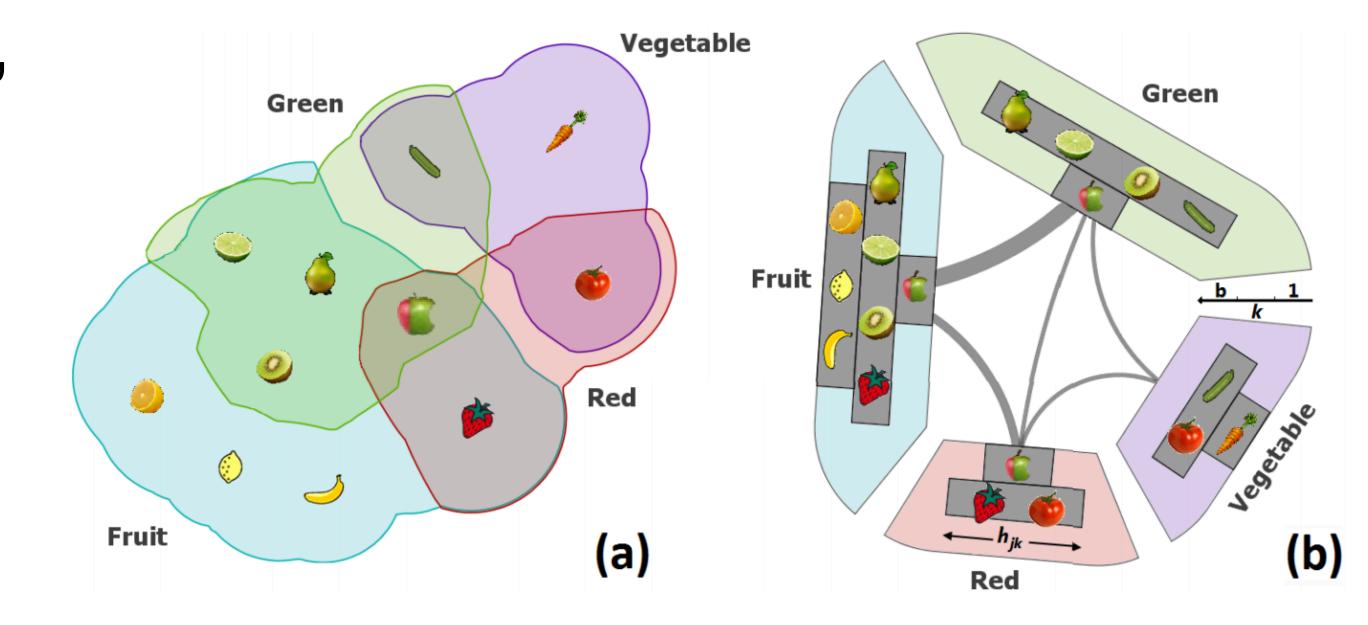
	School	Bl Hour	Duff for	(Bril)	male	Pu phont Age
Lisa	1/1/11					
bart	111111				12m	
Homer			Mun		Im	min
Marge		11/11				
Marge				1963		
maggie						
Barney			mu		111111	
Mr Burn	1 1			Mille	un	Mm
Mo			1mn		Mu	

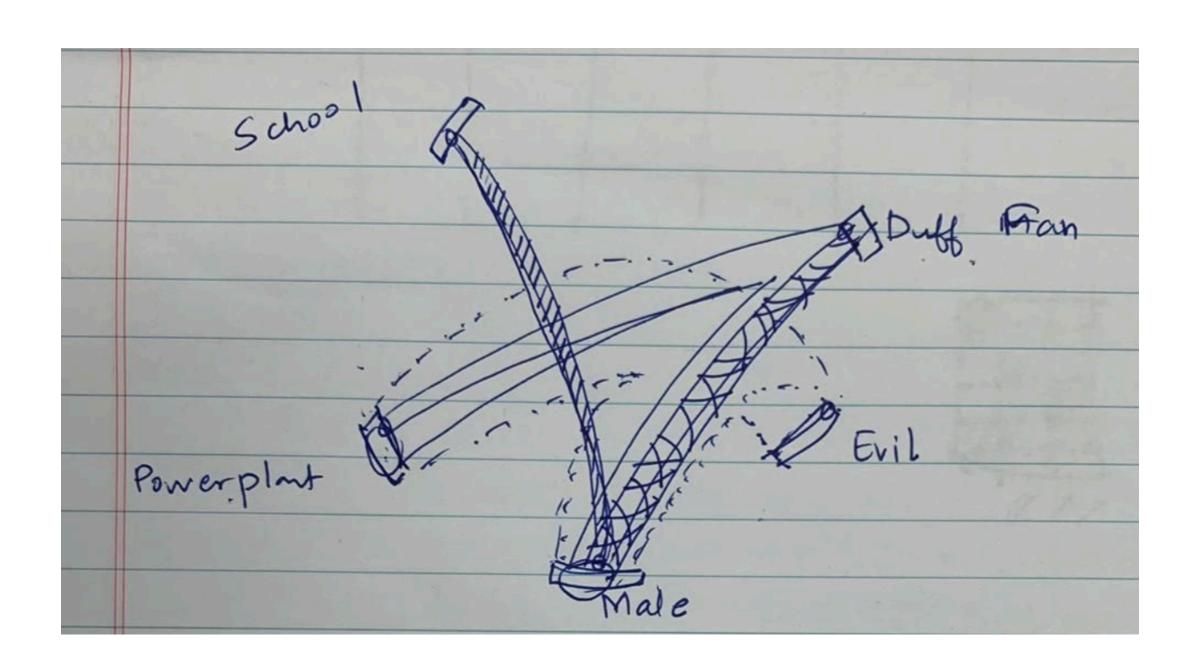
Radial Sets

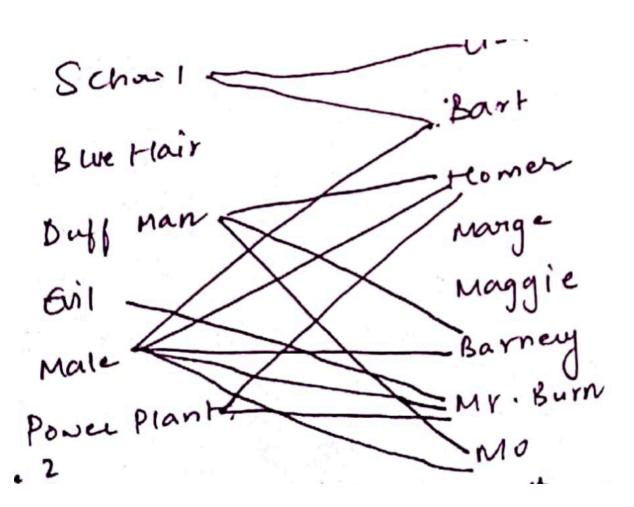
Sets are segments on a "circle" Relationships are encoded as ribbons

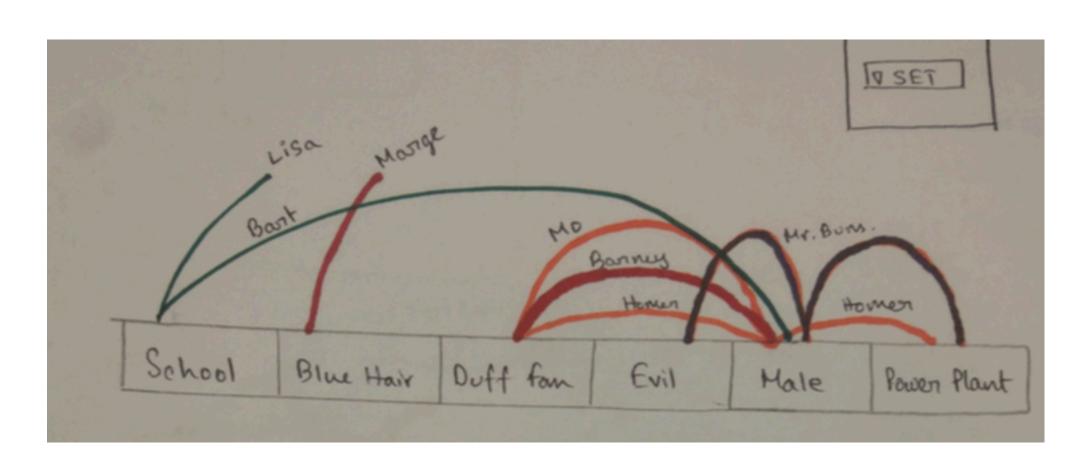
Size of segments encodes size of sets

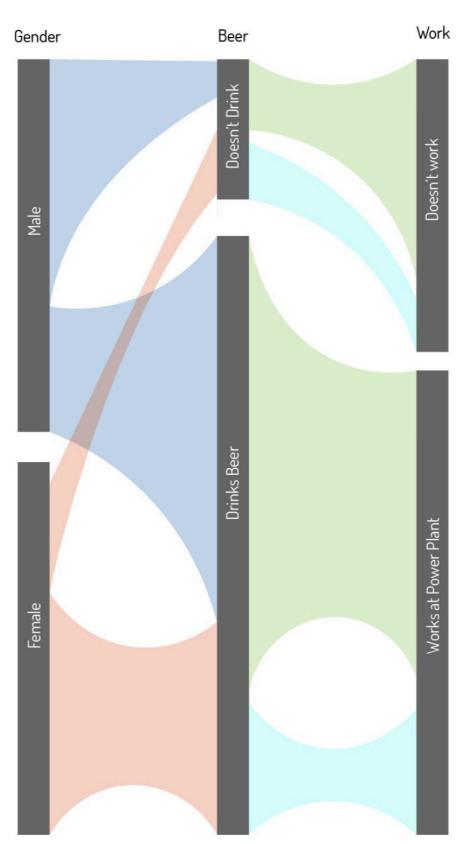
Histograms in segments show degrees







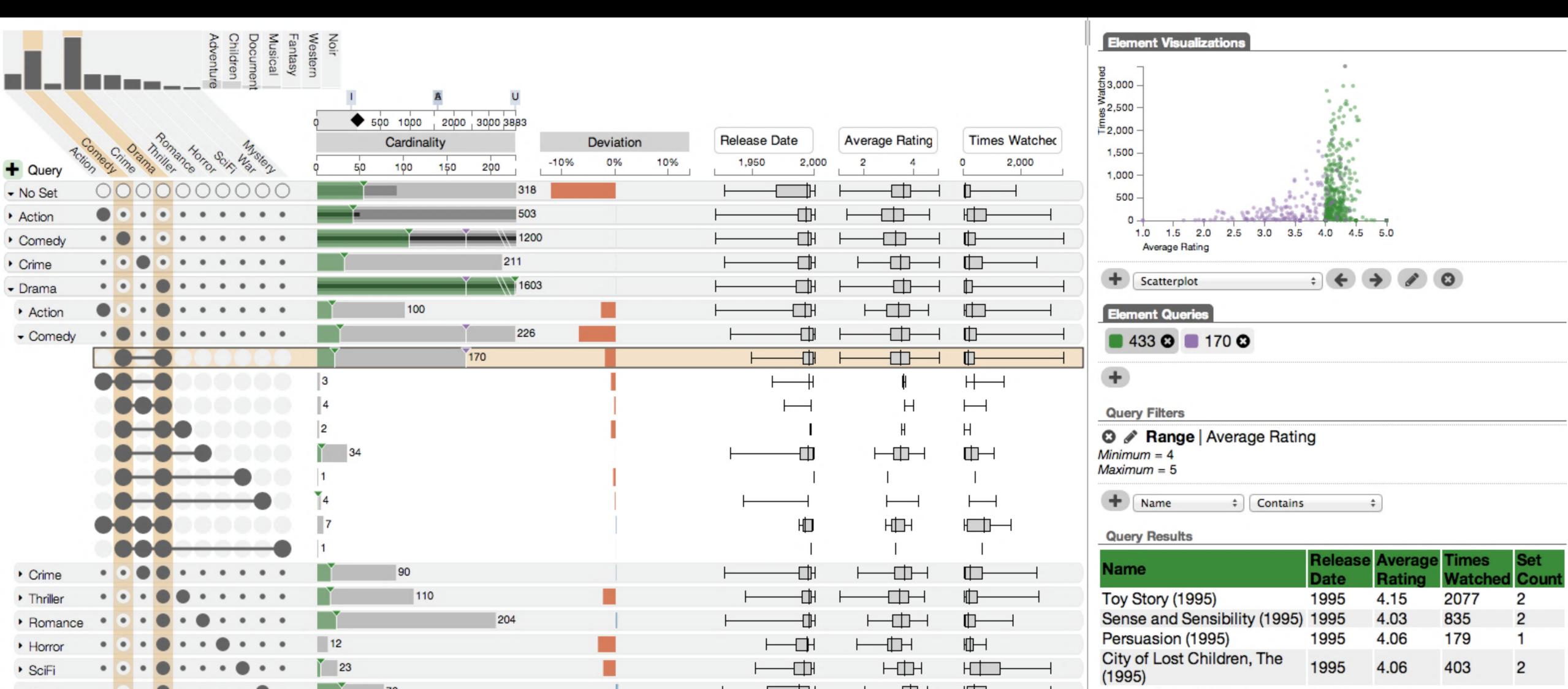




UpSet

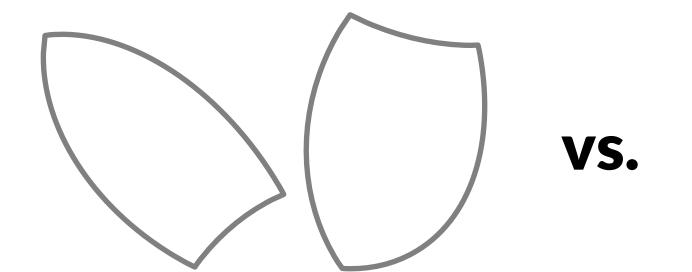
[InfoVis'14]

Visualizing Intersecting Sets

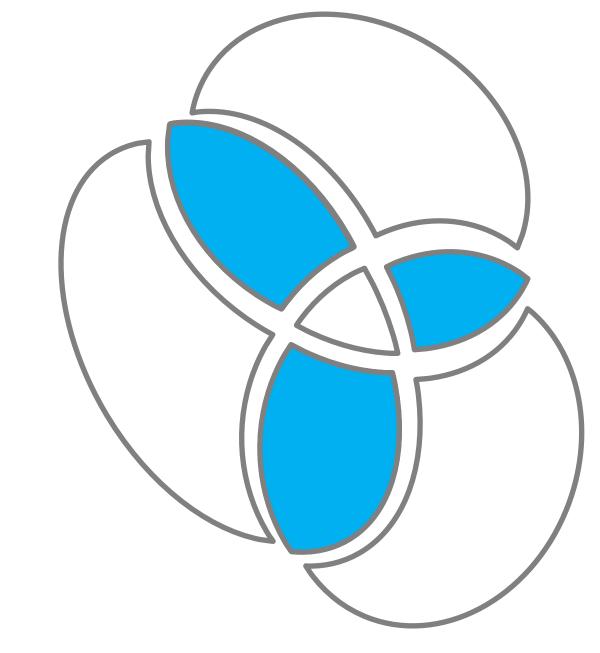


see Vis Croals

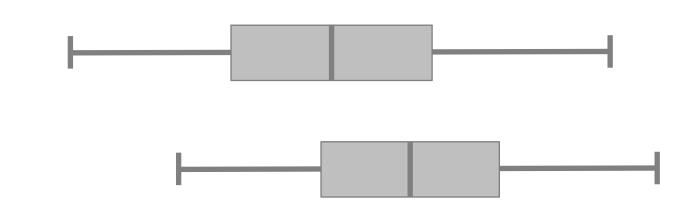
1. Efficient visual encoding



2. Creating complex slices of a dataset

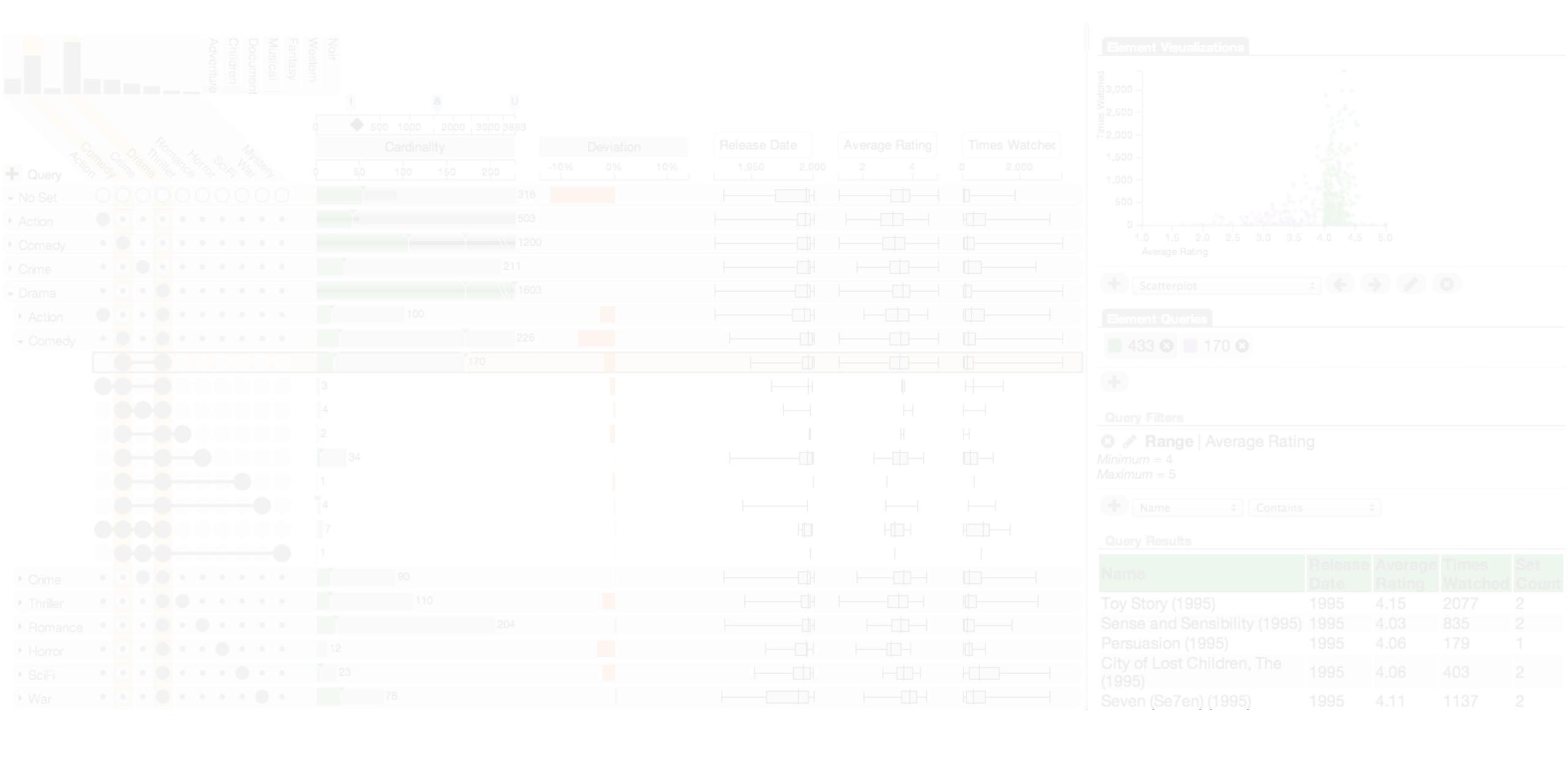


3. Visualize attributes



[Movie Lens Dataset]

Attribute Details

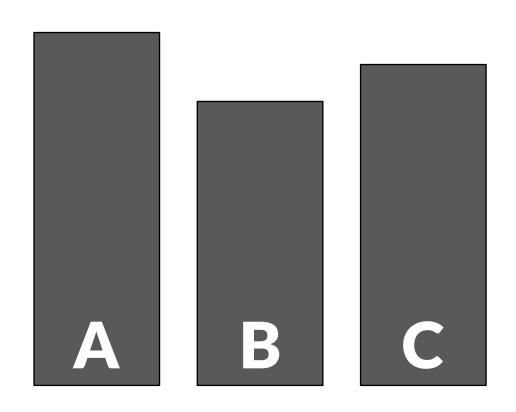


Visualizing Intersections

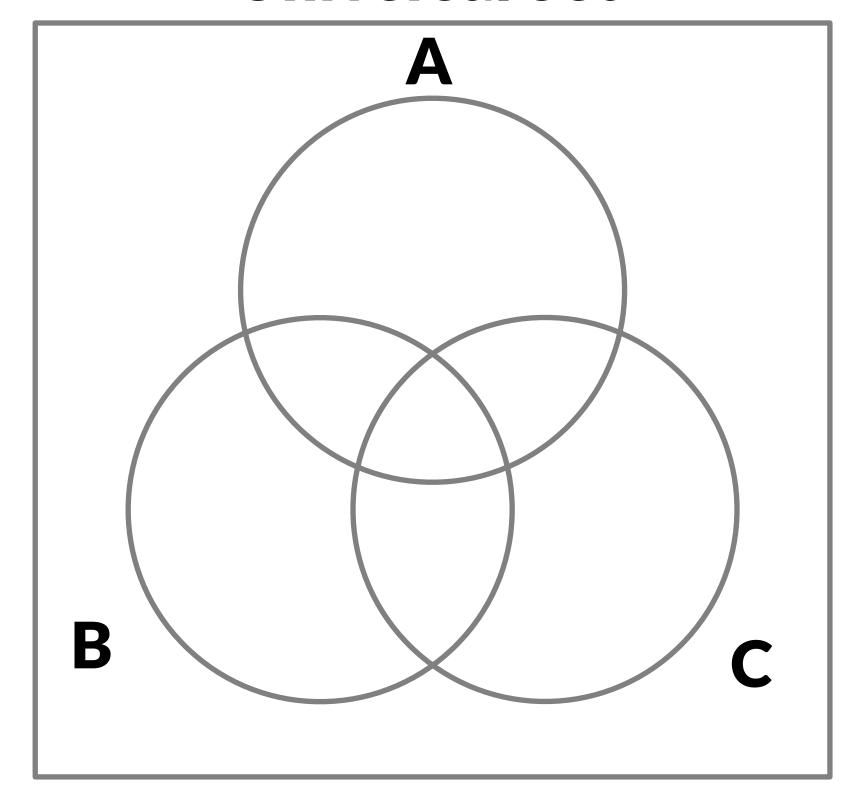
Visualizing Properties

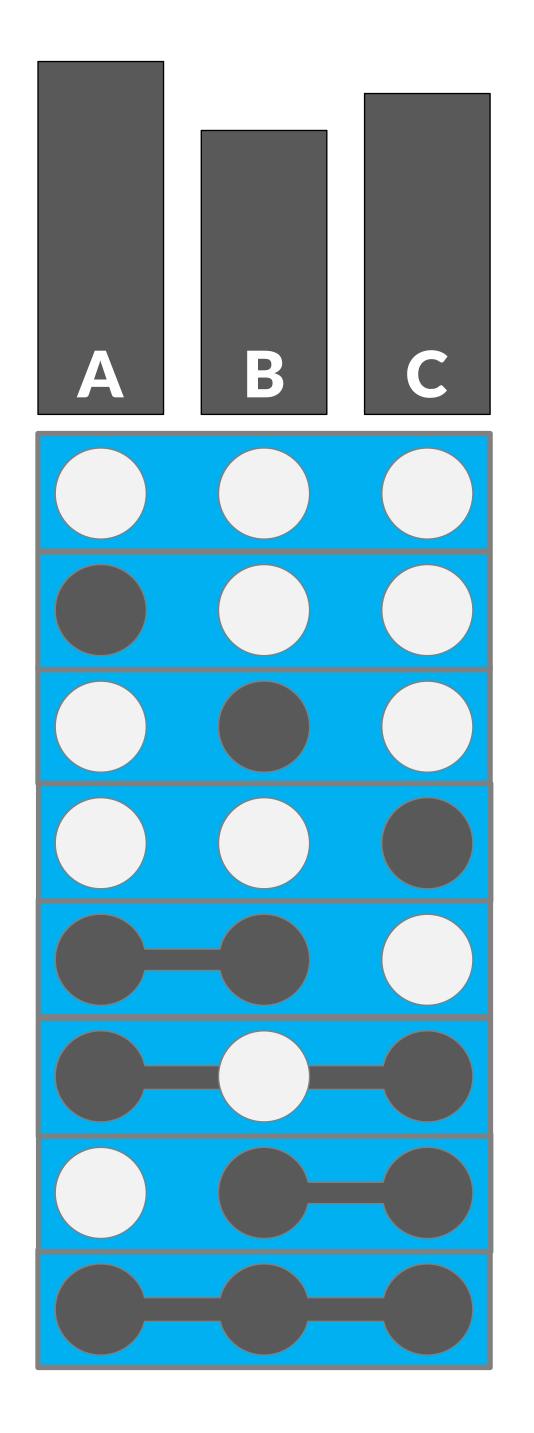
Element List & Queries

Visualizing



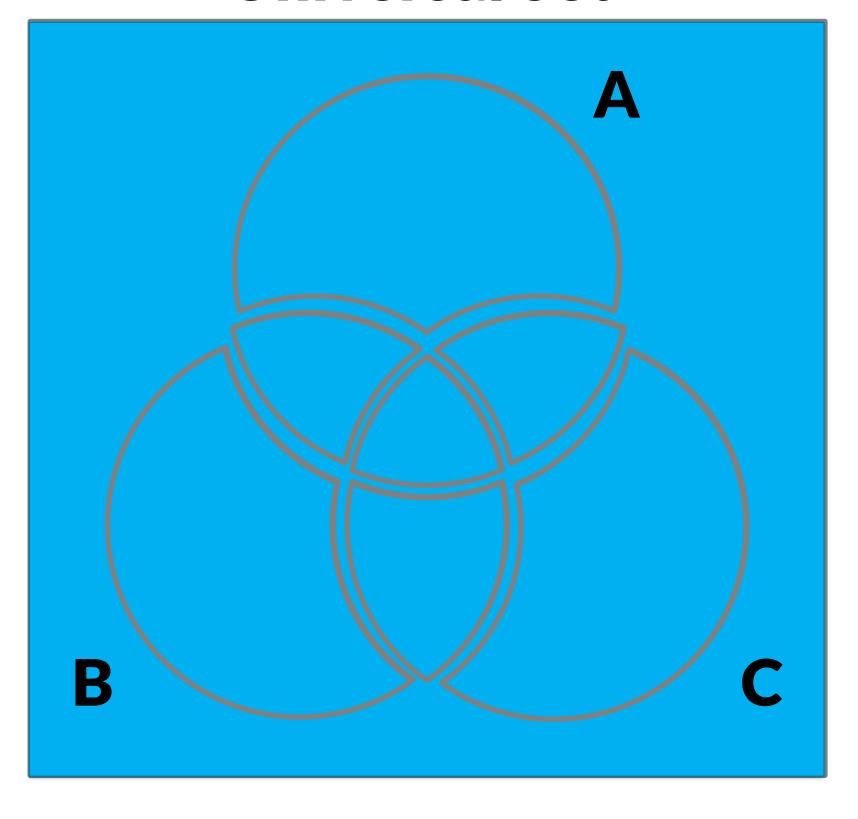
Universal Set

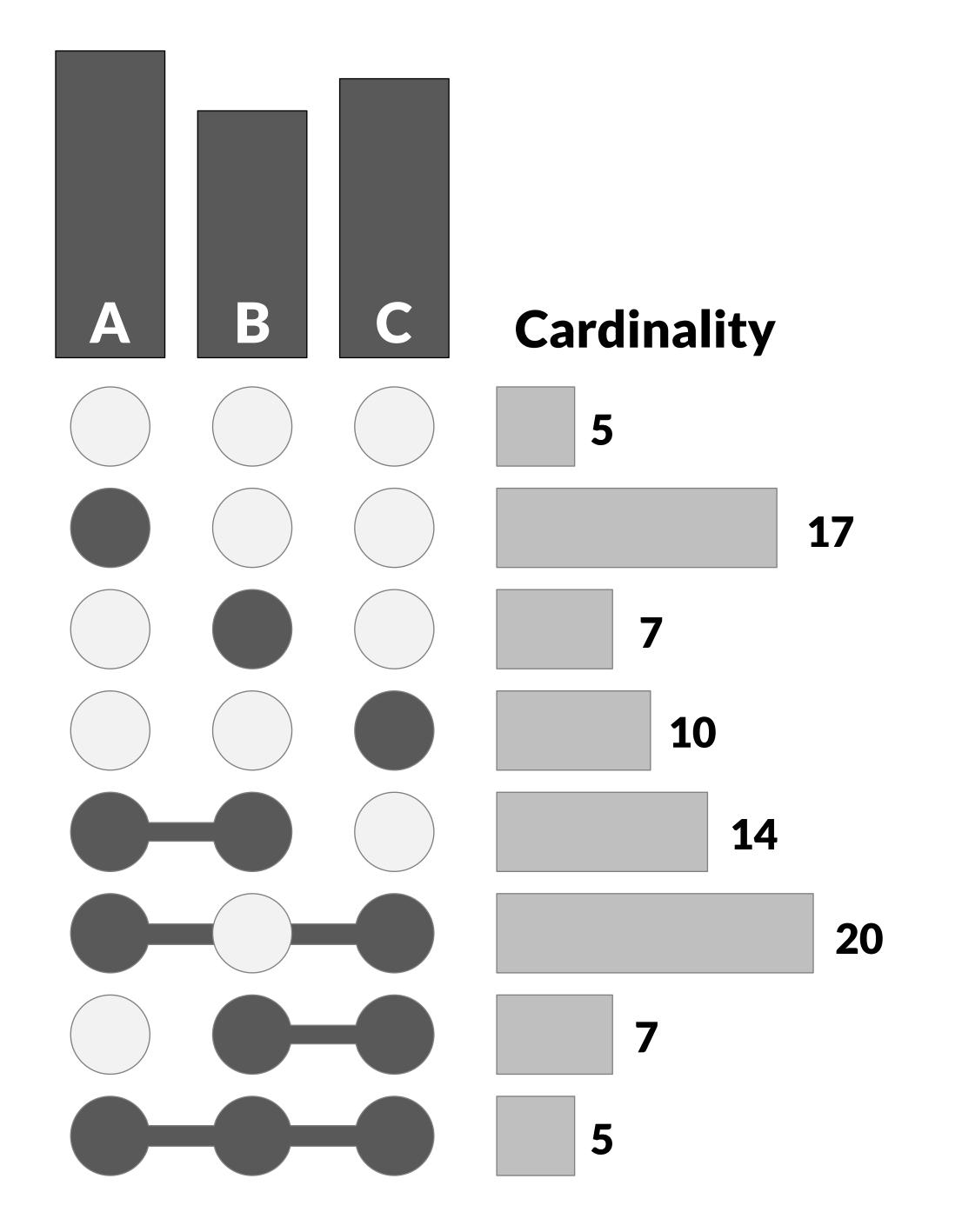


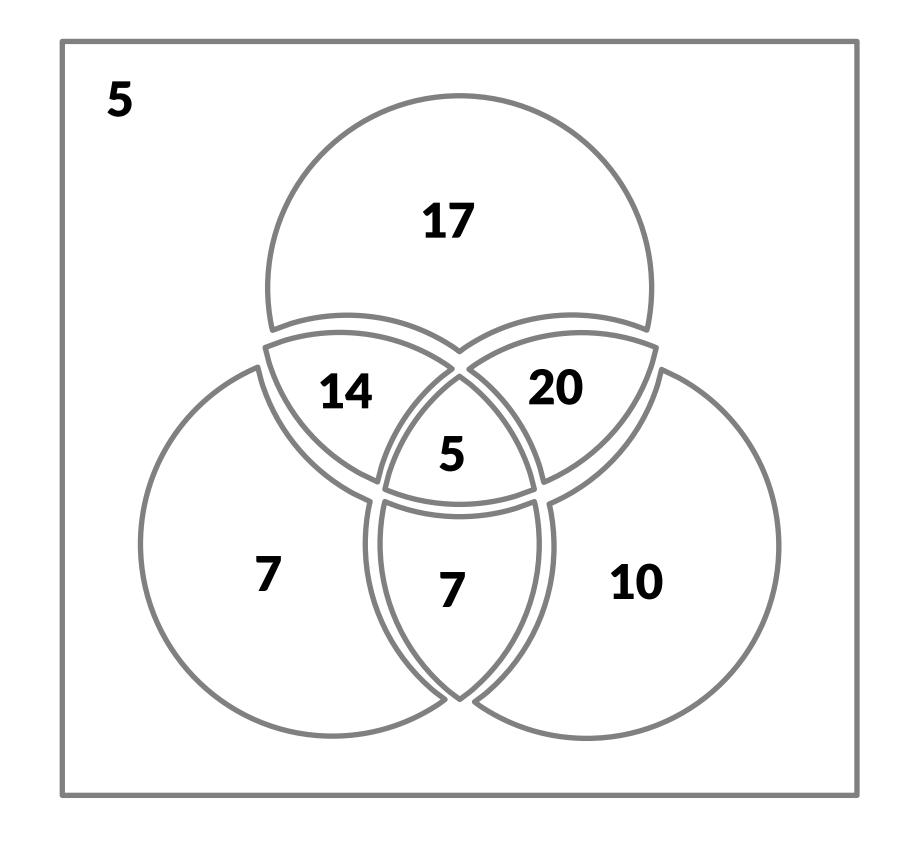




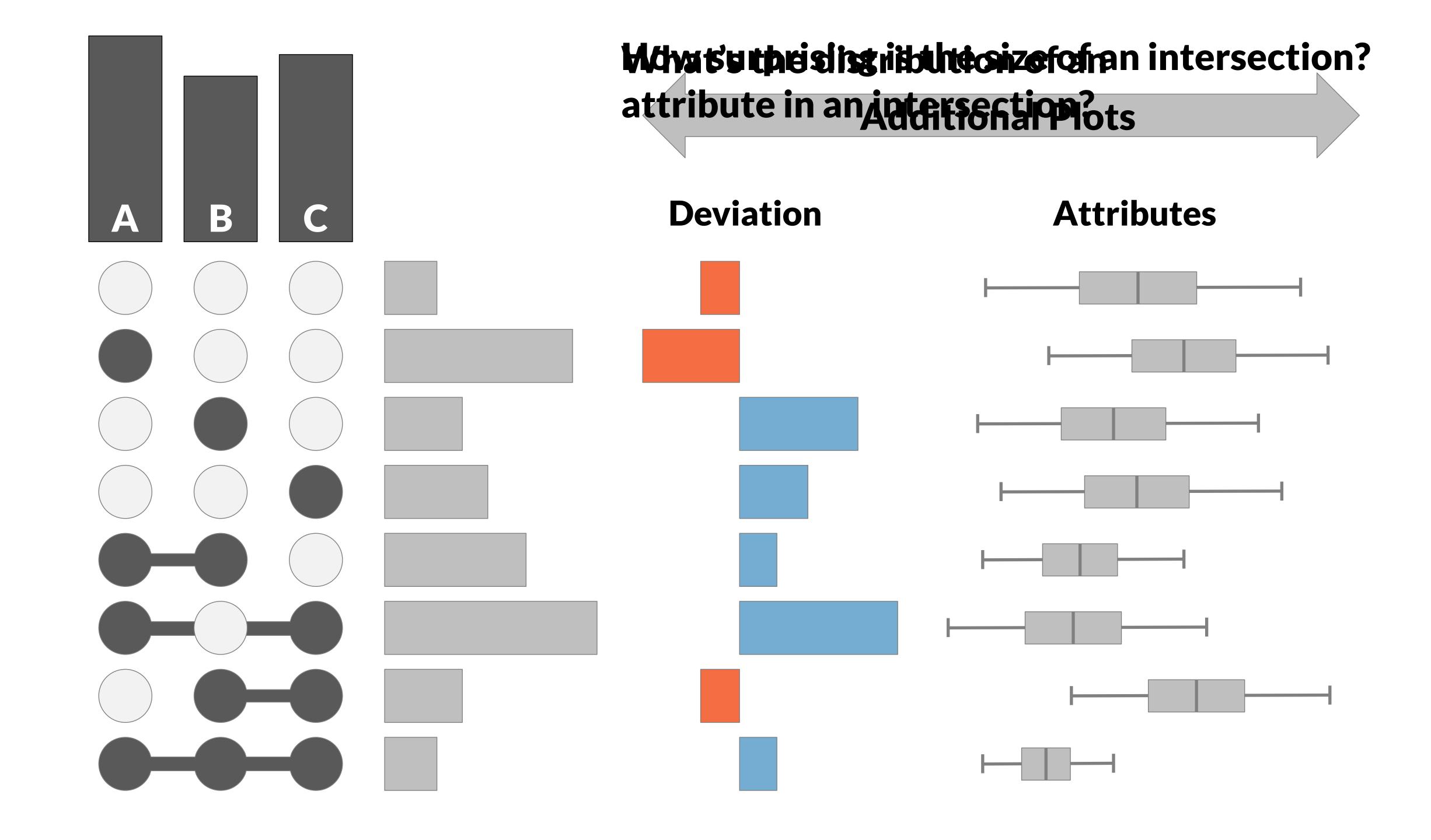
Universal Set

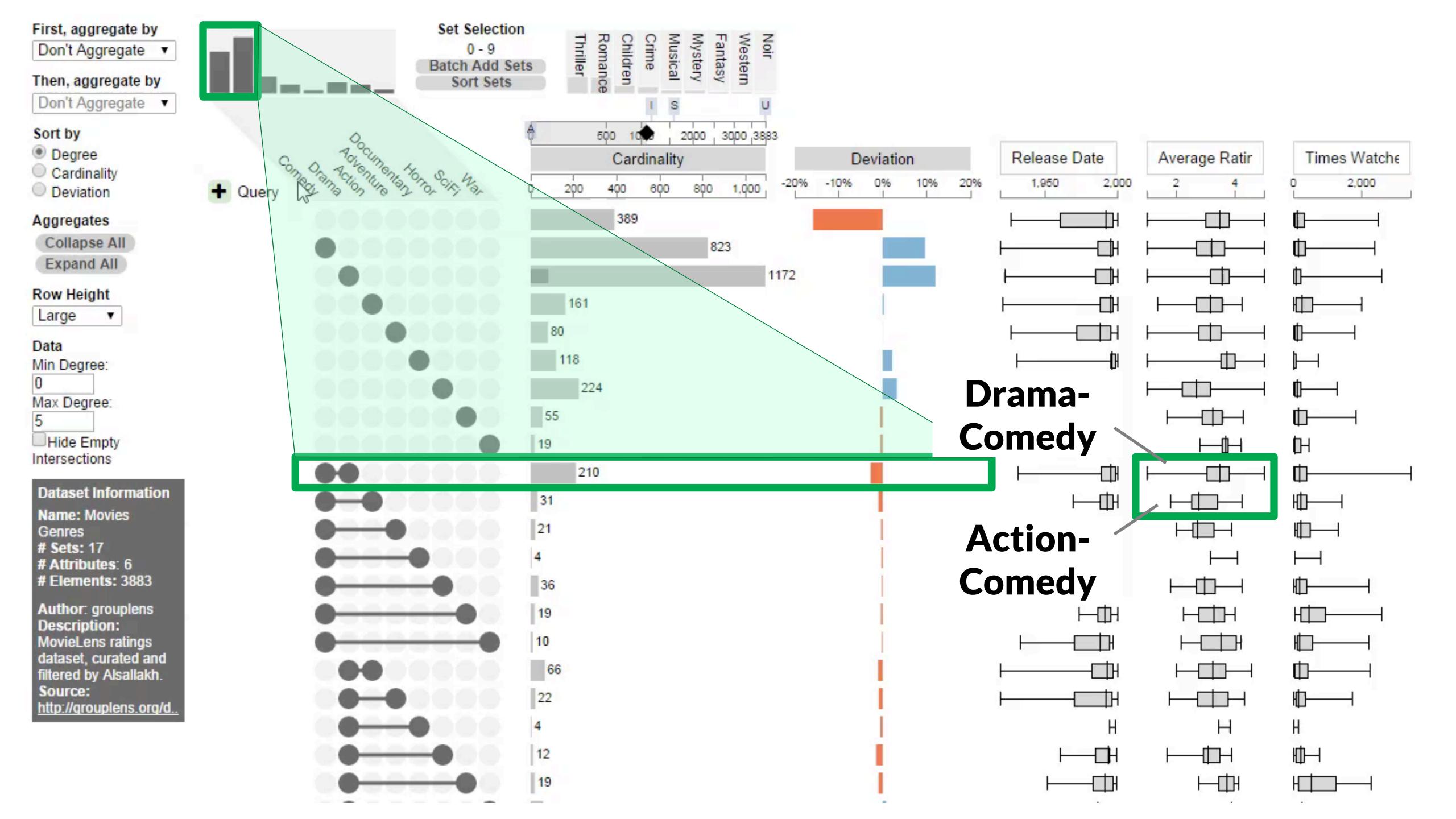


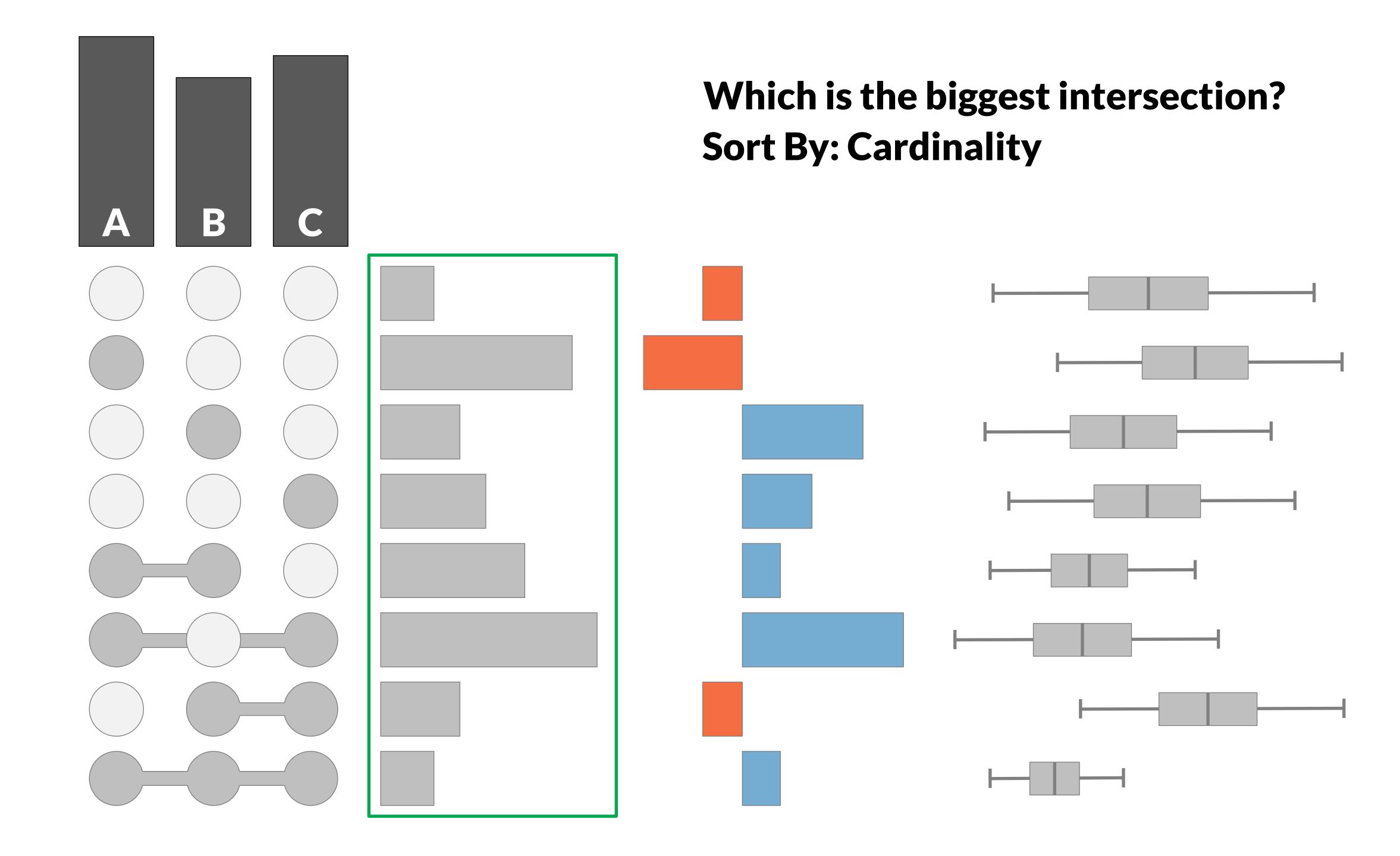


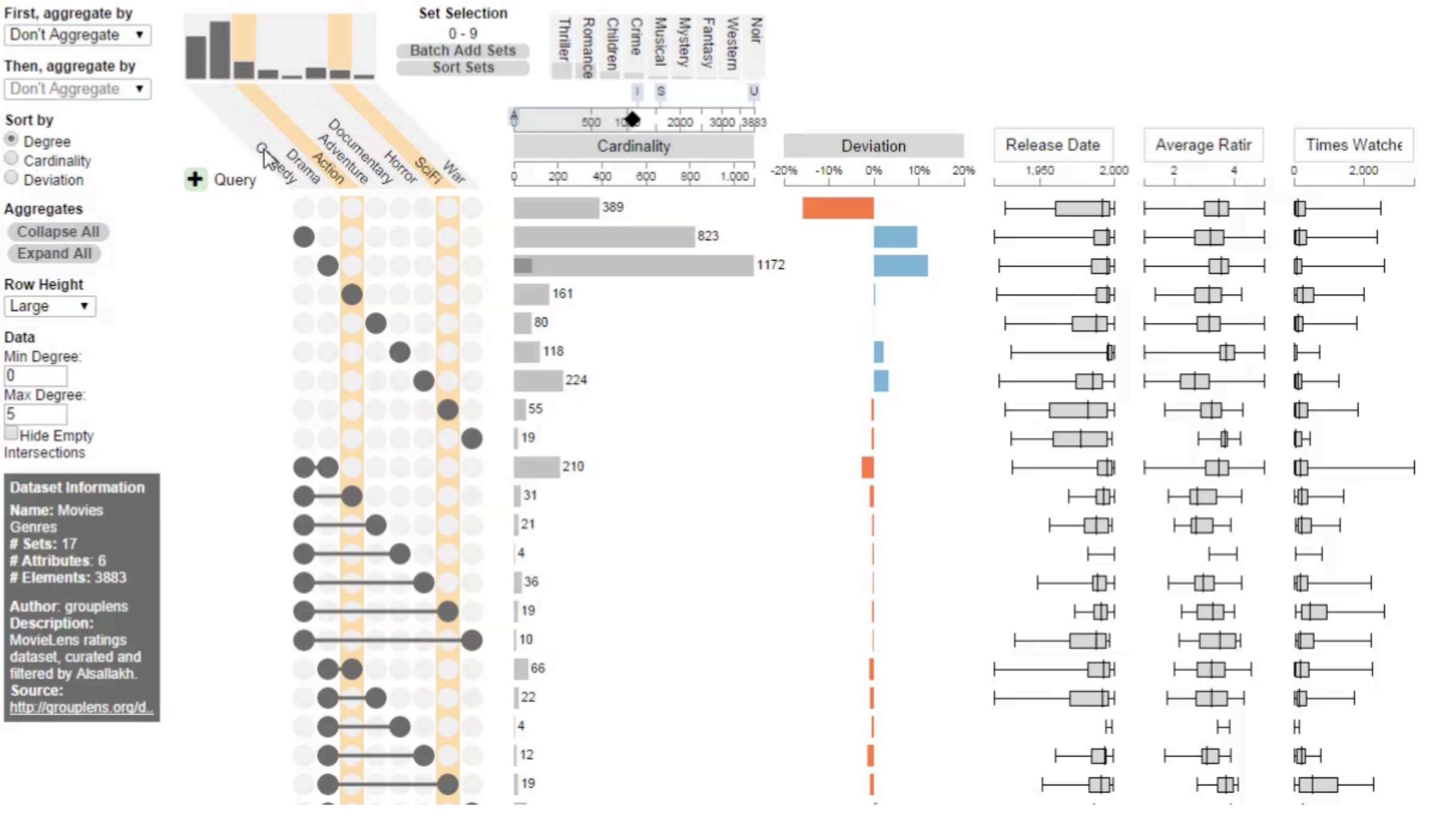


riceina Altributes

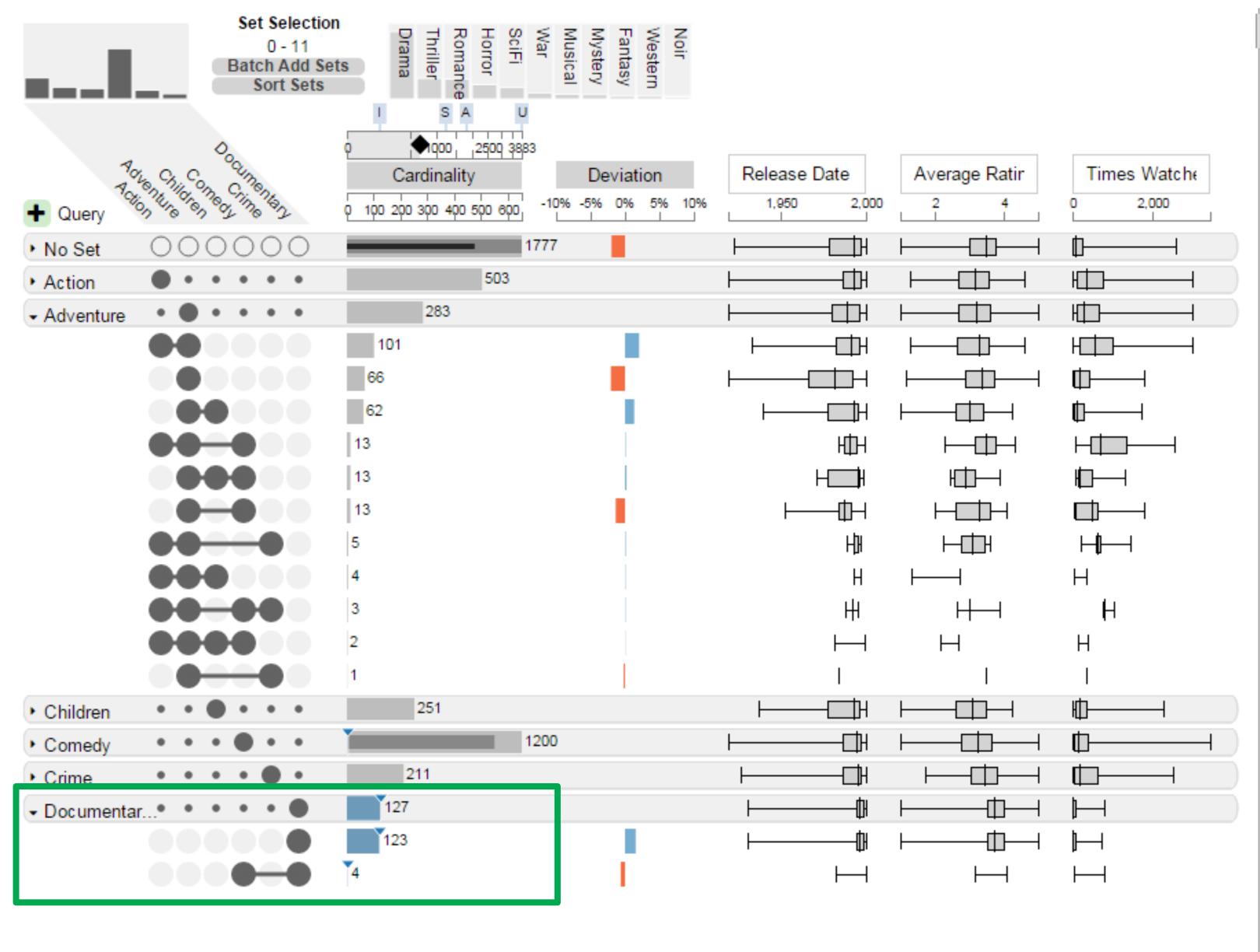


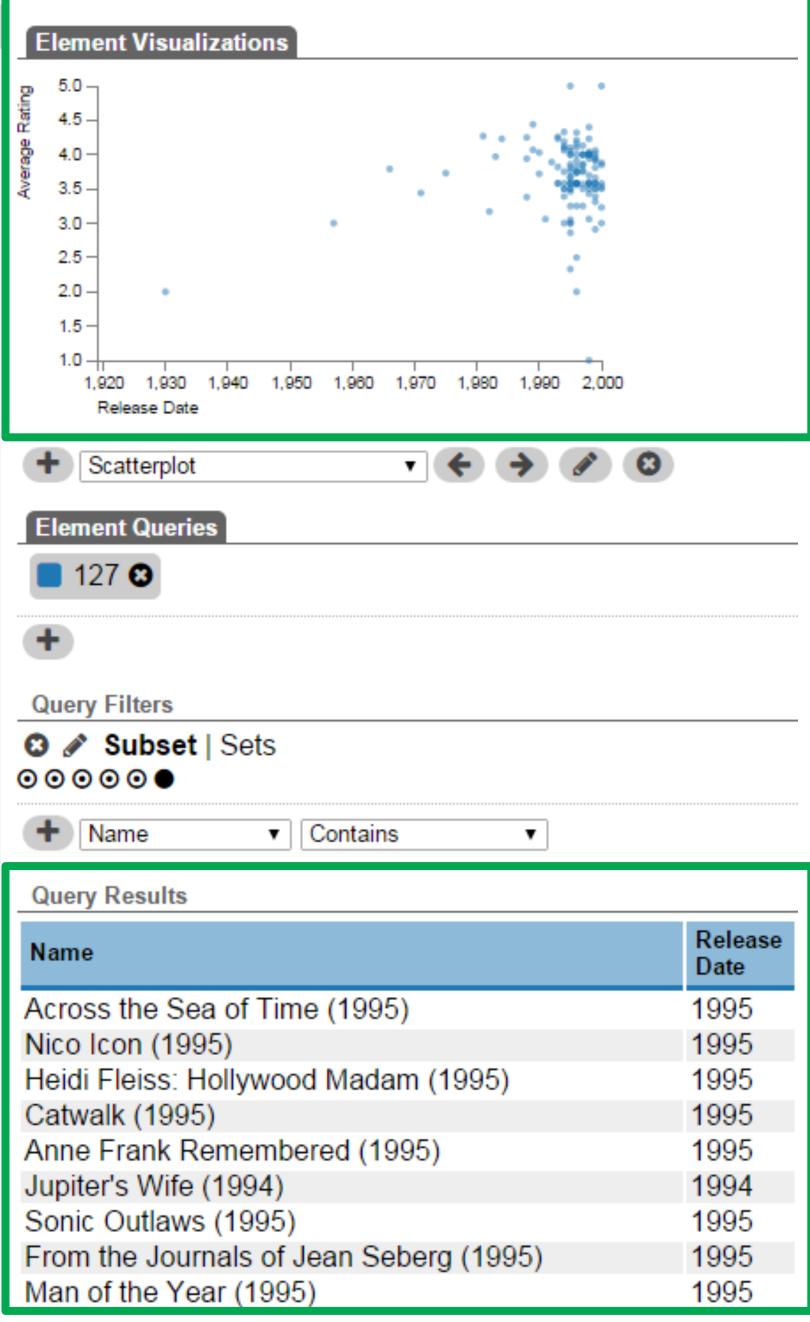






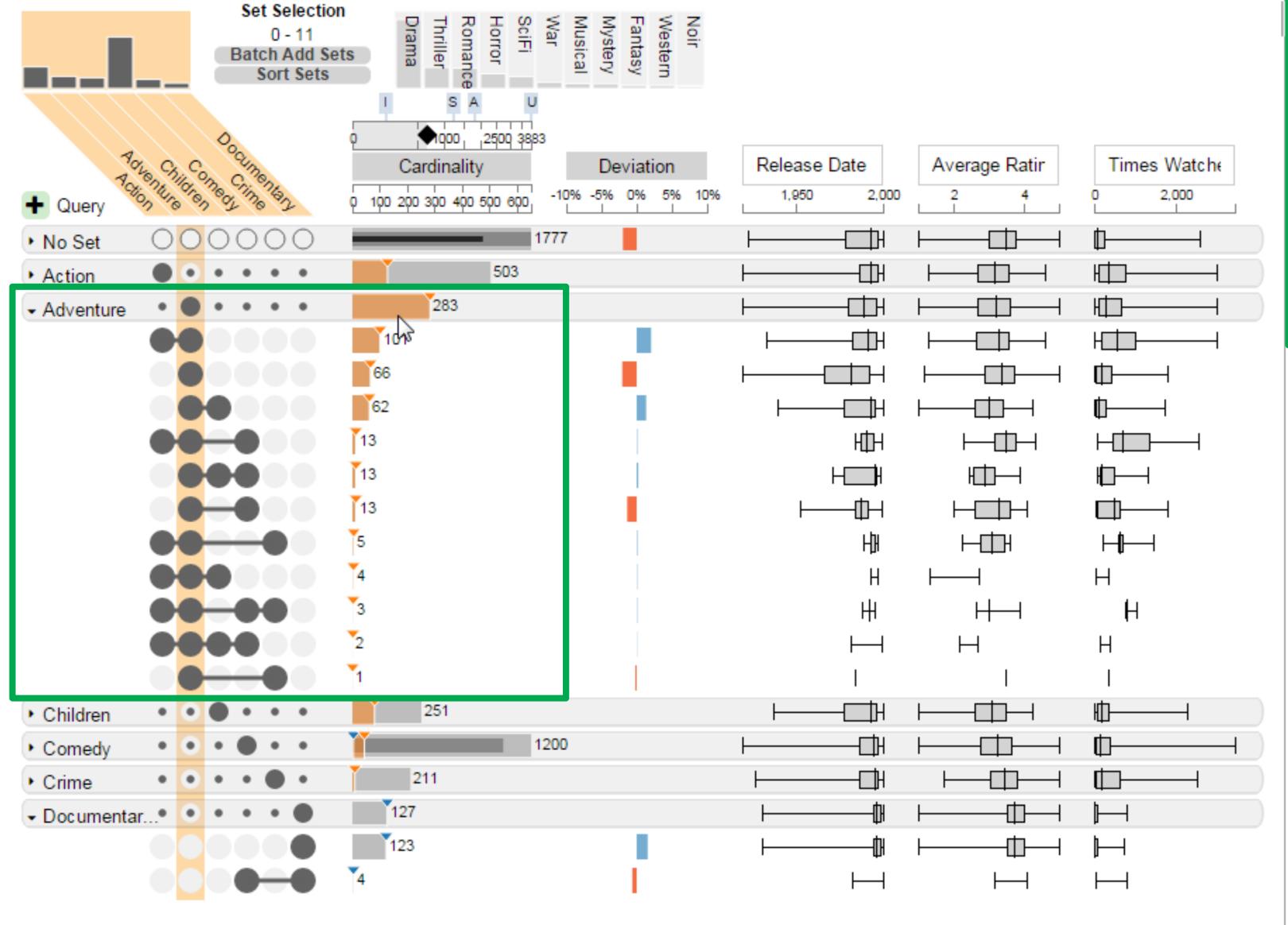
ELEMACINES STA



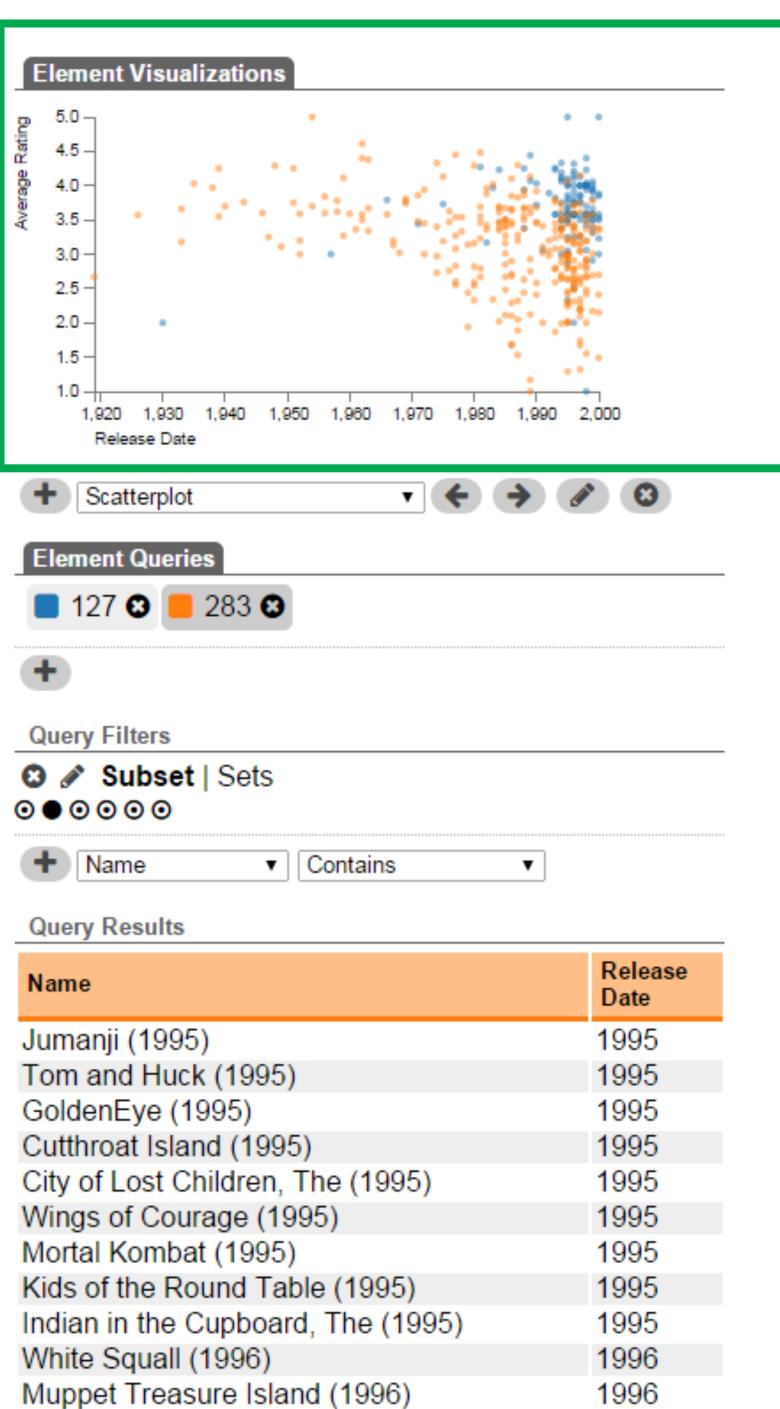




How do documentaries compare to adventure movies?



How do documentaries compare to adventure movies?

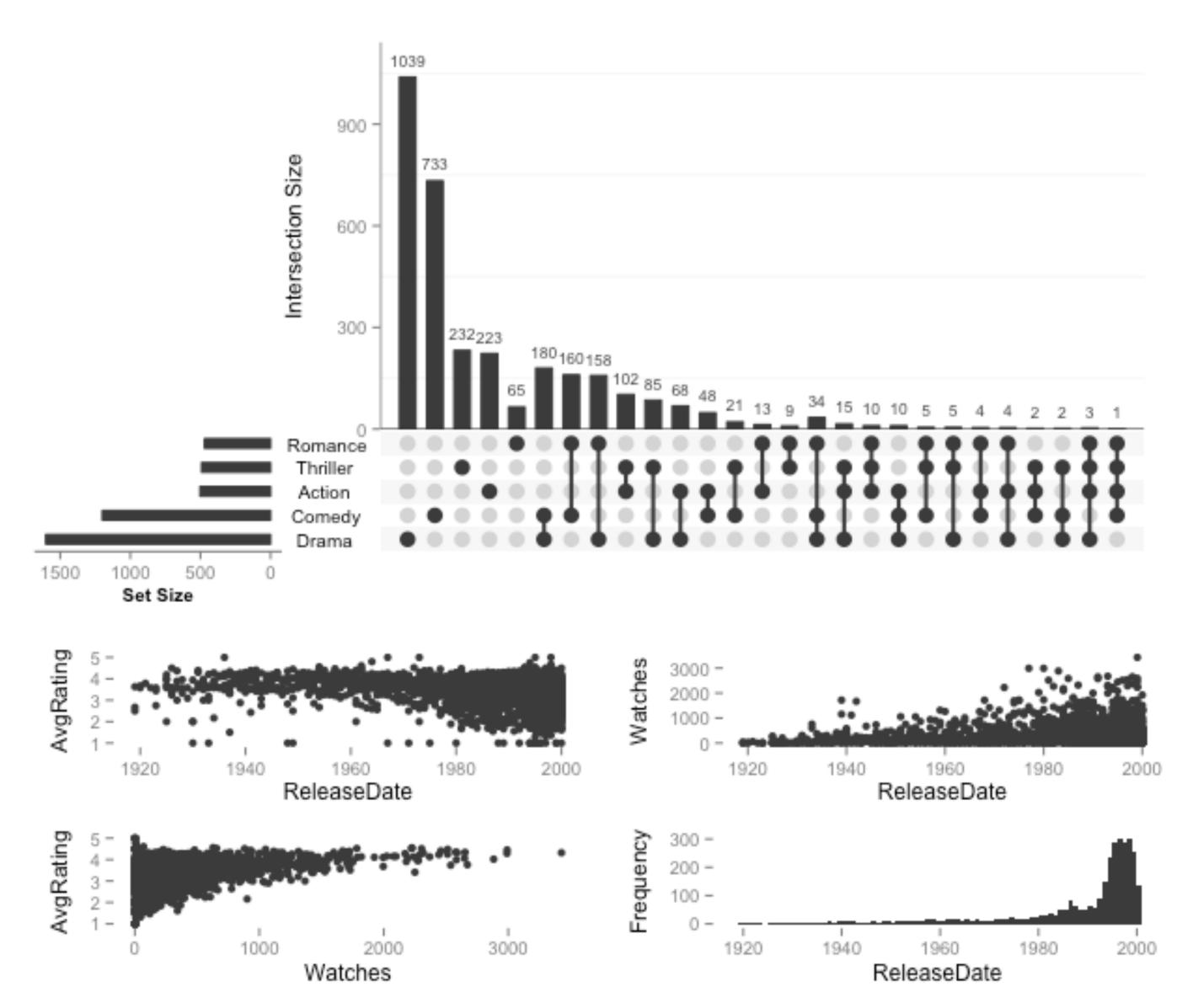


Applications

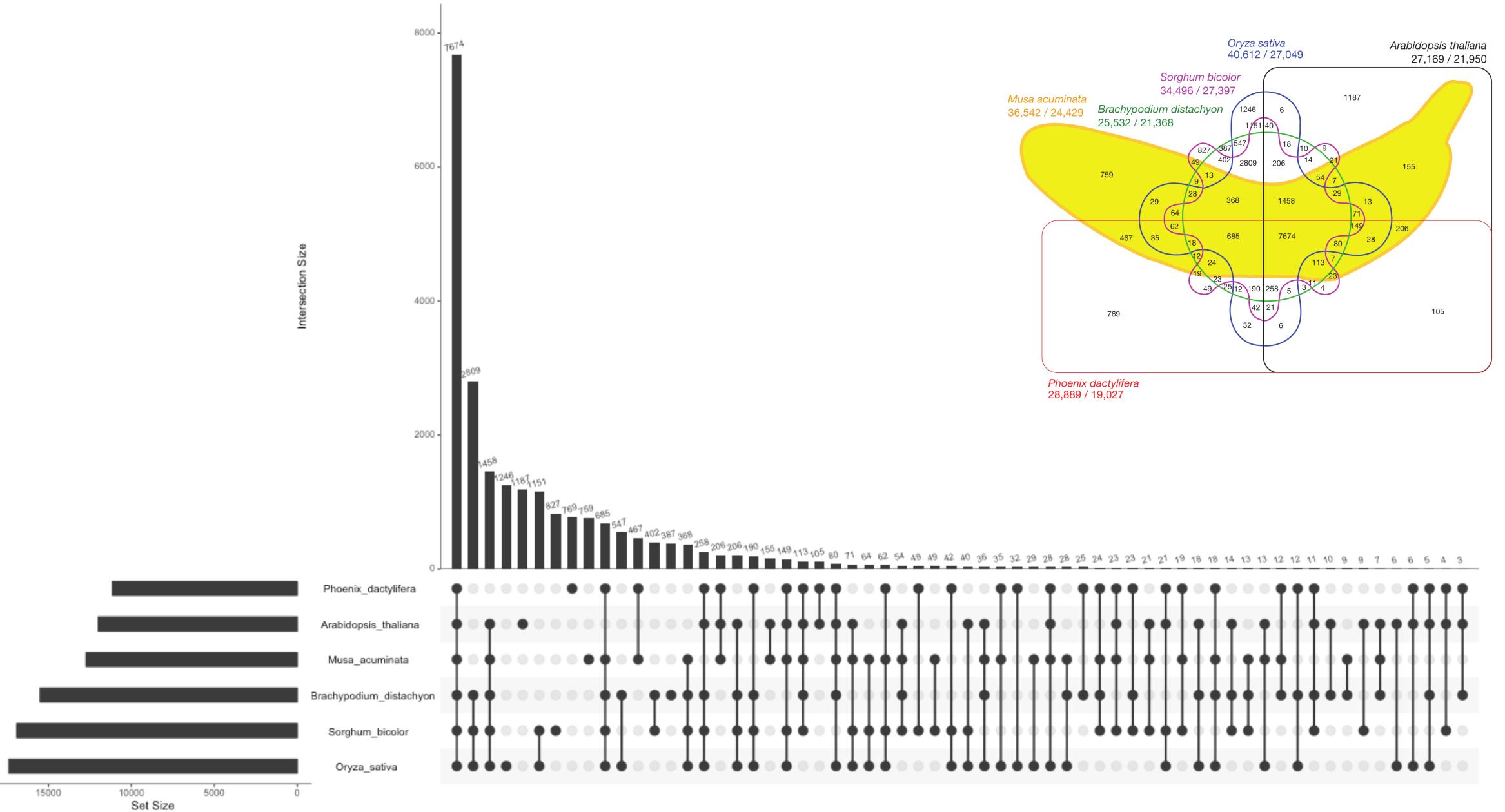
R-Version: UpSetR

Developed at HMS

Some design adaptions



The Banana Chart Redesigned



DEGIGIT E Male Dufffan Bluellair Values. Matrix 1 0 0 0 matrix 2 0 0

Other Options

