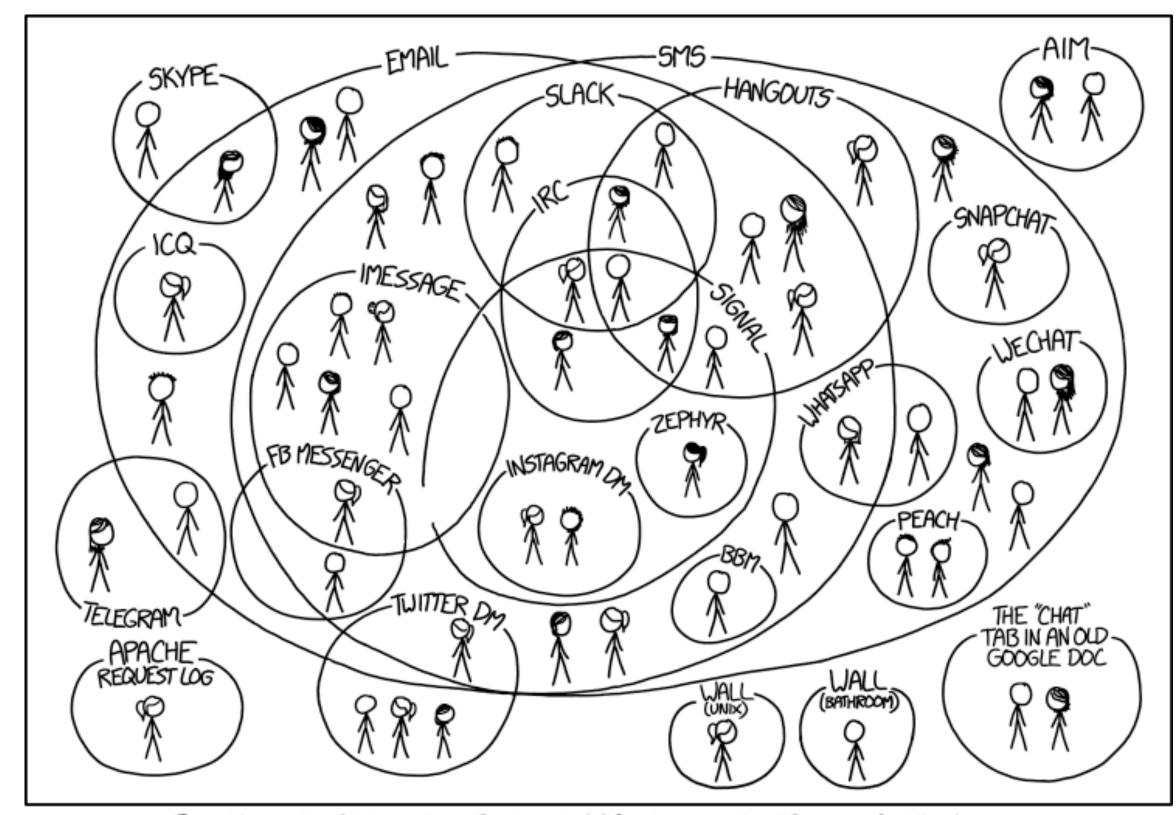
CS-5630 / CS-6630 Visualization for Data Science Set Visualization

Alexander Lex alex@sci.utah.edu





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

LETTER

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

Angélique D'Hont¹*, France Denoeud²,3,4*, Jean-Marc Aury², Franc-Christophe Baurens¹, Françoise Carreel¹,5, Olivier Garsmeur¹, Benjamin Noel², Stéphanie Bocs¹, Gaëtan Droc¹, Mathieu Rouard⁶, Corinne Da Silva², Kamel Jabbari²,4, Céline Cardi¹, Julie Poulain², Marlène Souquet¹, Karine Labadie², Cyril Jourda¹, Juliette Lengellé¹, Marguerite Rodier-Goud¹, Adriana Alberti², Maria Bernard², Margot Correa², Saravanaraj Ayyampalayam³, Michael R. Mckain³, Jim Leebens-Mack³, Diane Burgess³, Mike Freeling³, Didier Mbéguié-A-Mbéguié³, Matthieu Chabannes⁵, Thomas Wicker¹0, Olivier Panaud¹¹, Jose Barbosa¹¹, Eva Hribova¹², Pat Heslop-Harrison¹³, Rémy Habas⁵, Ronan Rivallan¹, Philippe Francois¹, Claire Poiron¹, Andrzej Kilian¹⁴, Dheema Burthia¹, Christophe Jenny¹, Frédéric Bakry¹, Spencer Brown¹⁵, Valentin Guignon¹,⁶, Gert Kema¹⁶, Miguel Dita¹ゥ, Cees Waalwijk¹⁶, Steeve Joseph¹, Anne Dievart¹, Olivier Jaillon²,³,⁴, Julie Leclercq¹, Xavier Argout¹, Eric Lyons¹⁵, Ana Almeida⁶, Mouna Jeridi¹, Jaroslav Dolezel¹², Nicolas Roux⁶, Ange-Marie Risterucci¹, Jean Weissenbach²,³,⁴, Manuel Ruiz¹, Jean-Christophe Glaszmann¹, Francis Quétier¹8, Nabila Yahiaoui¹ & Patrick Wincker²,³,⁴

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

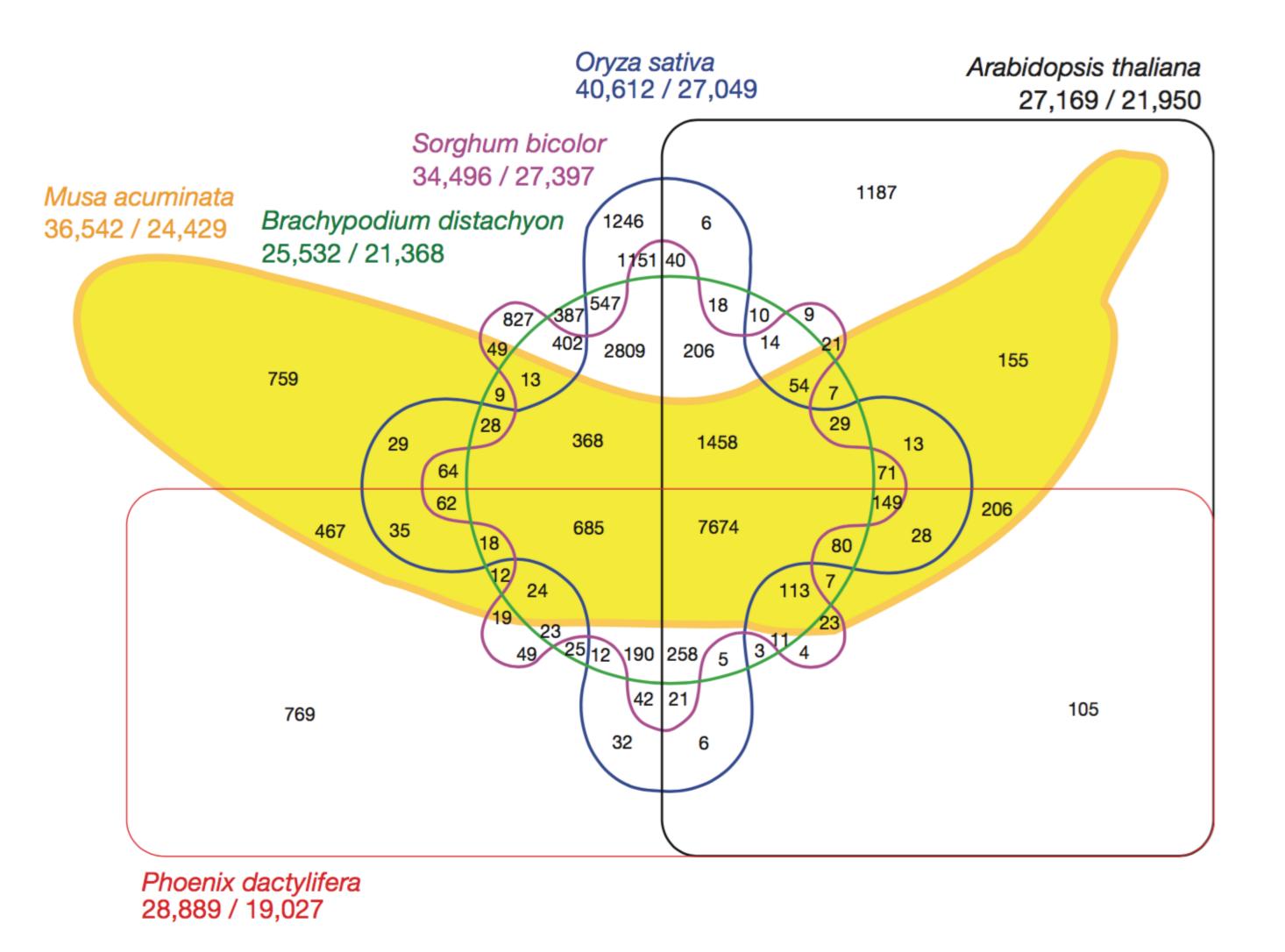
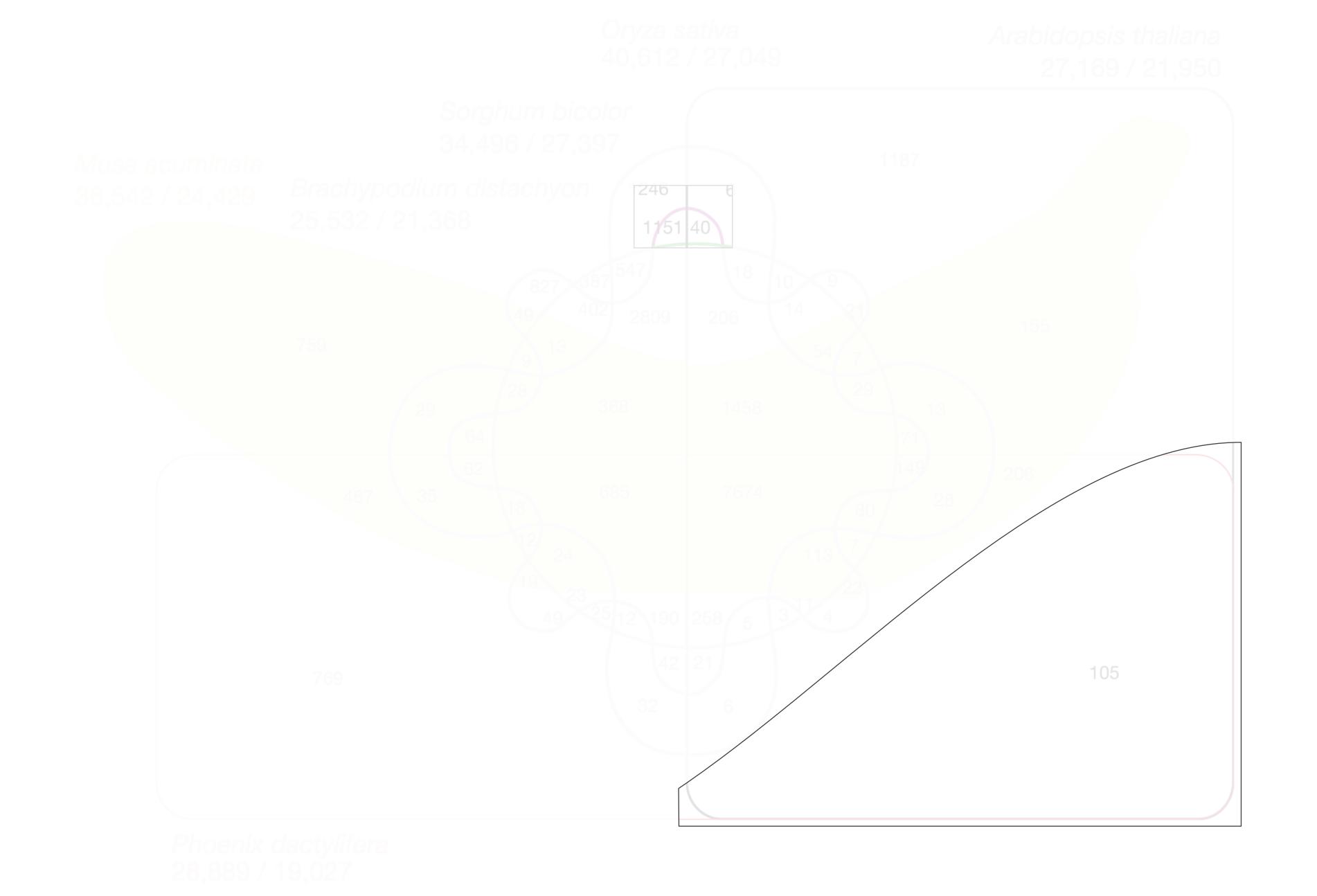
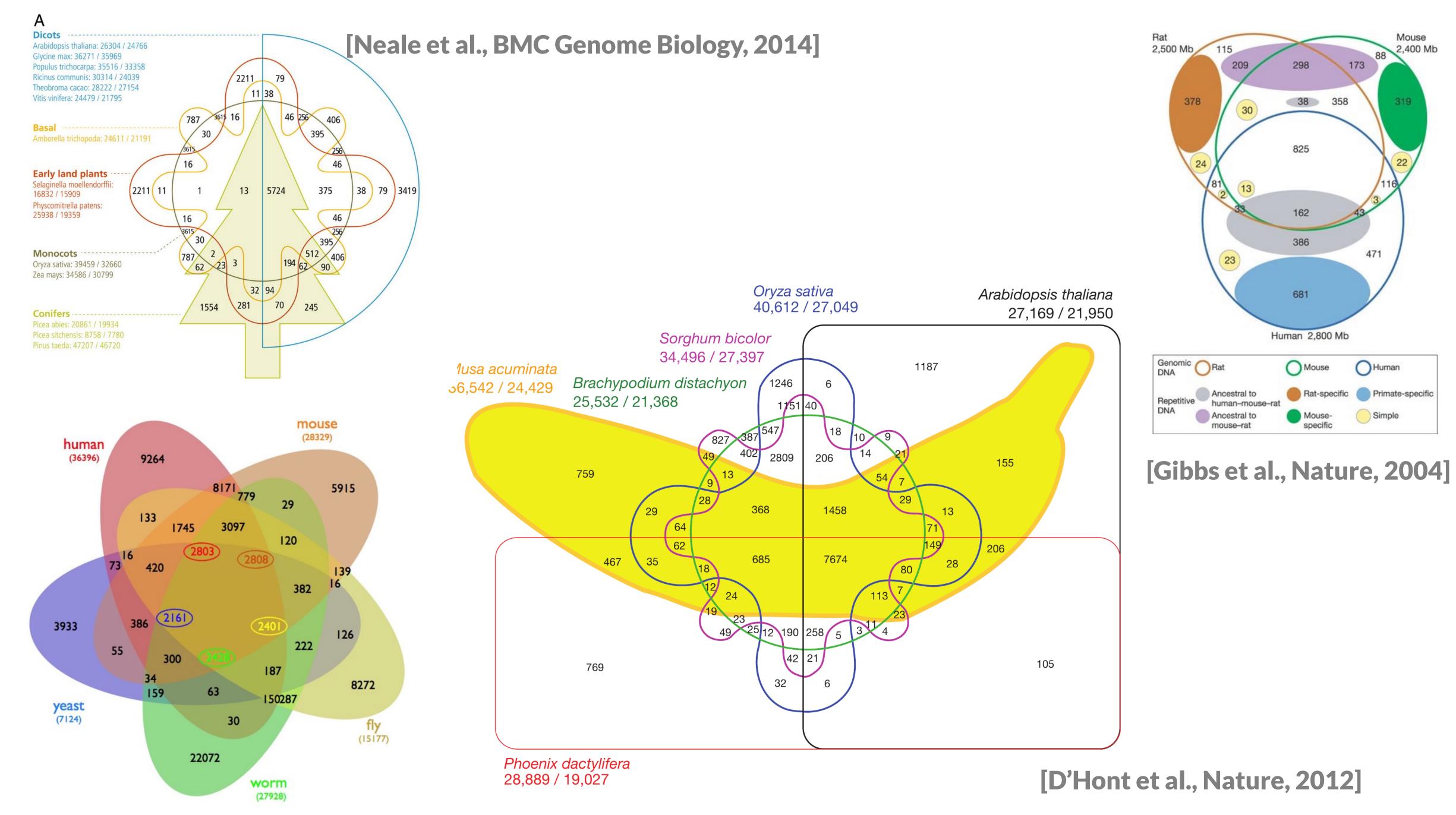


Figure 4 | Six-way Venn diagram showing the distribution of shared gene families (sequence clusters) among *M. acuminata*, *P. dactylifera*, *Arabidopsis thaliana*, *Oryza sativa*, *Sorghum bicolor* and *Brachypodium distachyon* genomes. Numbers of clusters are provided in the intersections. The total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

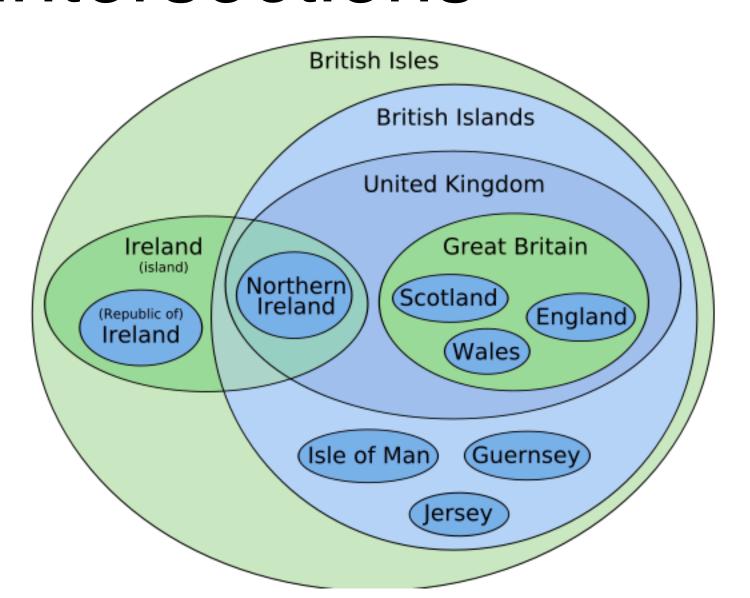
Uenn and Euler Diagrams

Venn vs Euler

Euler Diagram

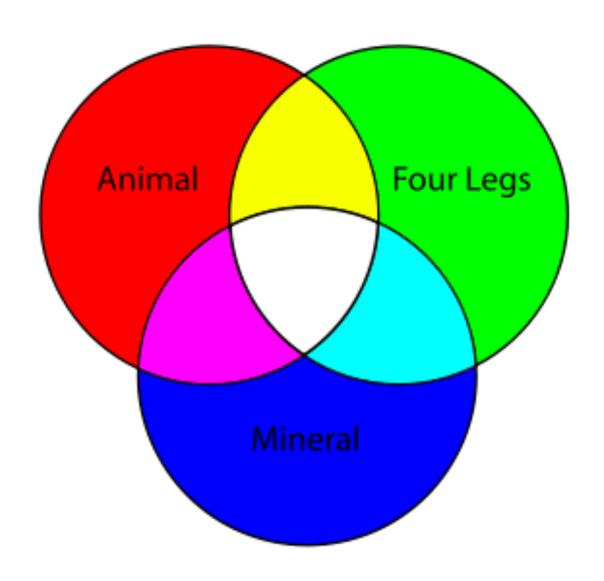
Shows logical relations

May omit empty intersections



Venn Diagram

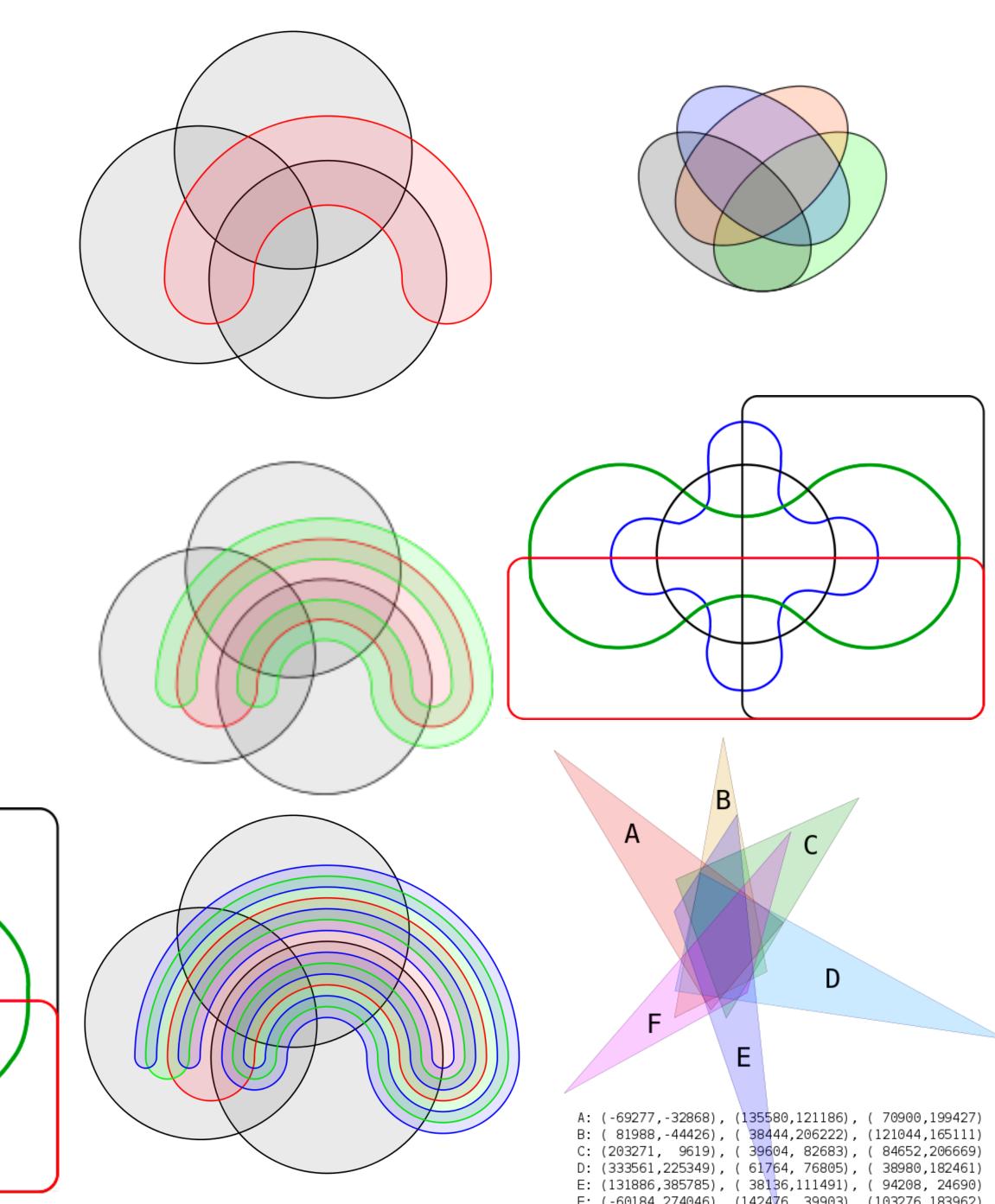
Shows all possible logical relations between sets (even if empty)

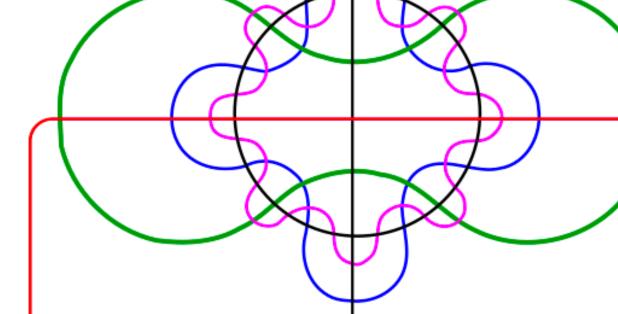


Venn Diagrams

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.

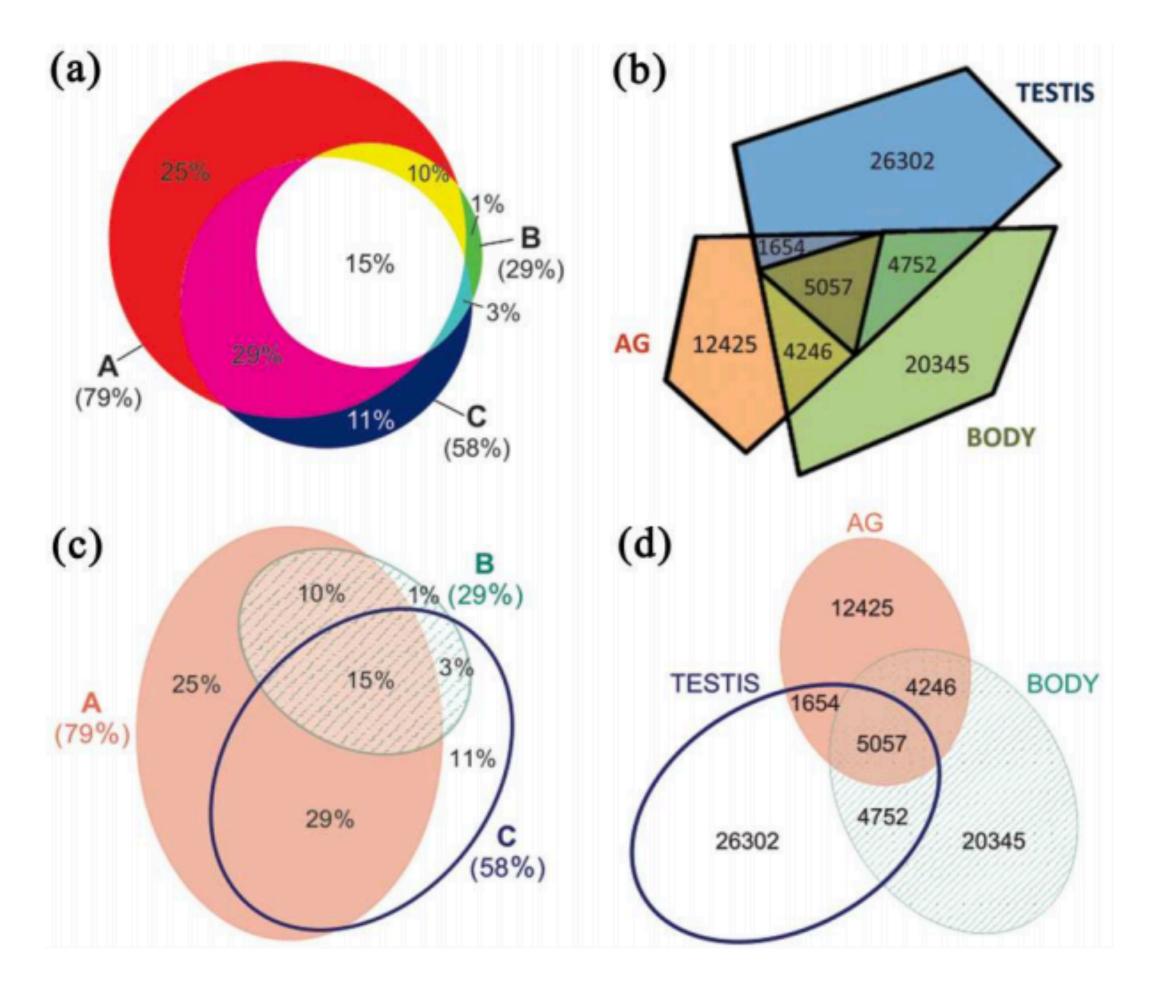
Layout criteria:

area proportional

simple curves (circles are best)

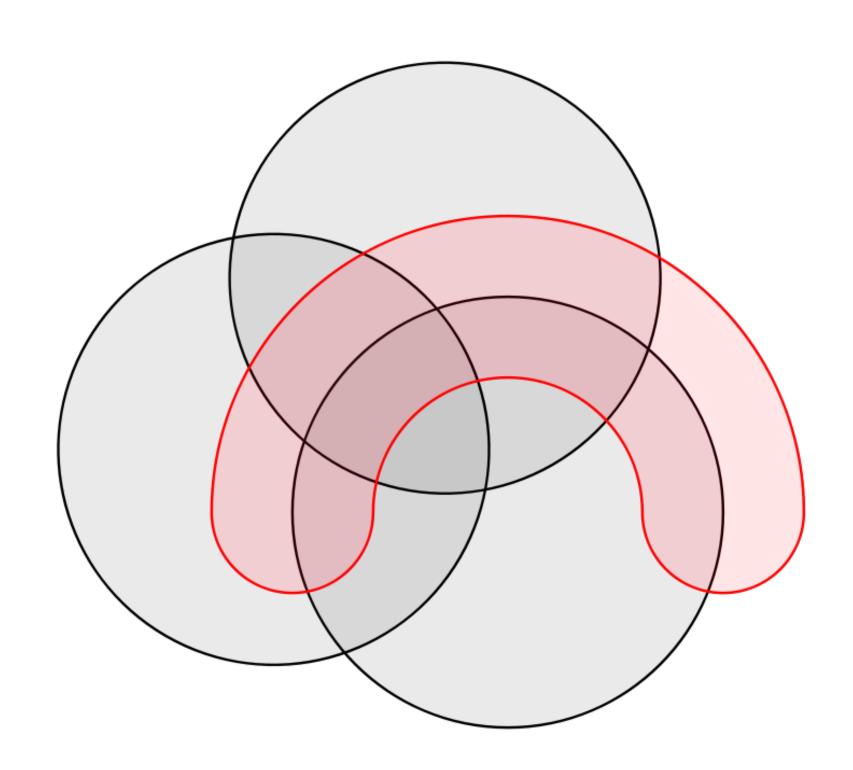
makes it easy to identify which sets are participating in intersection

Gestalt-principle: good continuation

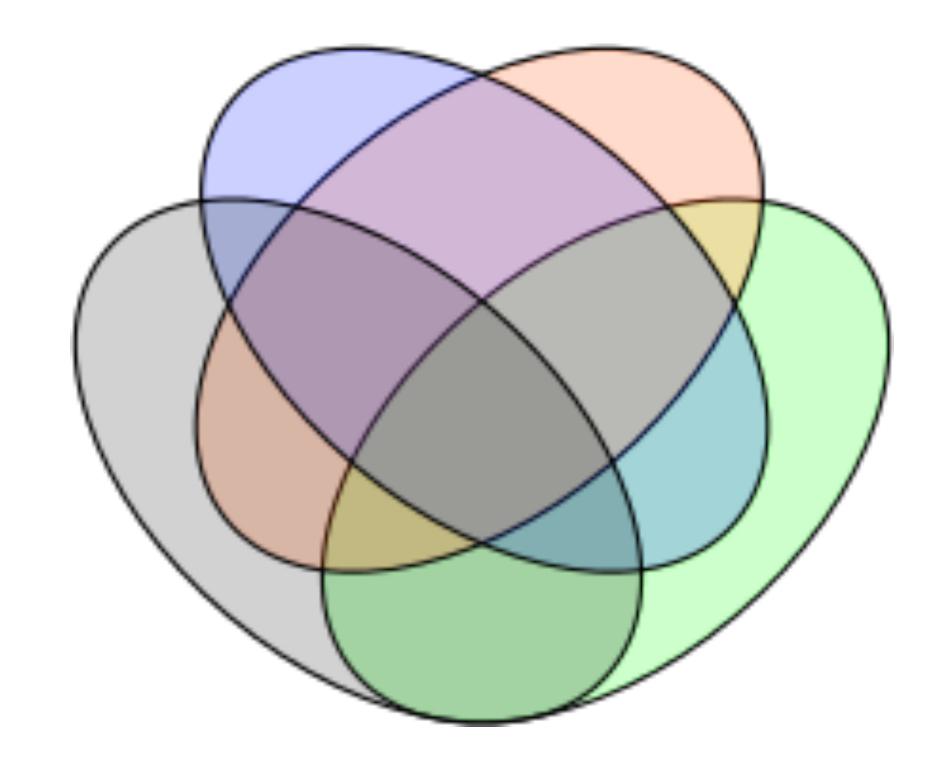


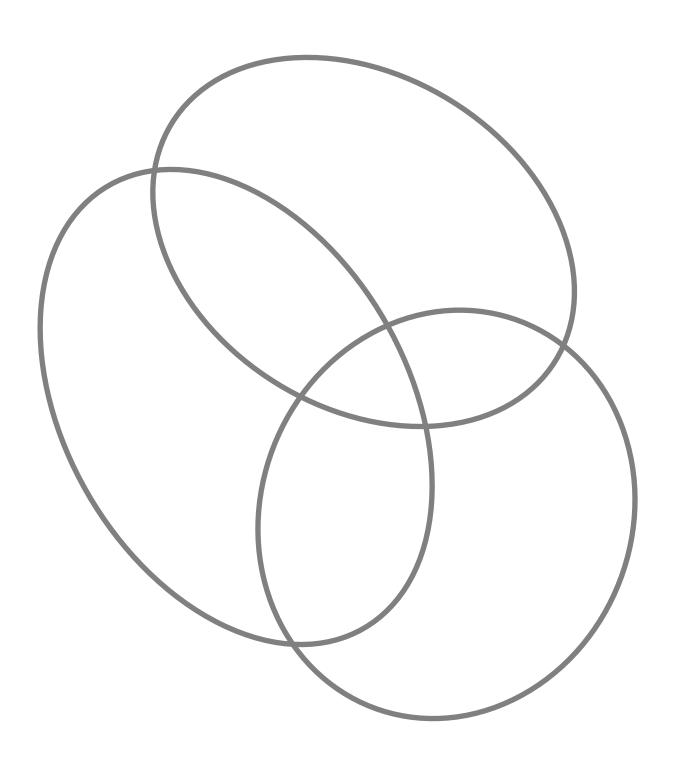
Compare Simple vs Complex Shape

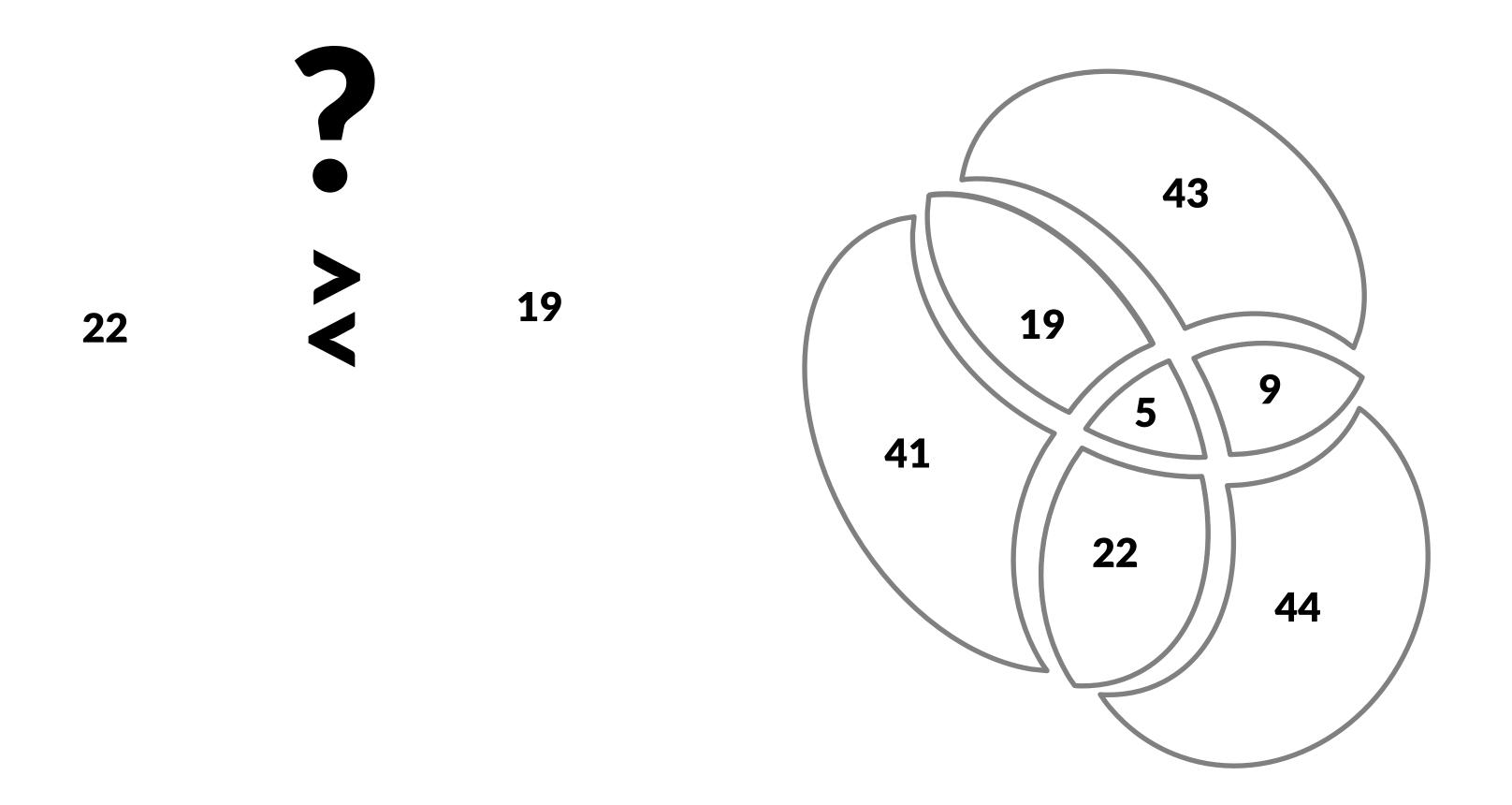
Complex



Simple







Venn-Euler Pros/Cons

Pros

Familiar

Intuitive

Work well for 2-4 sets

Cons

Doesn't work well for more

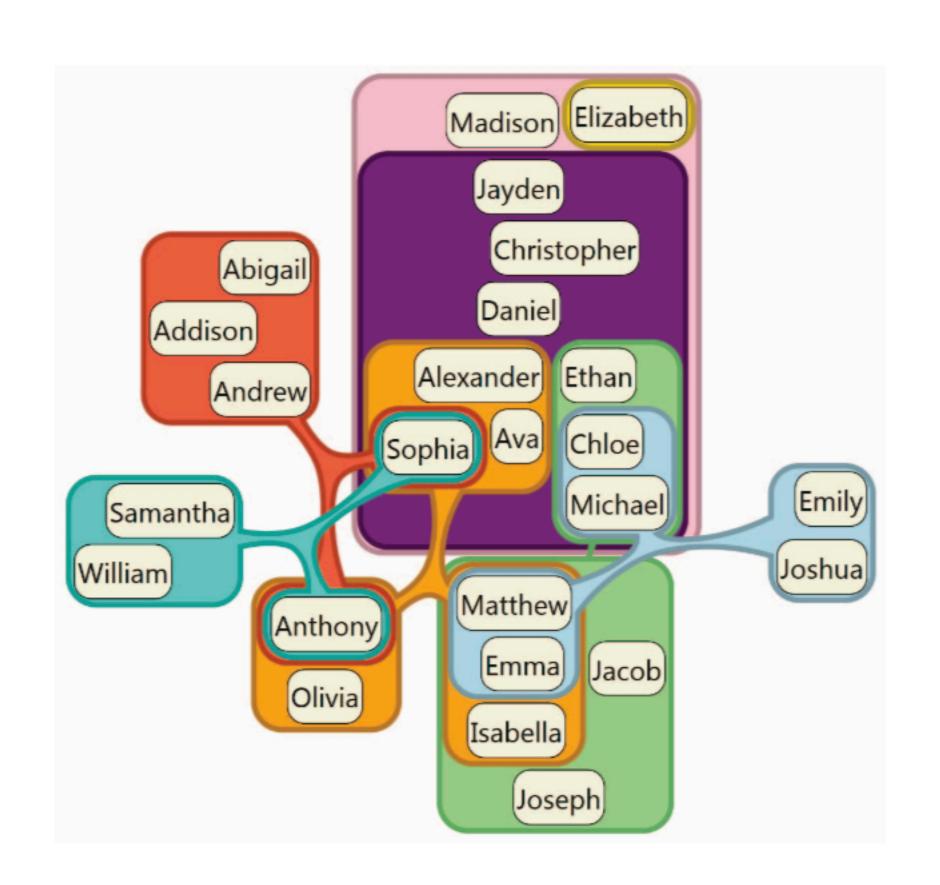
than 4 sets

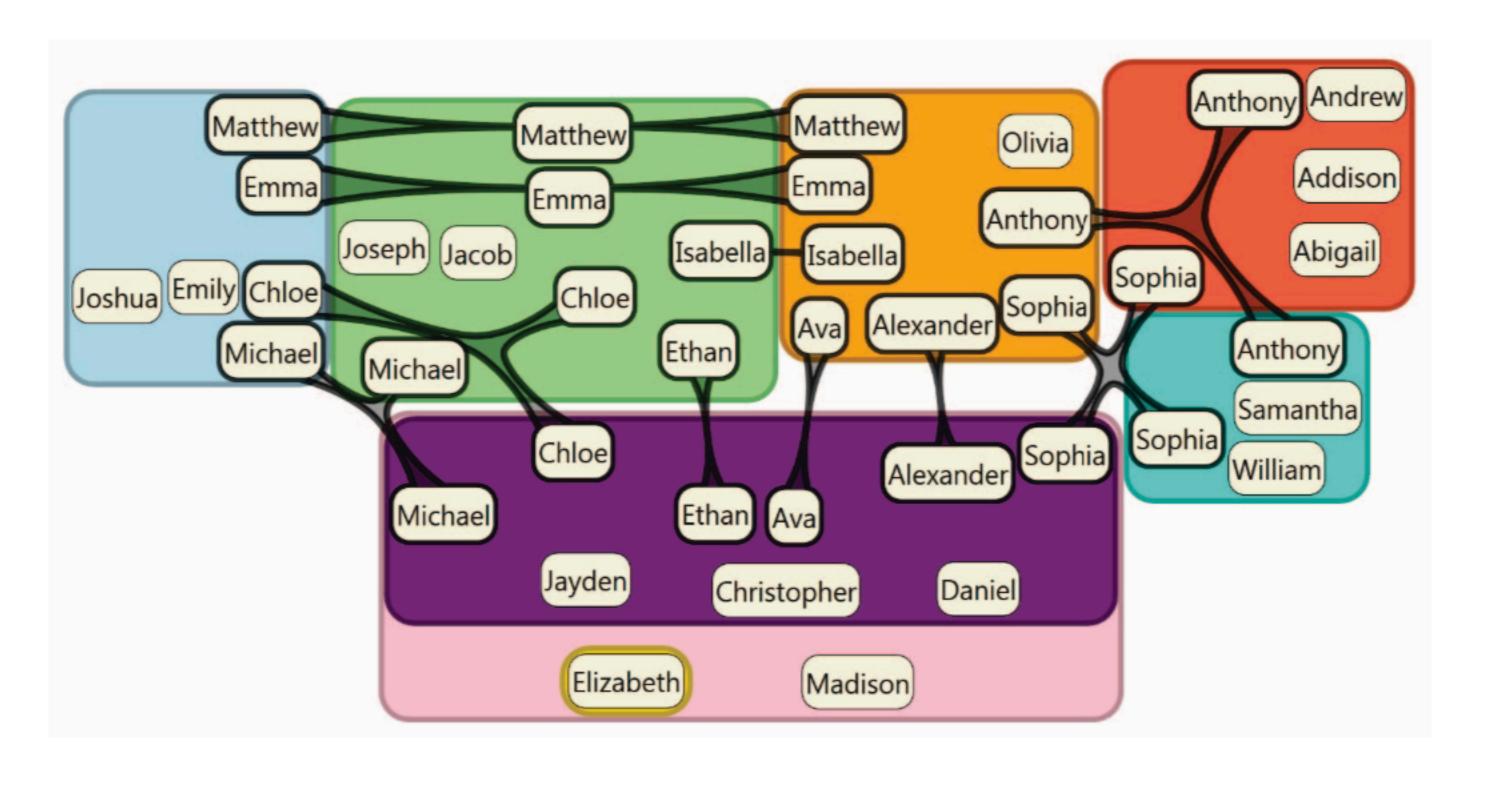
Area proportionality hard to do

Not well suited to show

attributes

Relationships for specific Items





No Duplicate Nodes Complex Shapes Notice the Nesting

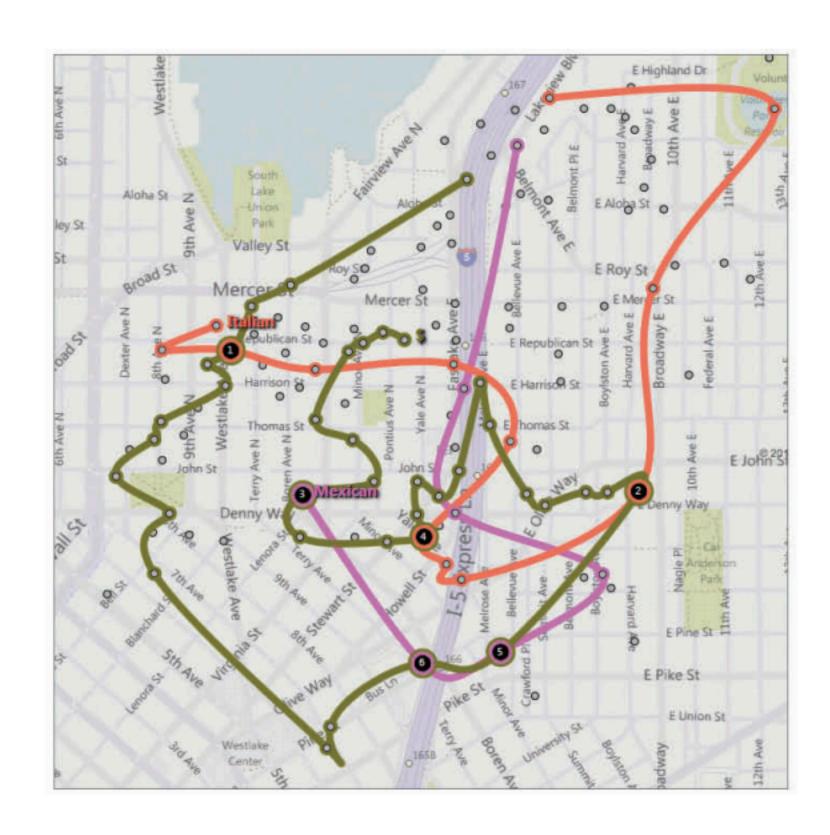
Duplicate Nodes
Simple Shapes

Sets on top of a fixed layout



Sets on top of a fixed layout

LineSets



Kelp Diagrams

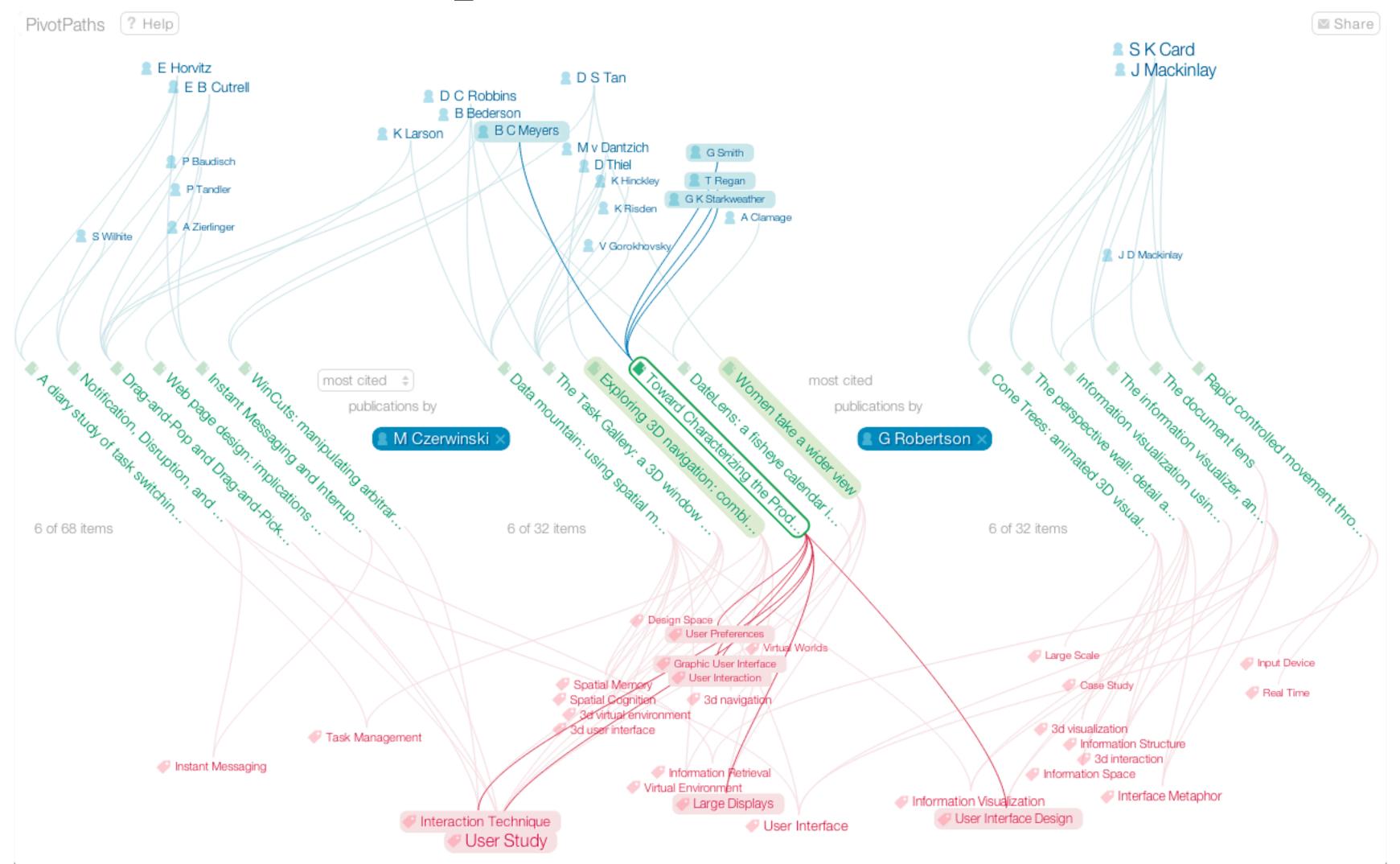


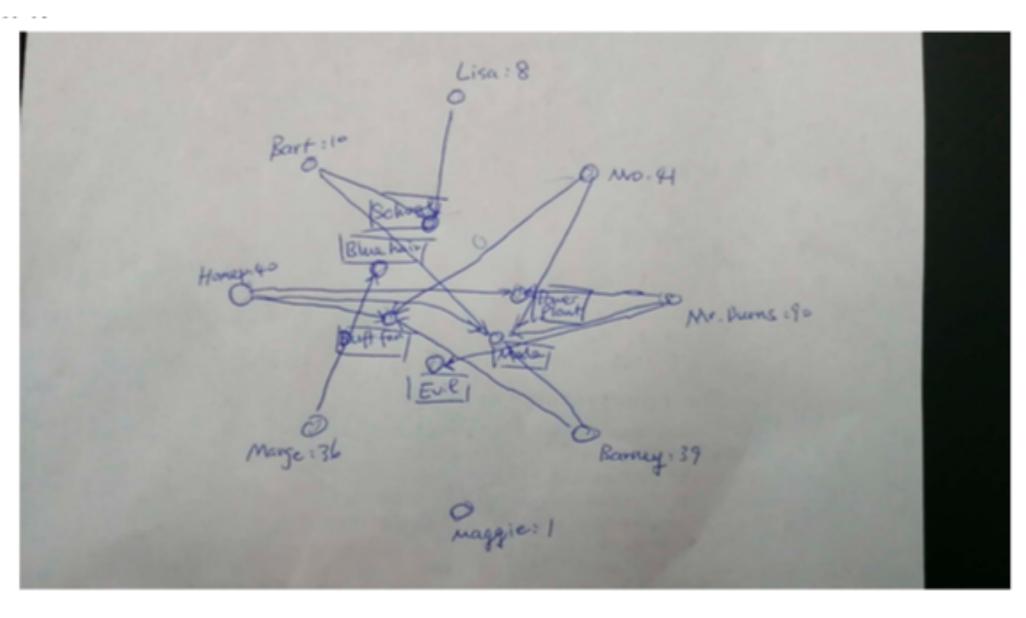
[Alper 2011] [Dinkla 2012]

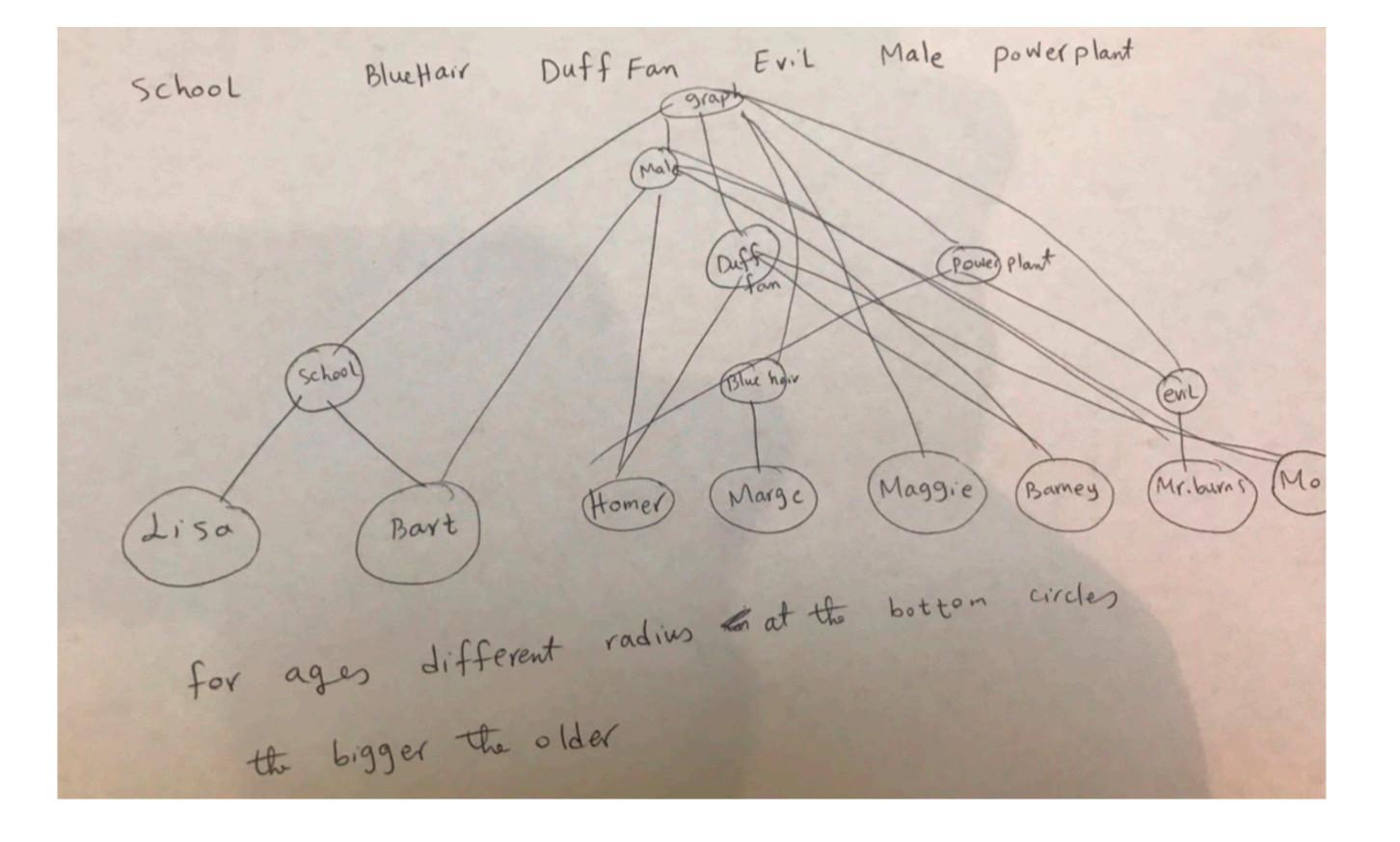
Node-Link Techniques

Treat sets as nodes

Connect to elements that are in set







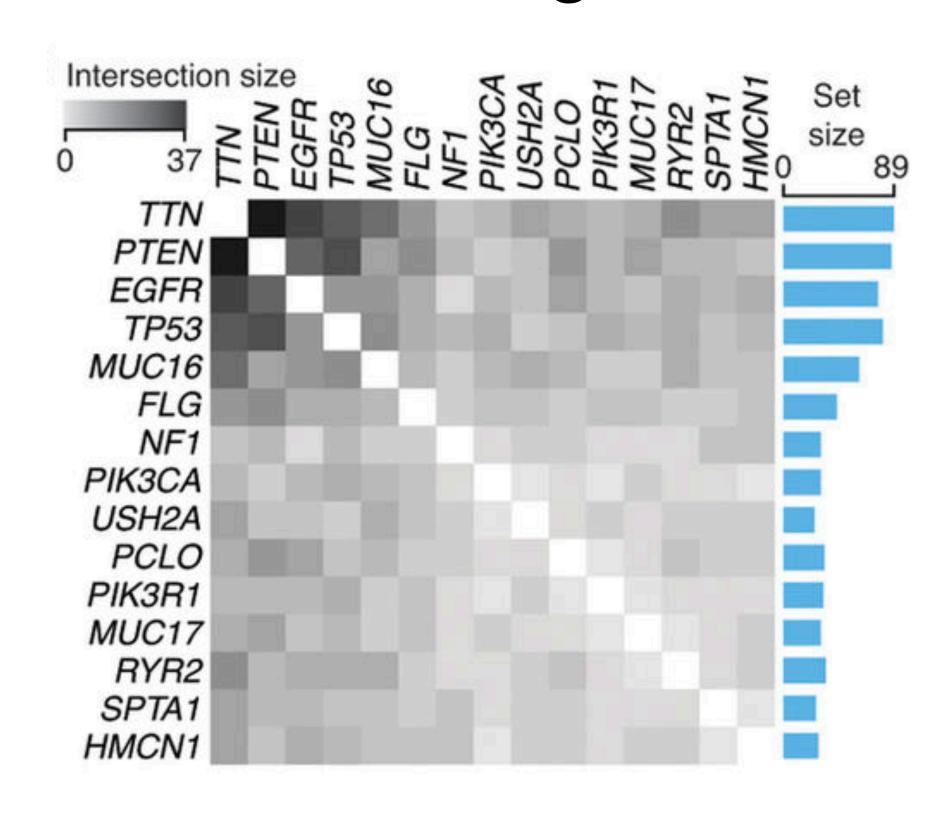
Showing Pairwise Overlap

Doesn't show higher-order overlaps

Very scalable

Can't show attributes

Co-Mutations of genes

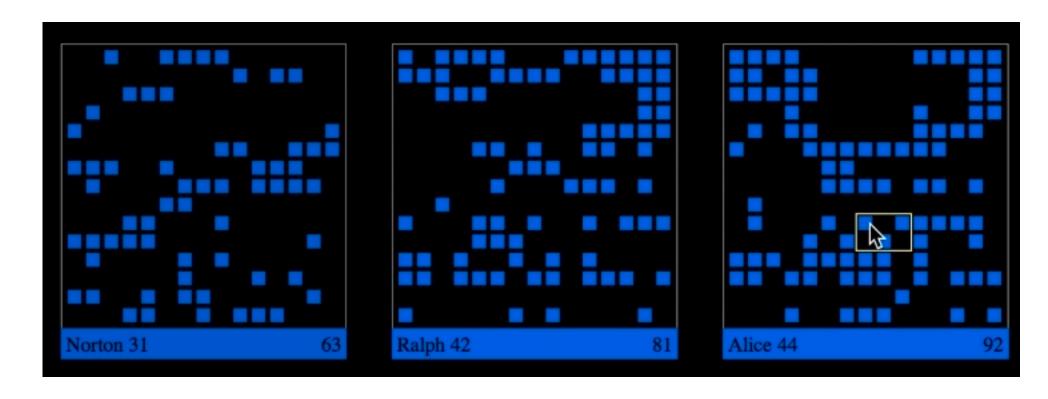


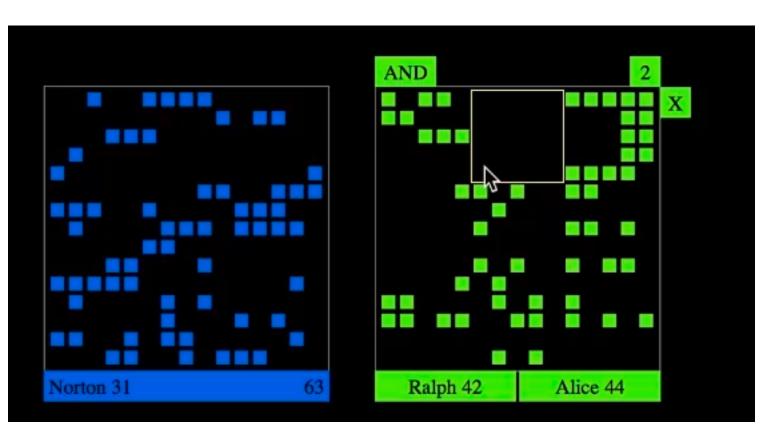
Set Matrices: OnSet

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

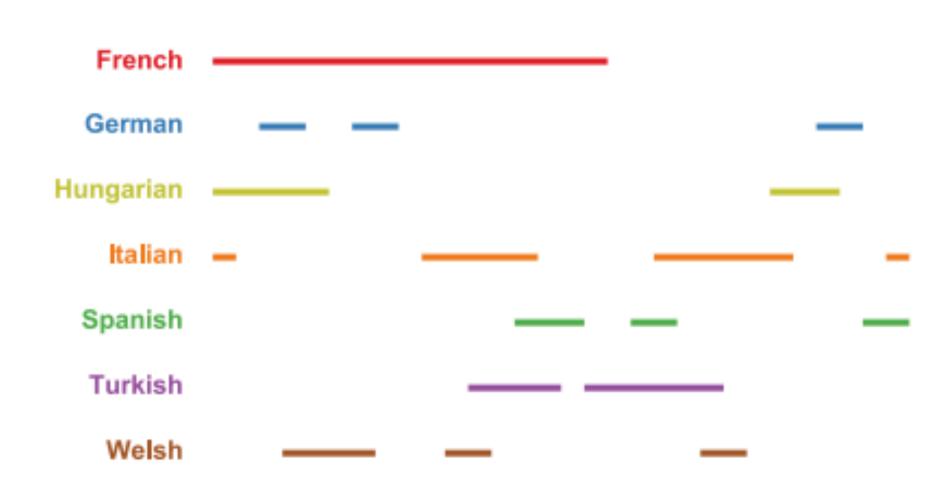


Fig. 1. Visualizing sets: linear diagrams.

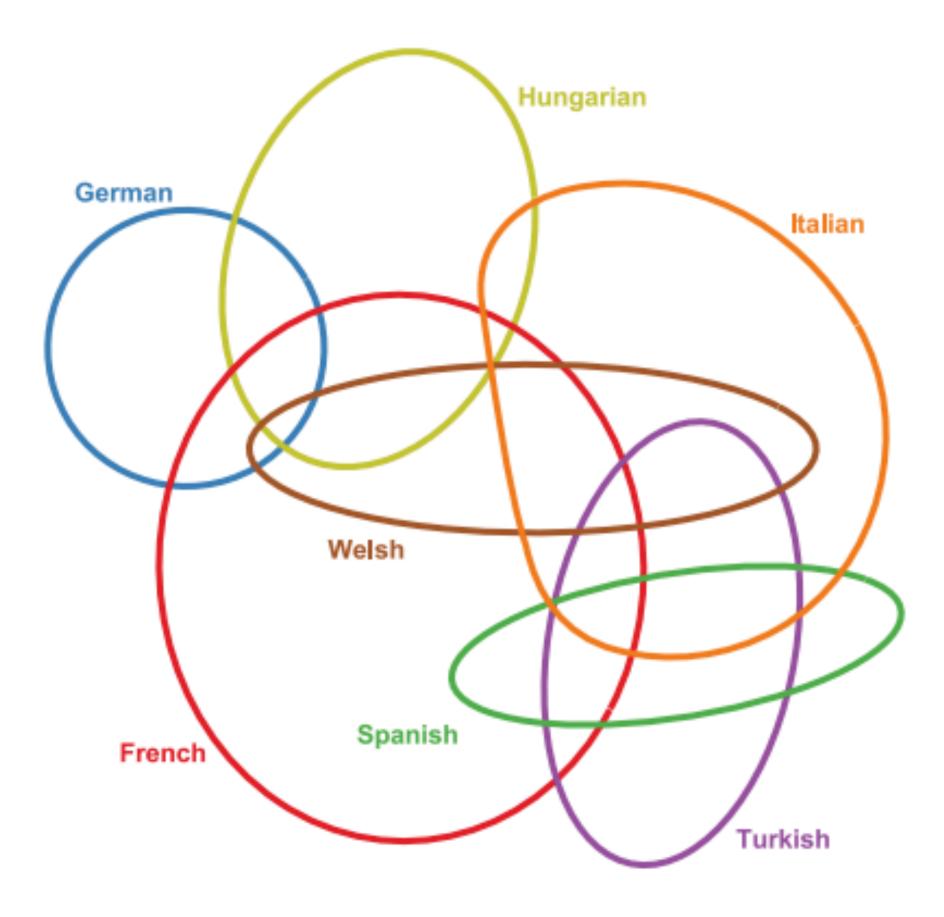
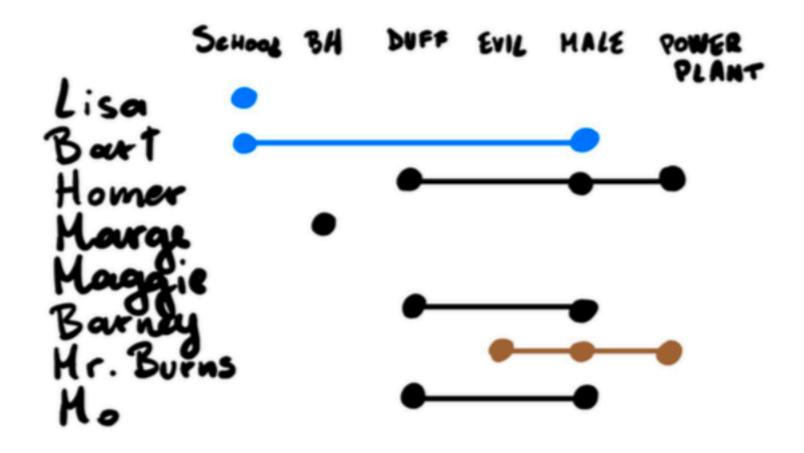
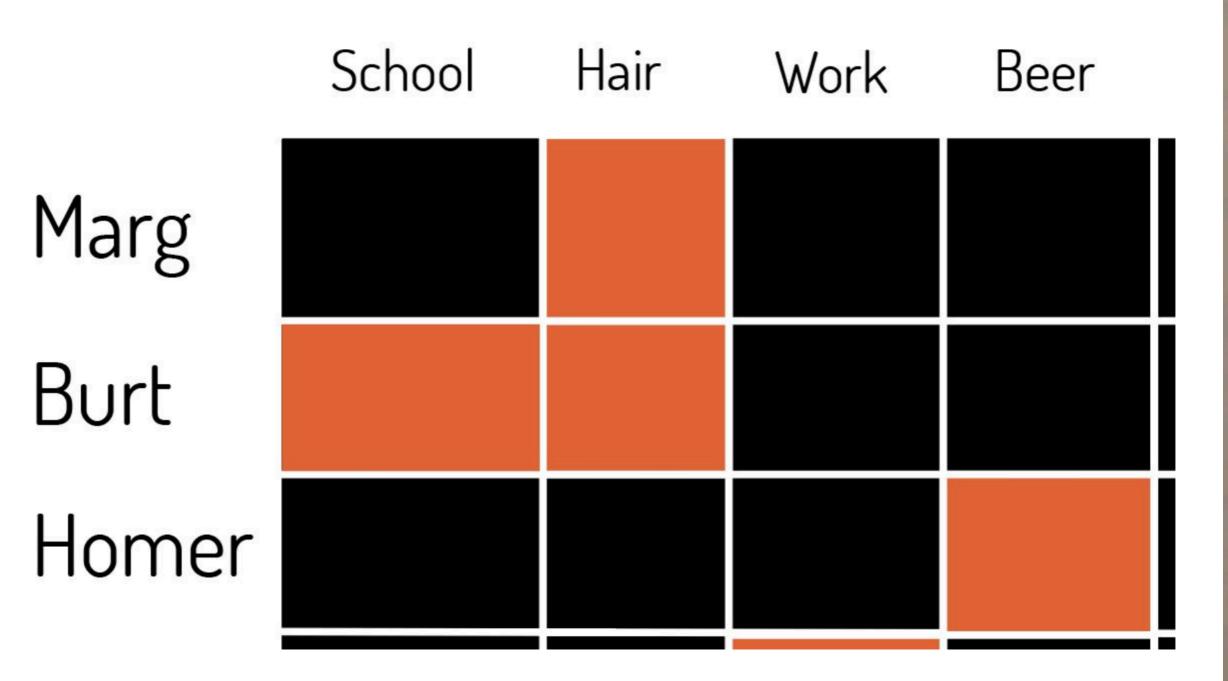


Fig. 2. Visualizing sets: Euler diagrams.





| | 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 | |

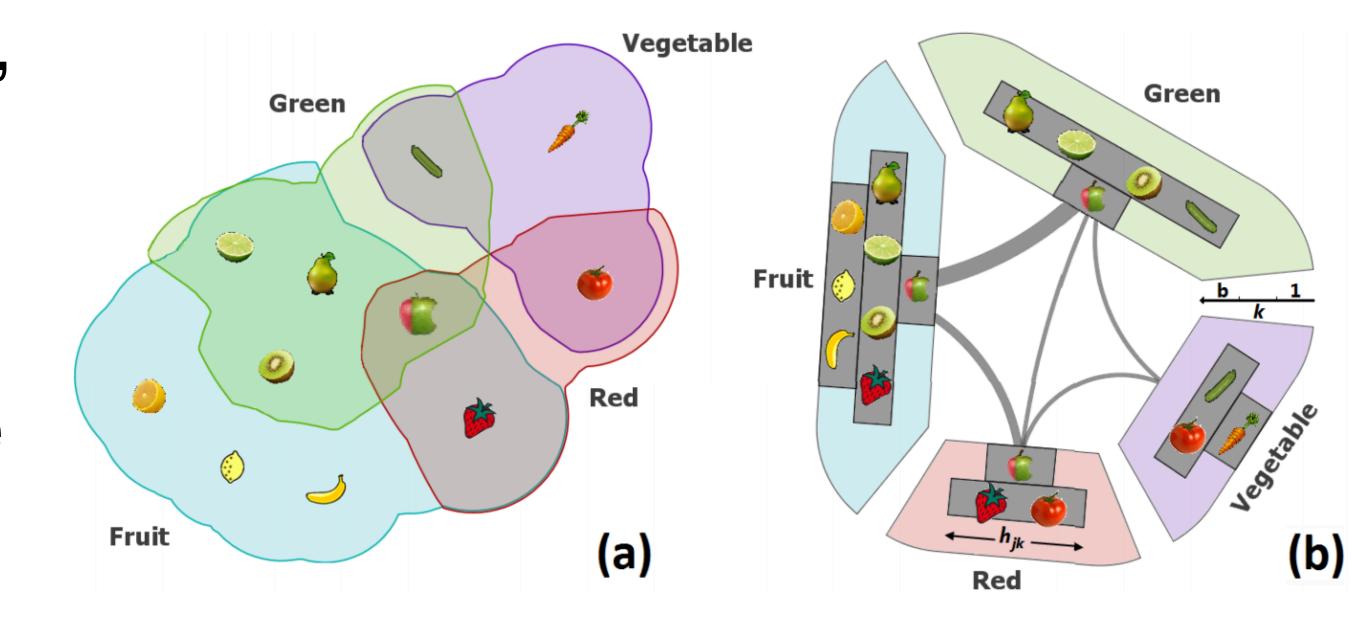
Radial Sets

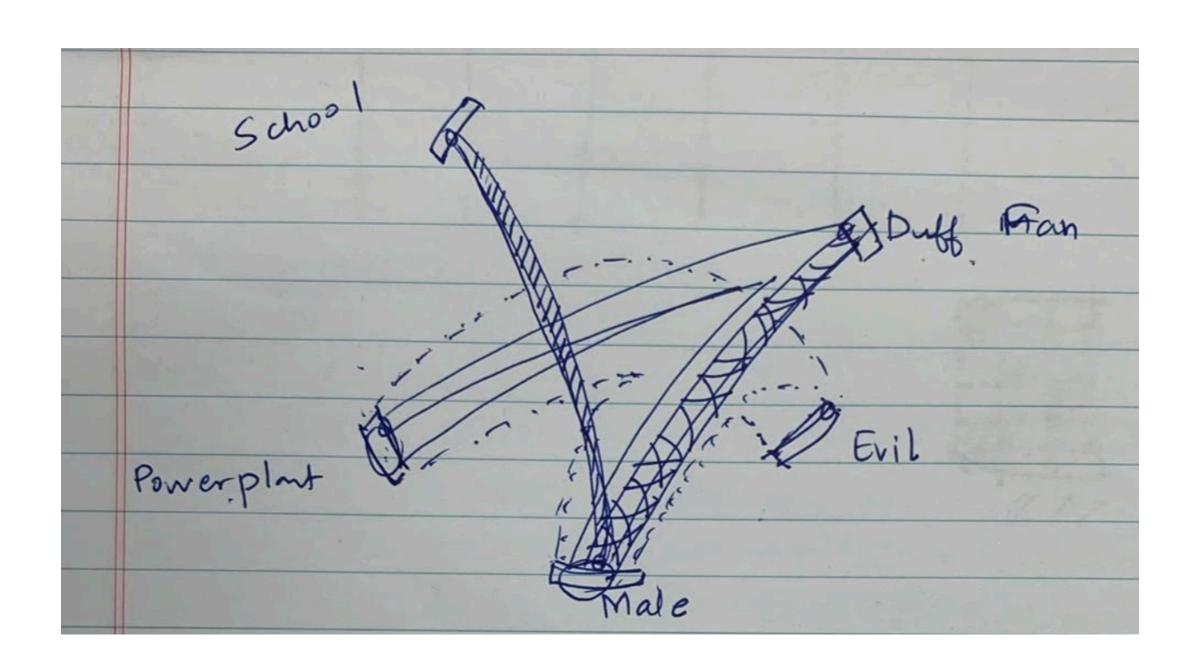
Sets are segments on a "circle" Relationships are encoded as

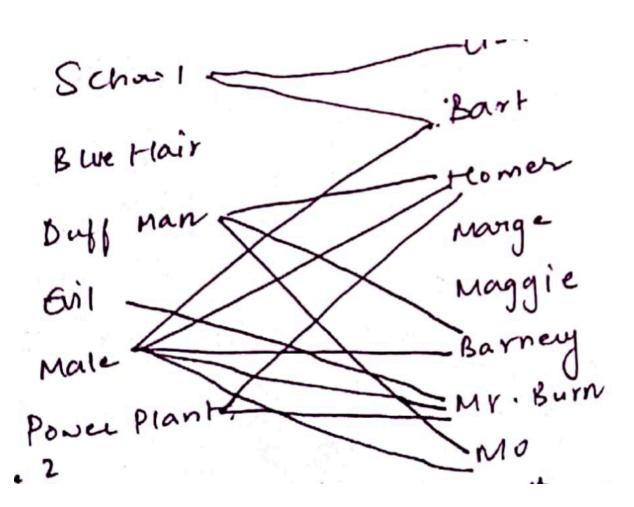
ribbons

Size of segments encodes size of sets

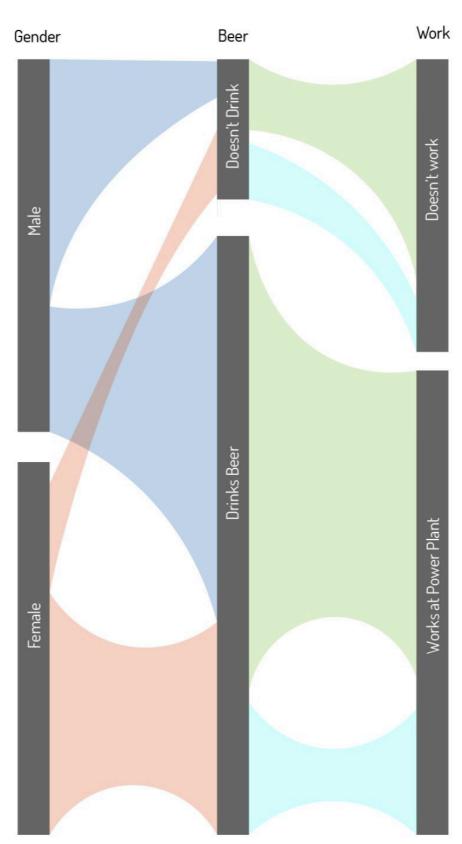
Histograms in segments show degrees







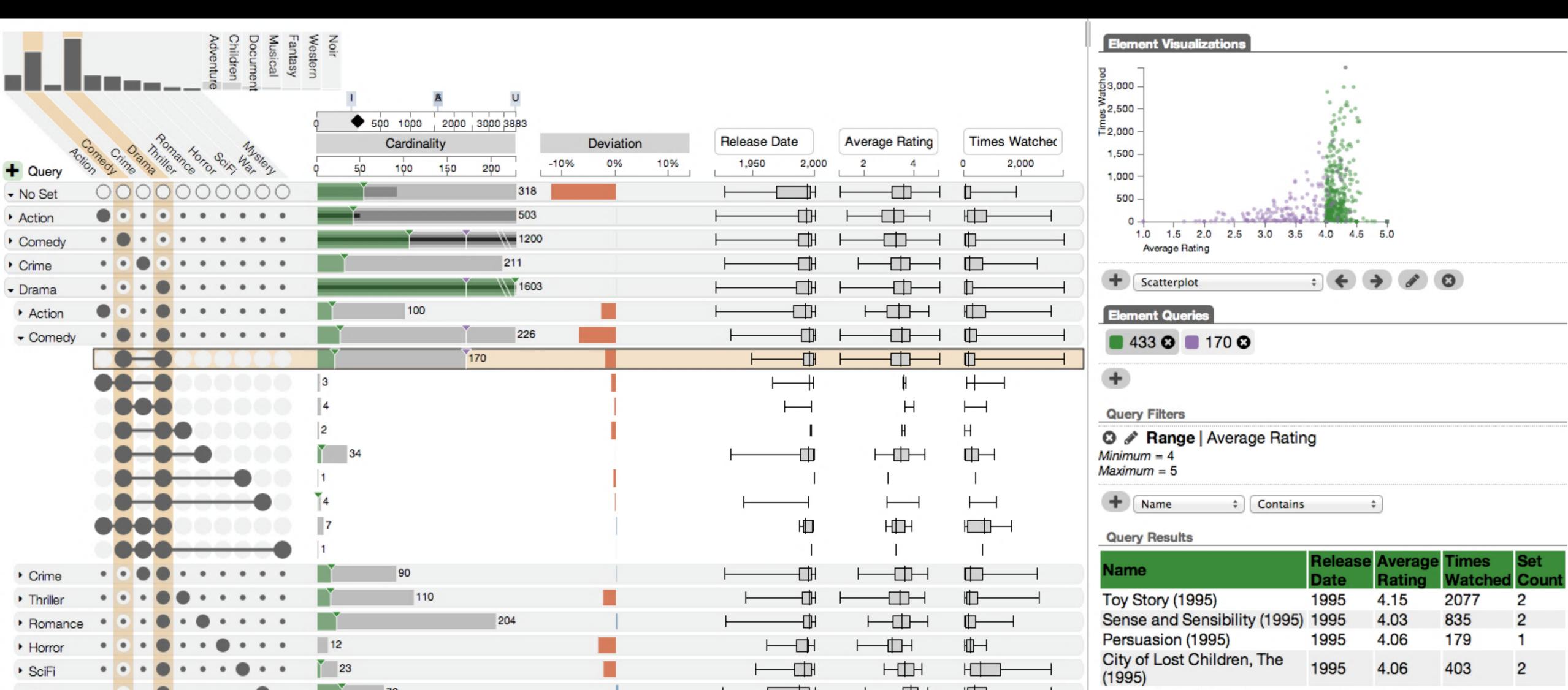




UpSet

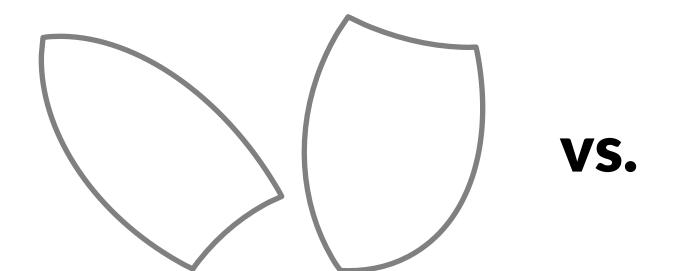
[InfoVis'14]

Visualizing Intersecting Sets

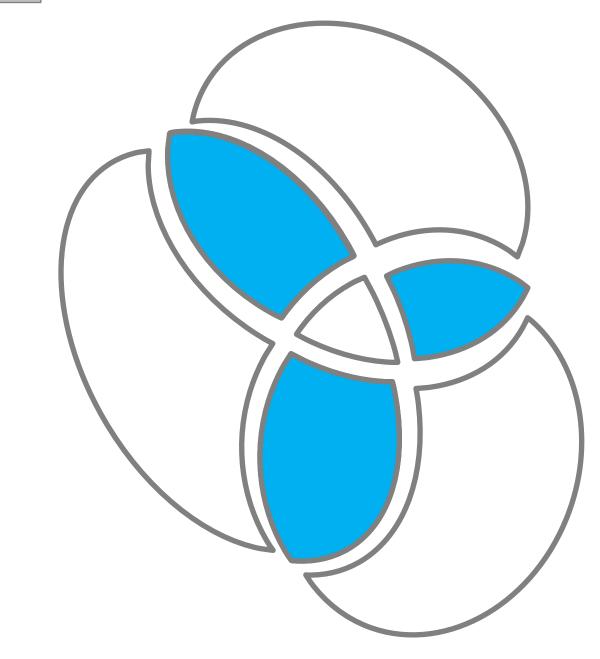


see Vis Croals

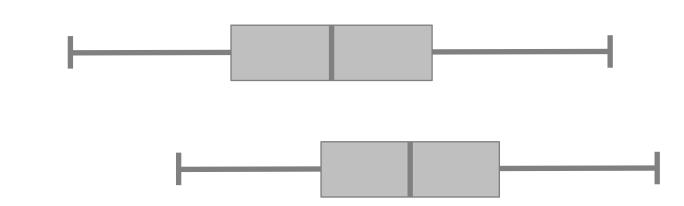
1. Efficient visual encoding



2. Creating complex slices of a dataset



3. Visualize attributes



[Movie Lens Dataset]

Attribute Details

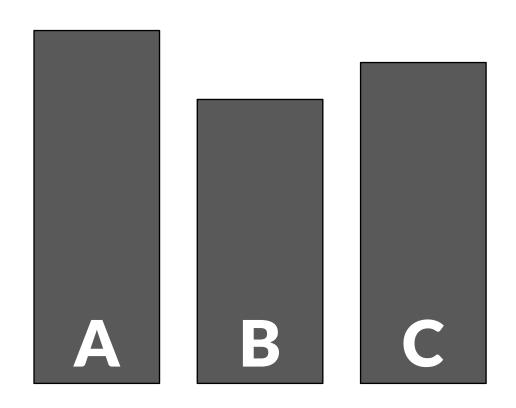


Visualizing Intersections

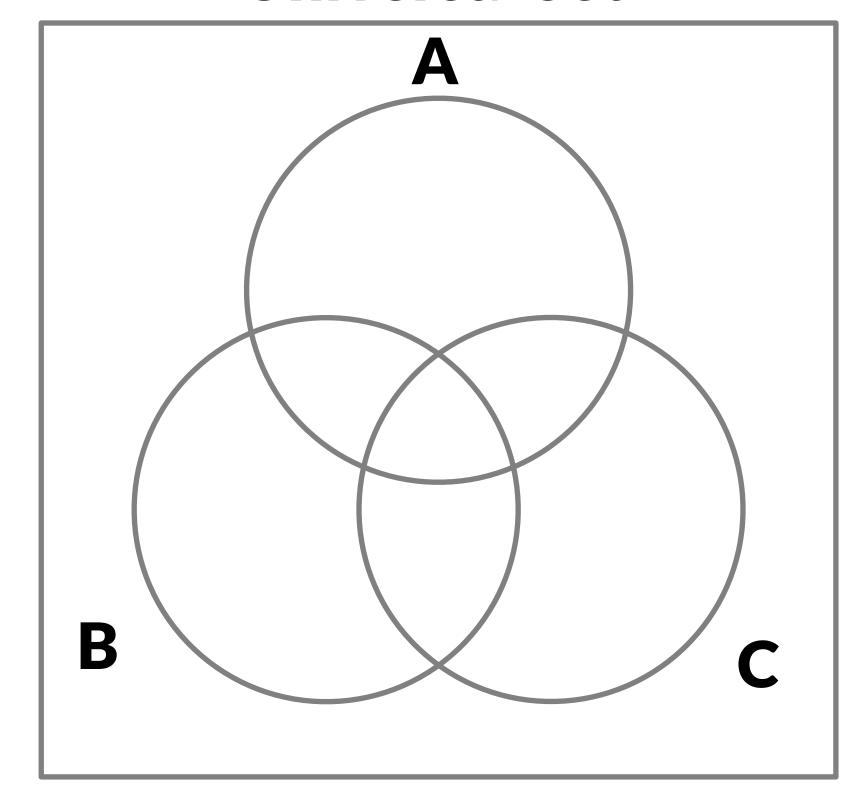
Visualizing Properties

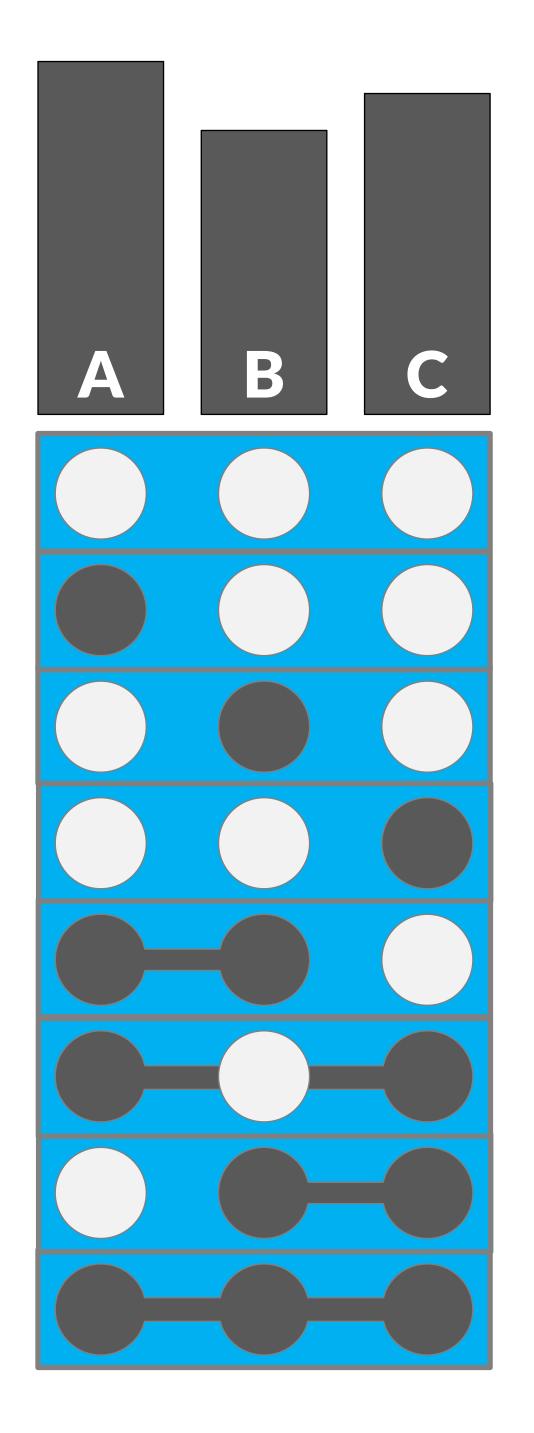
Element List & Queries

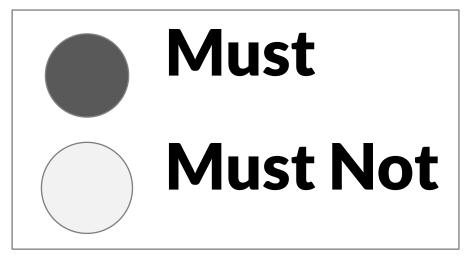
Visualizing



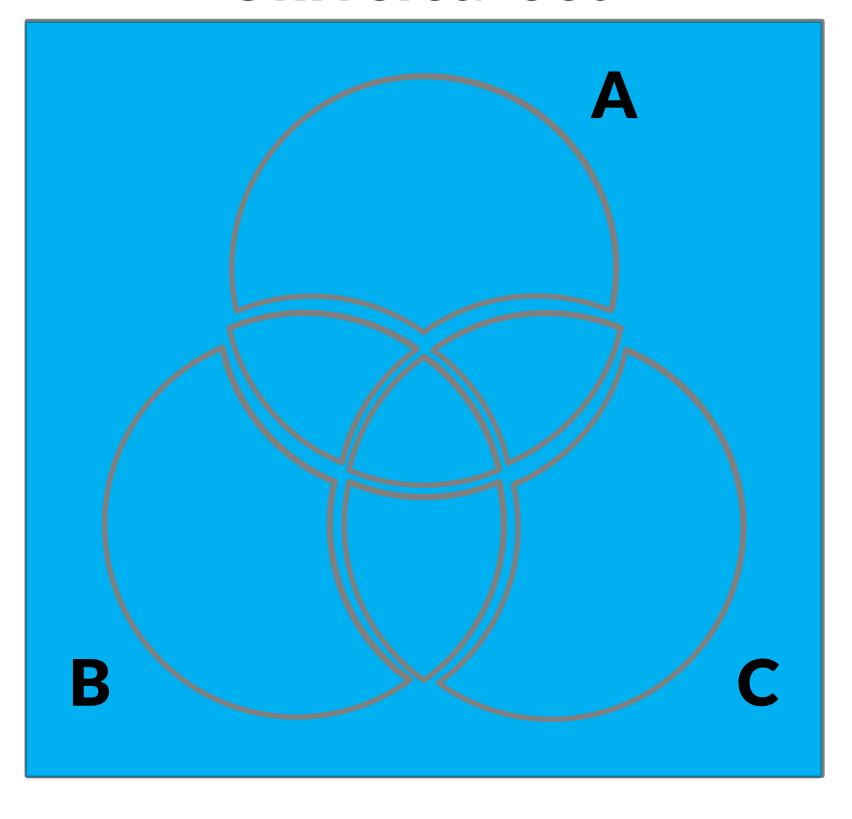
Universal Set

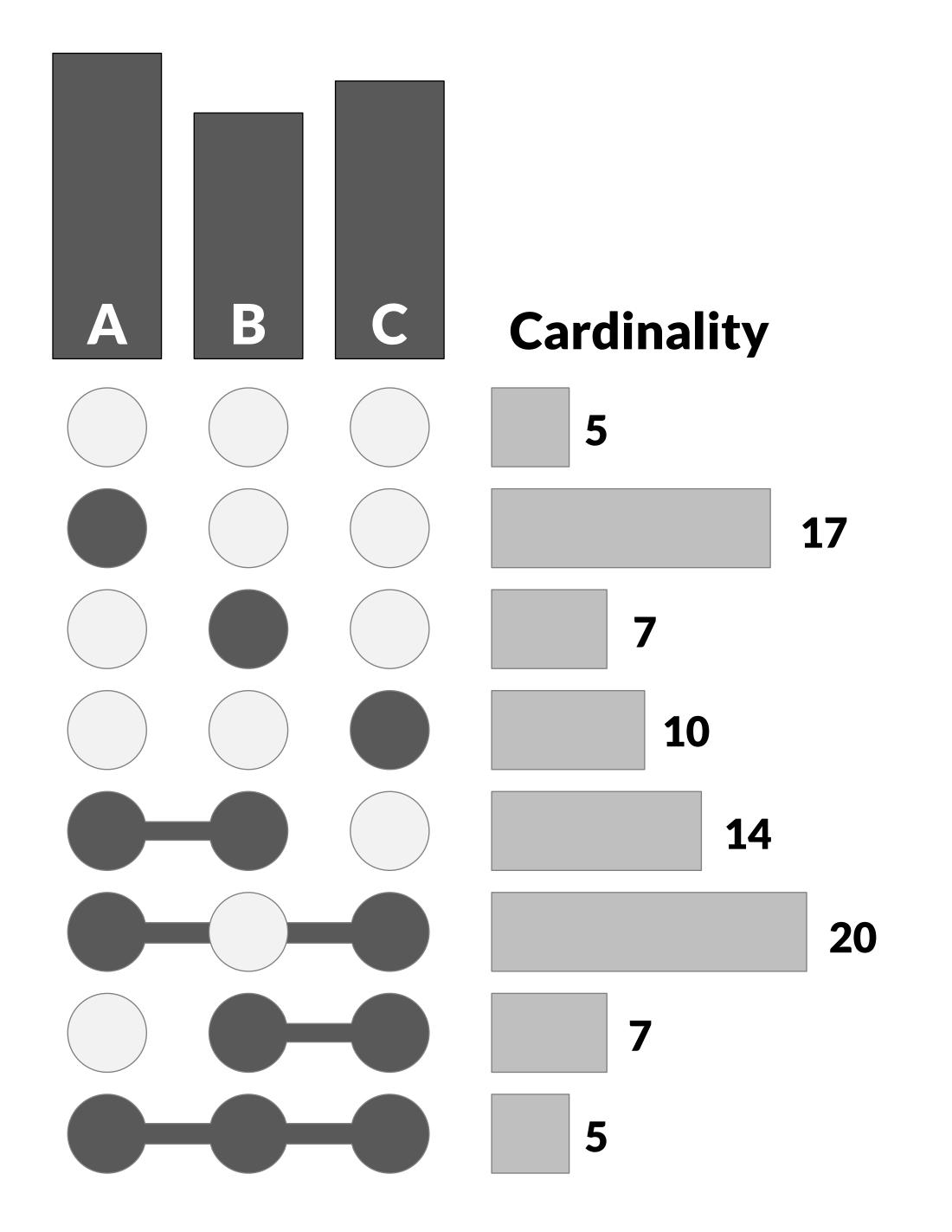


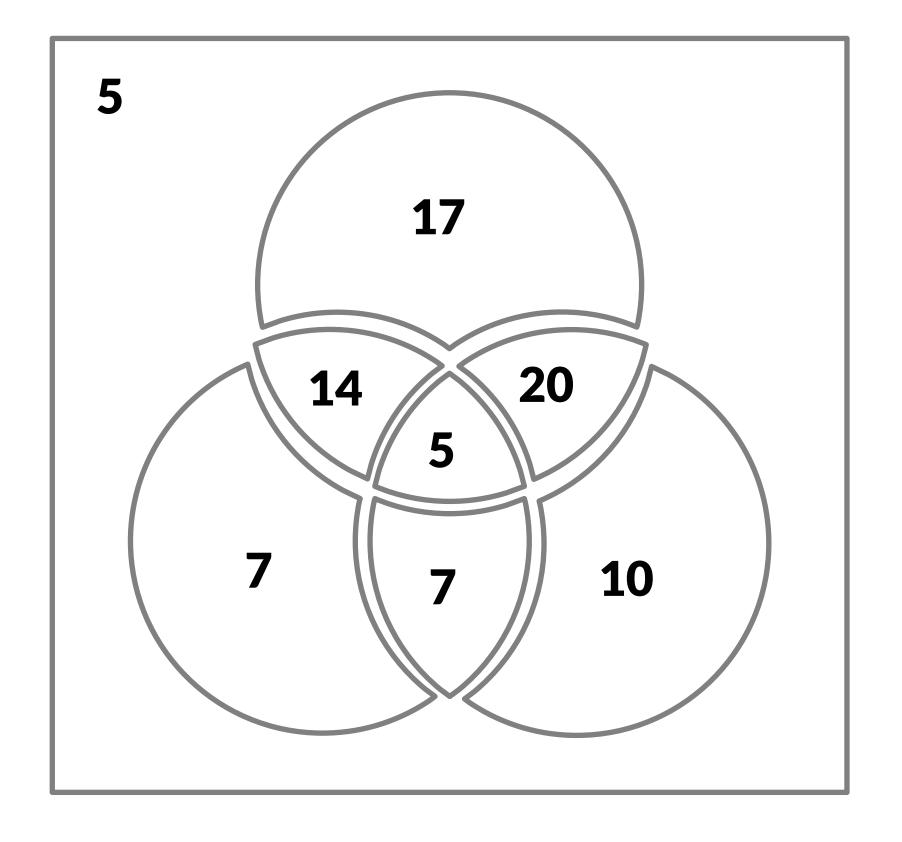




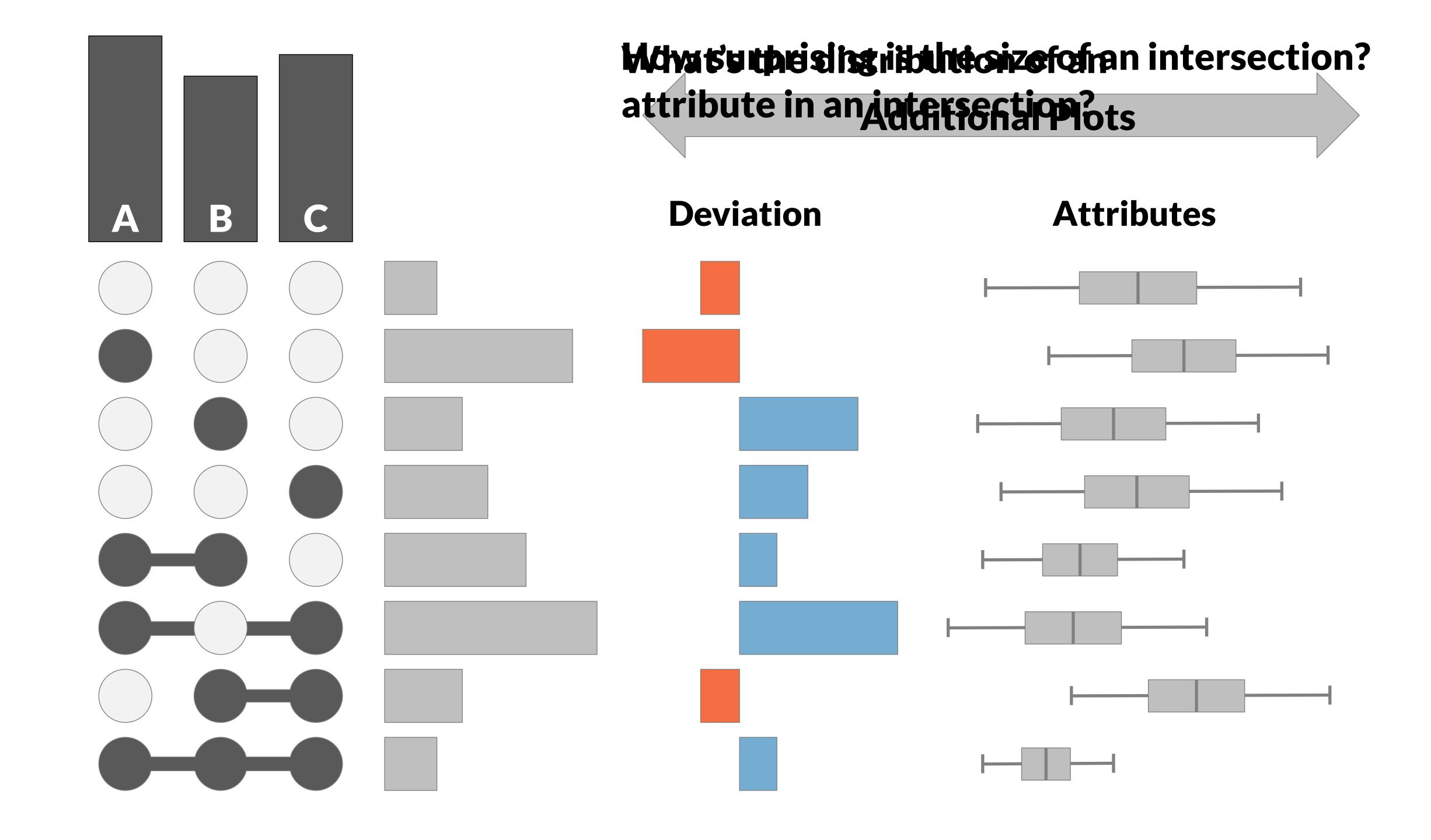
Universal Set

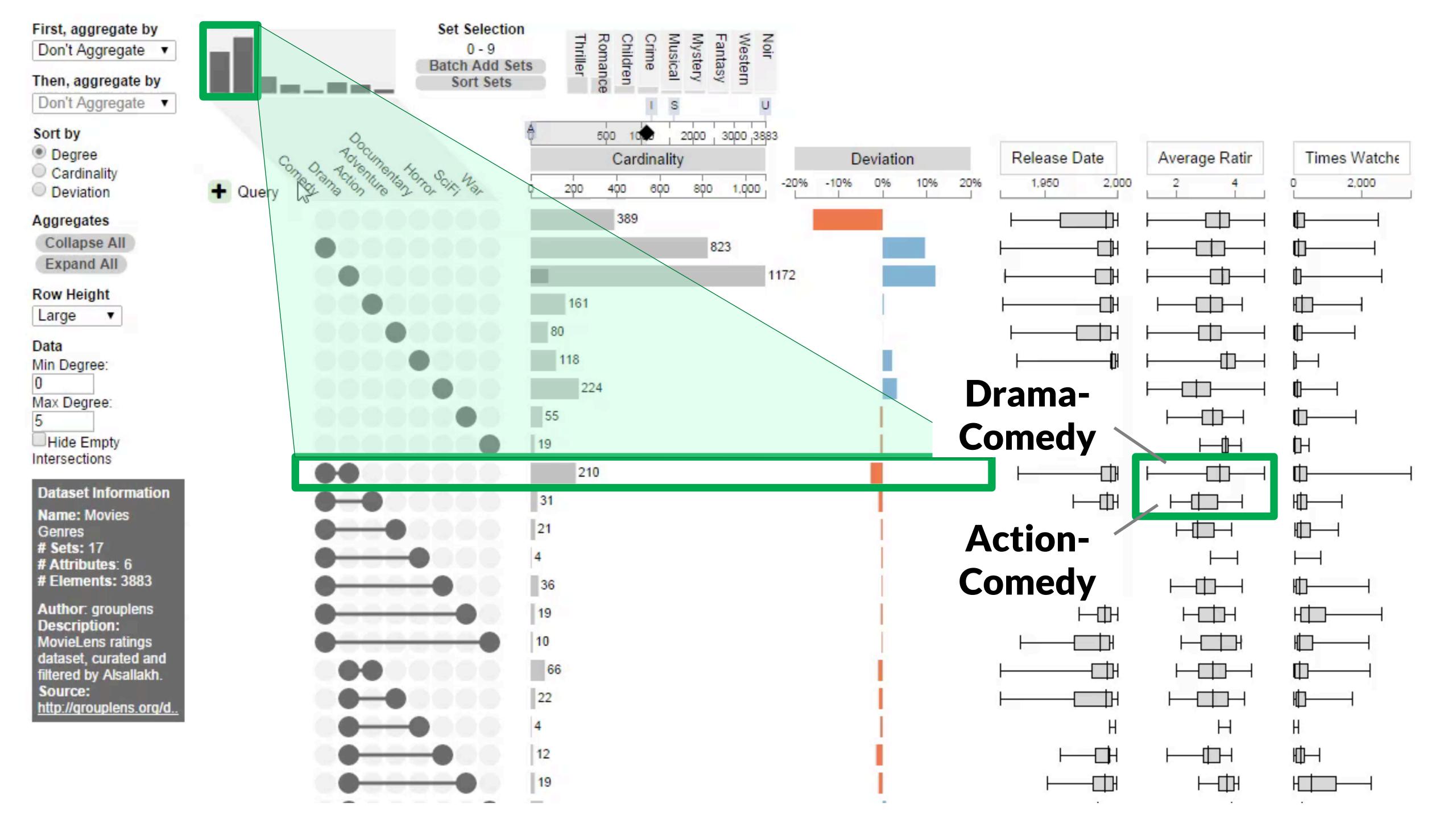


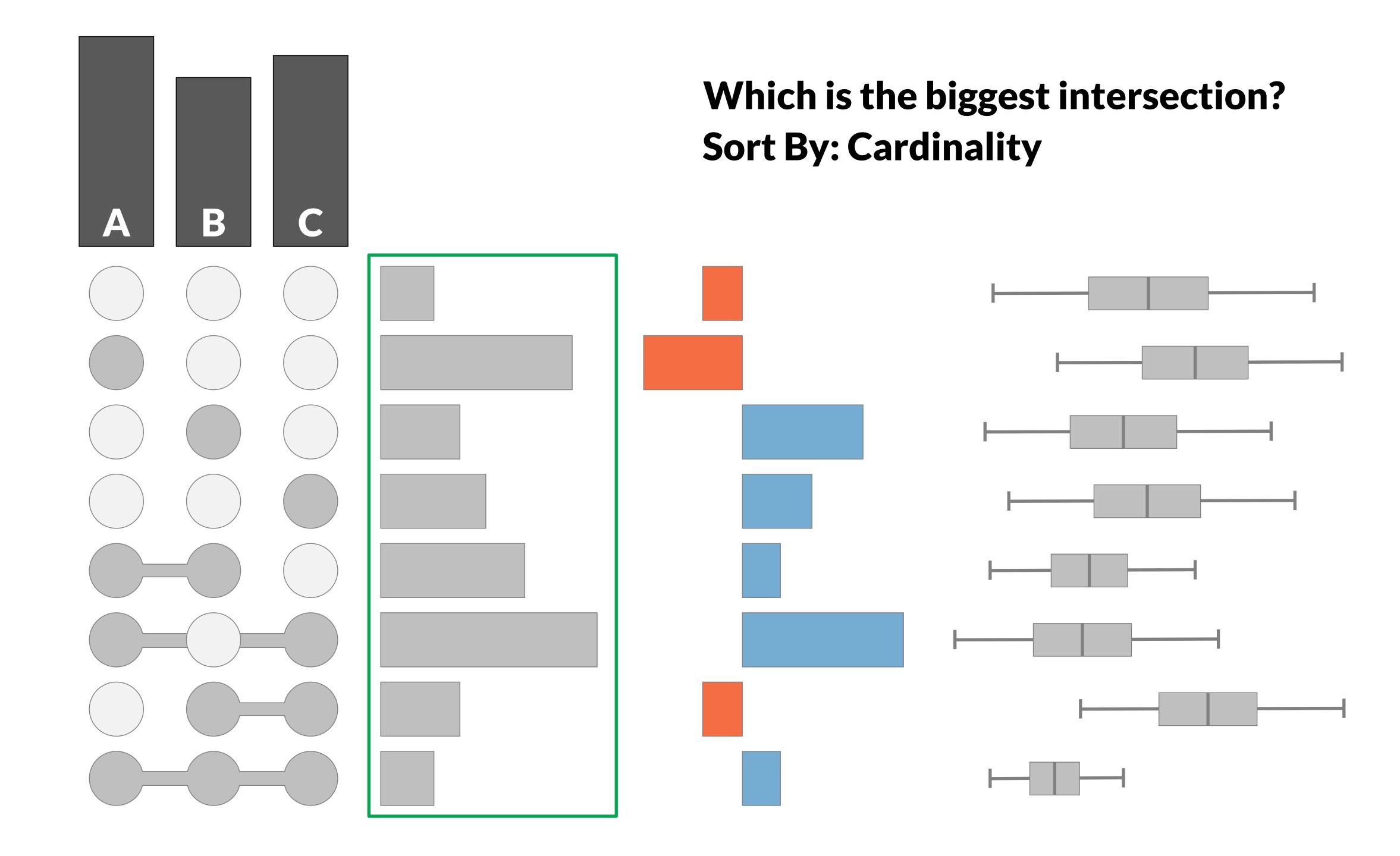


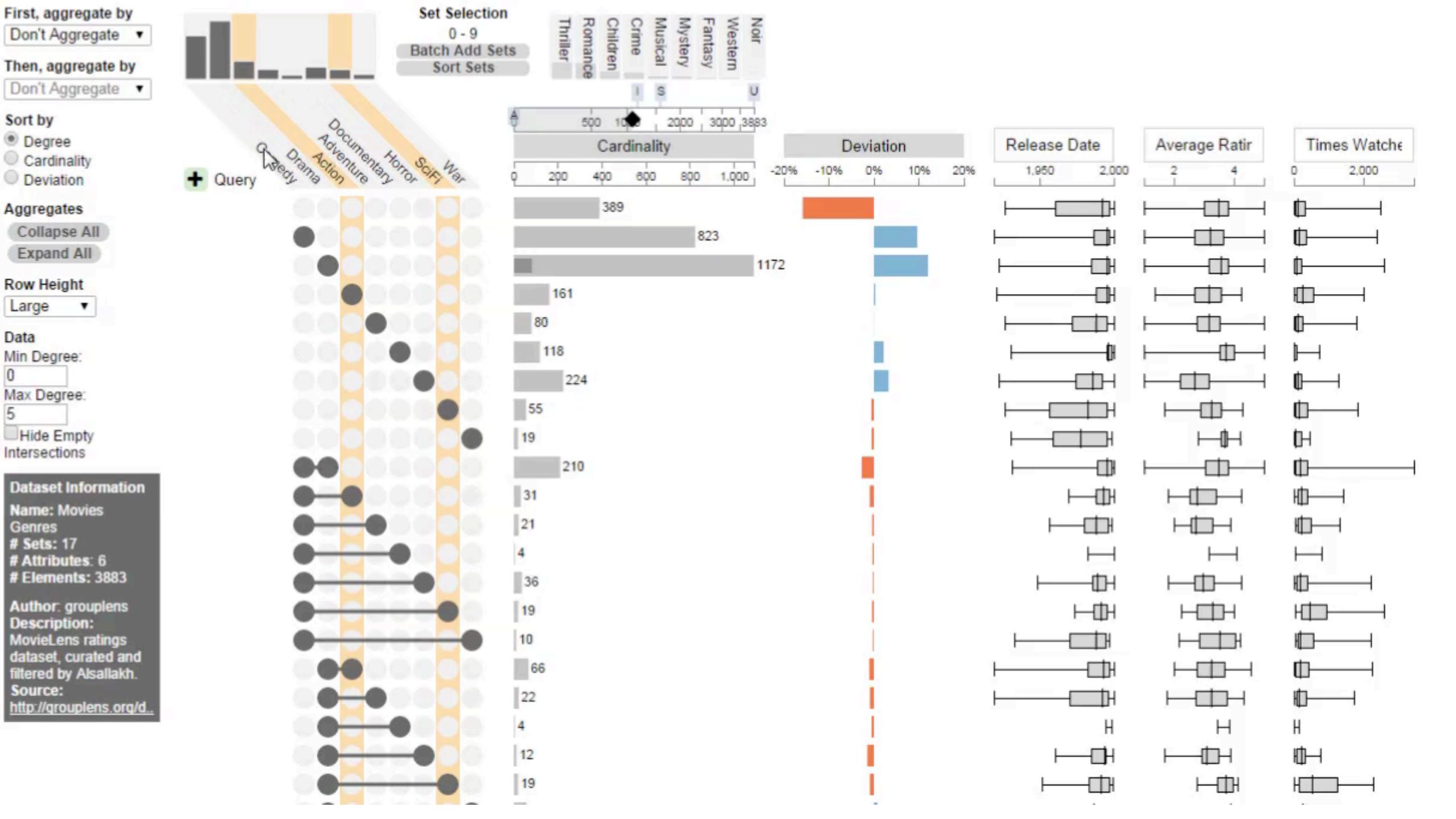


riceling Altributes

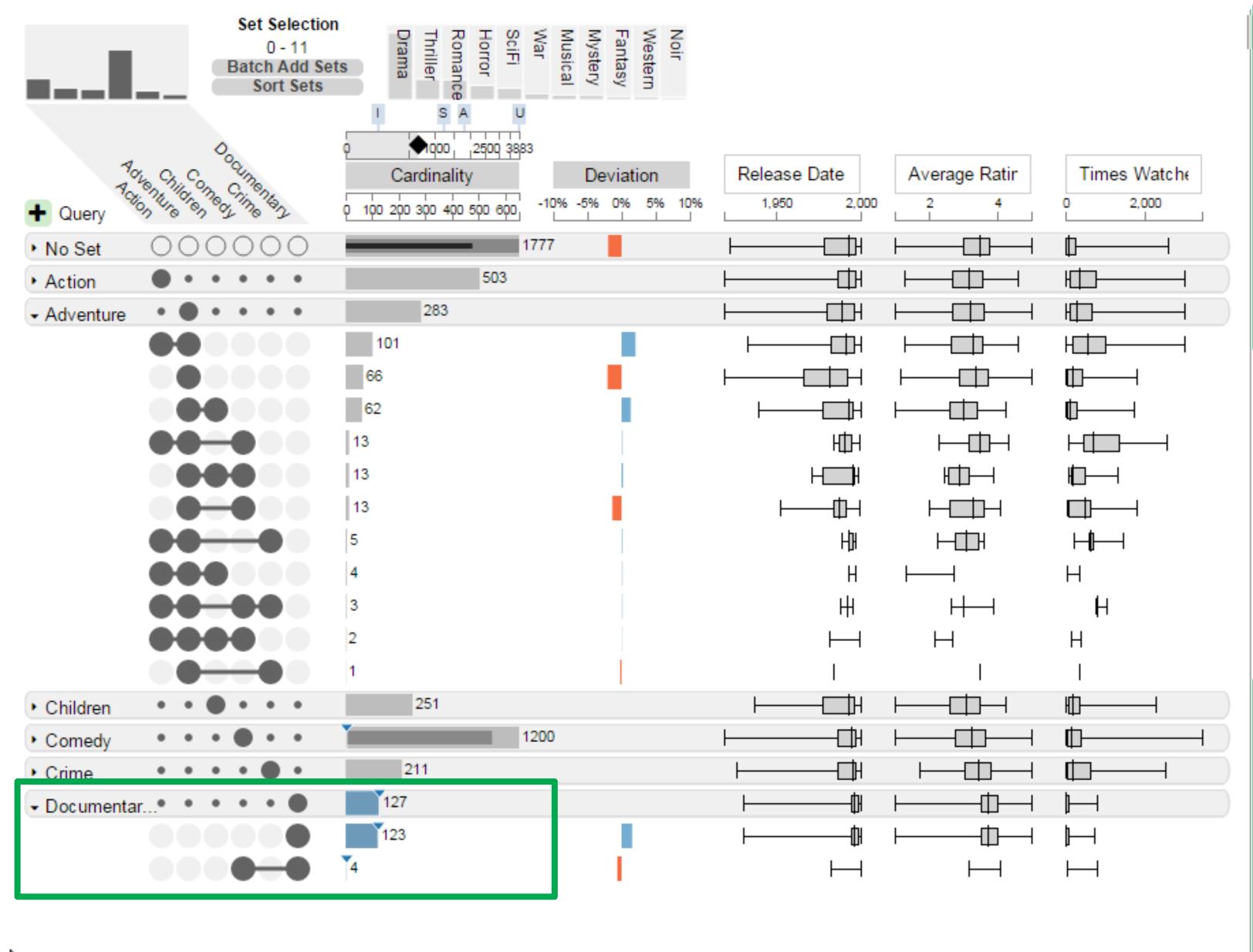


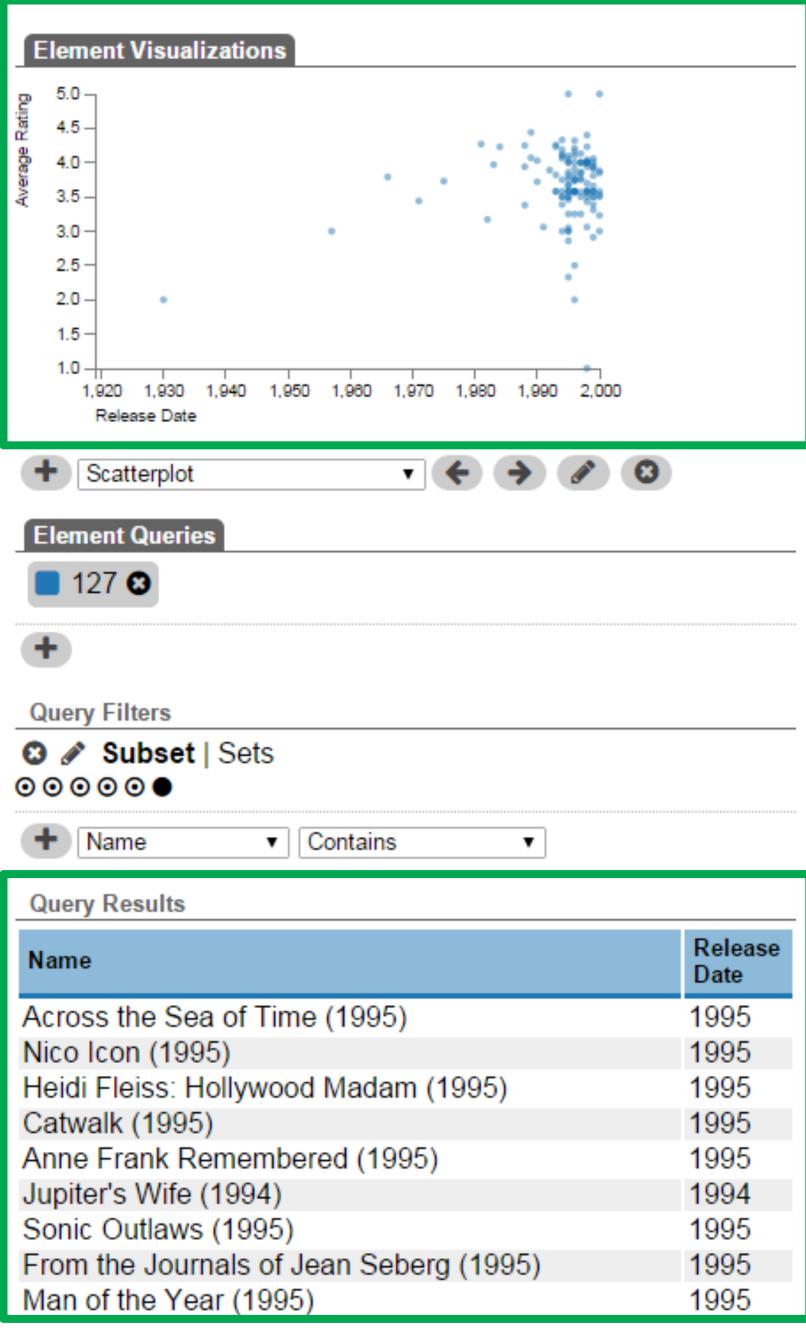






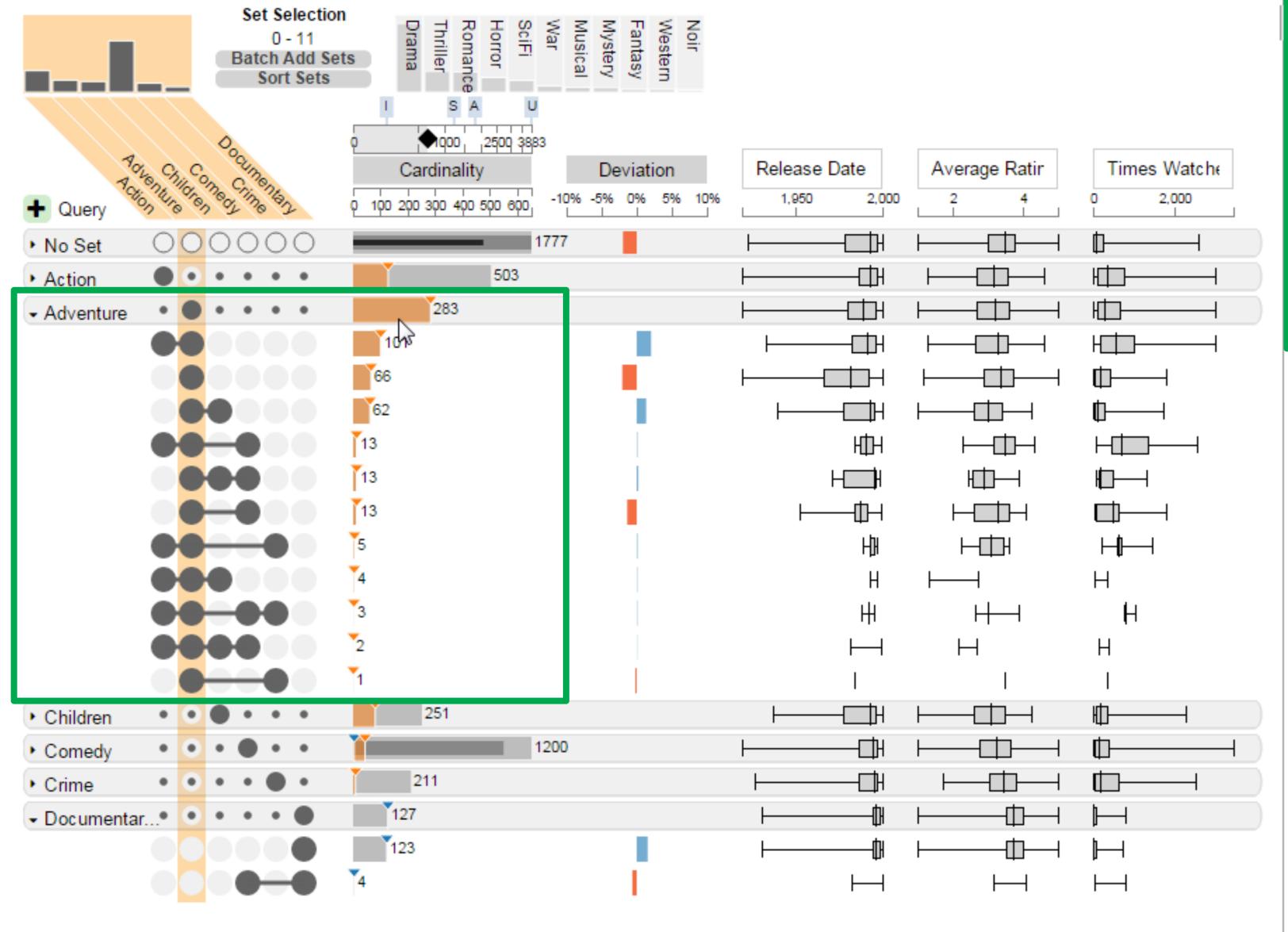
ELEMENTS STA



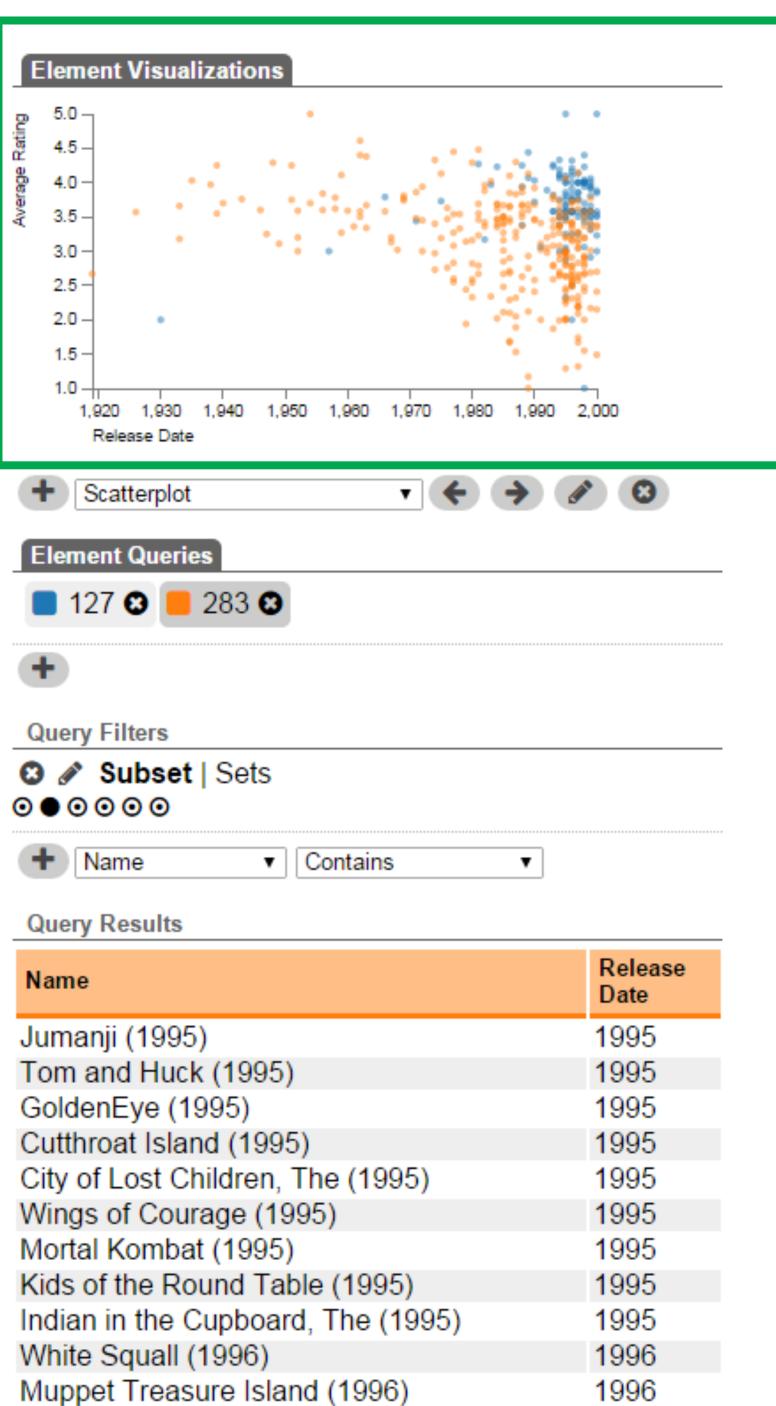




How do documentaries compare to adventure movies?



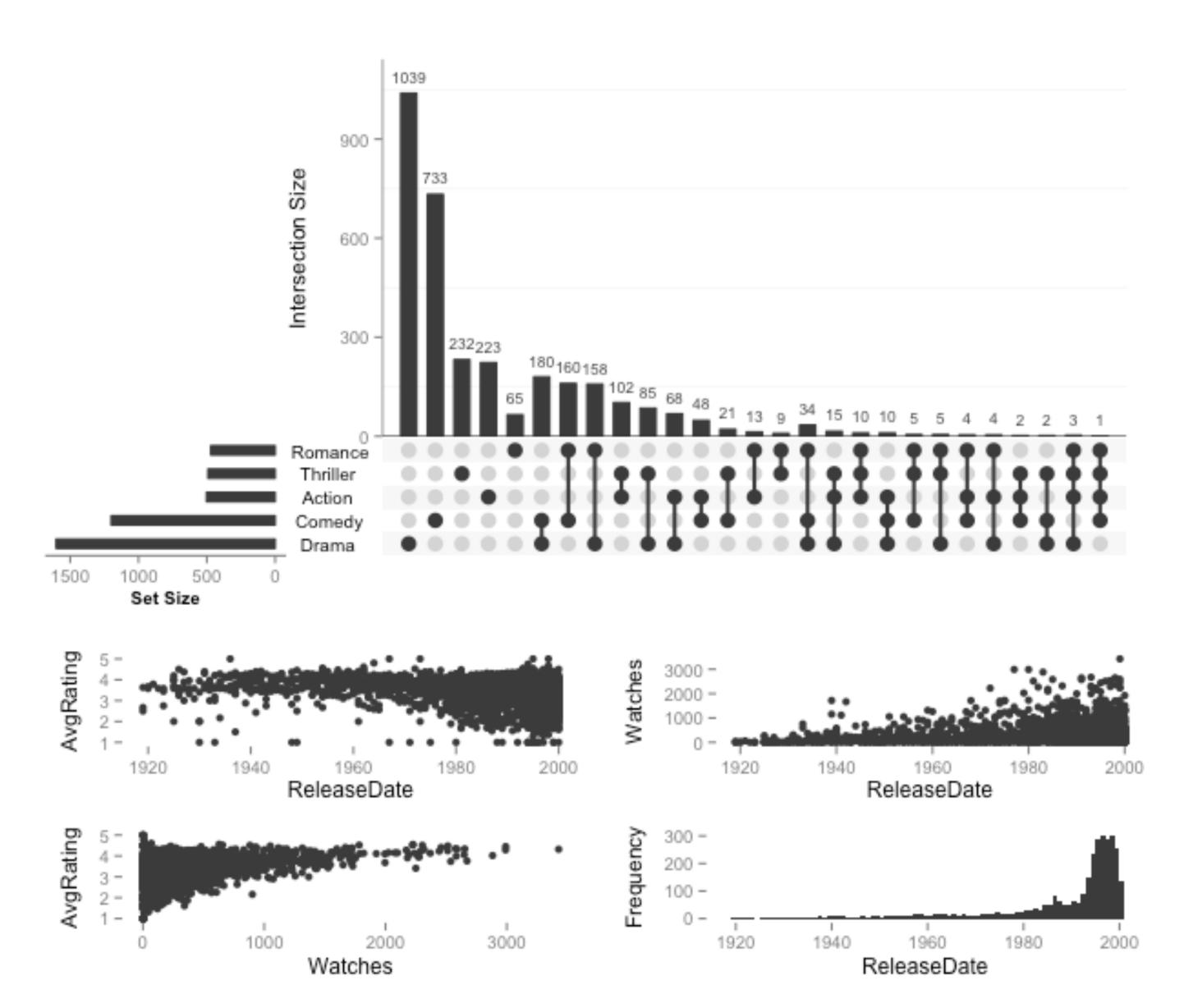
How do documentaries compare to adventure movies?



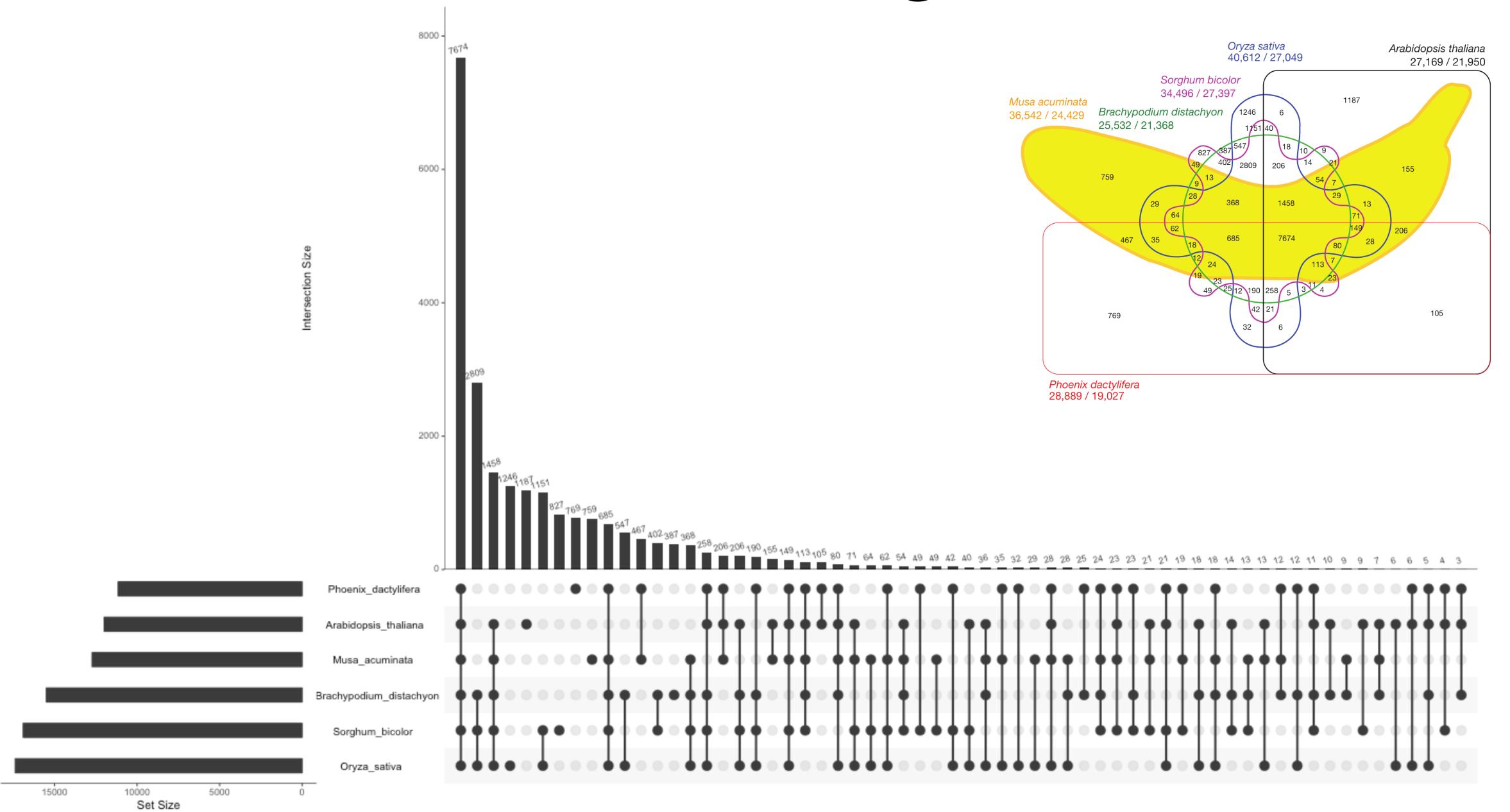
Applications

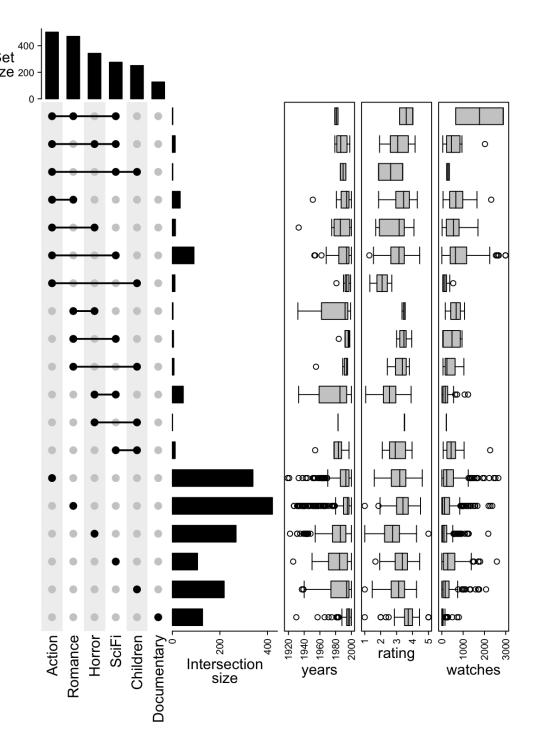
R-Version: UpSetR

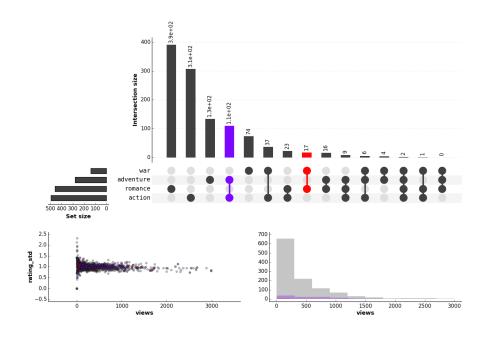
Developed at HMS Some design adaptions

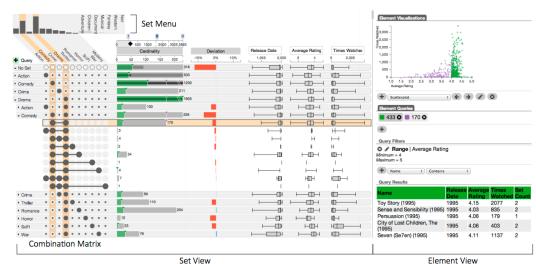


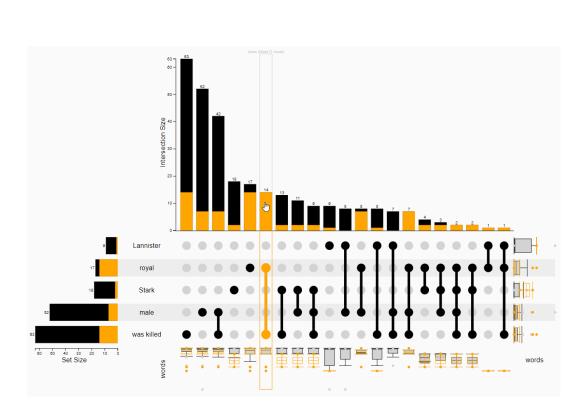
The Banana Chart Redesigned



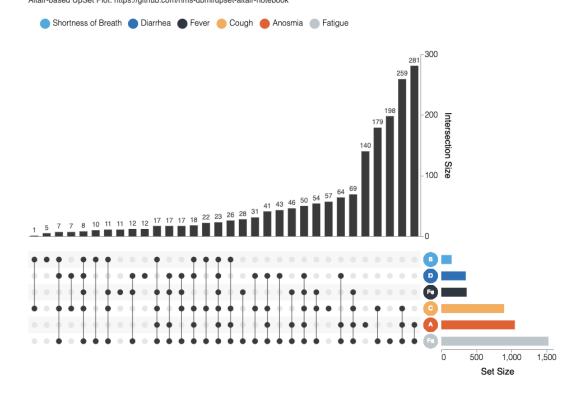




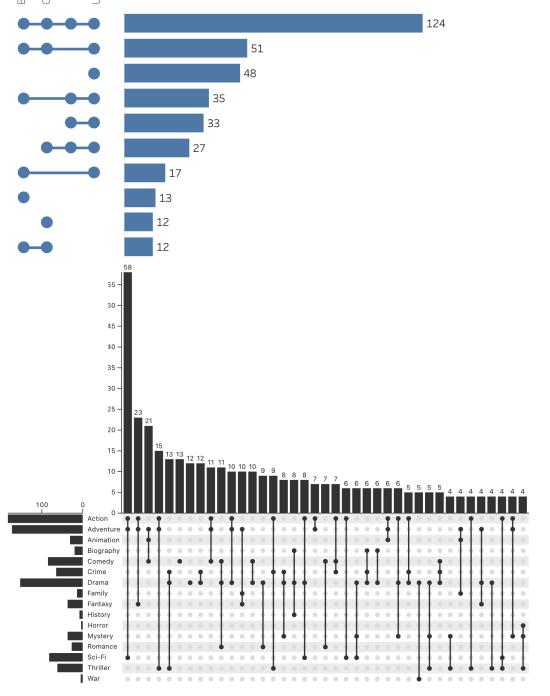


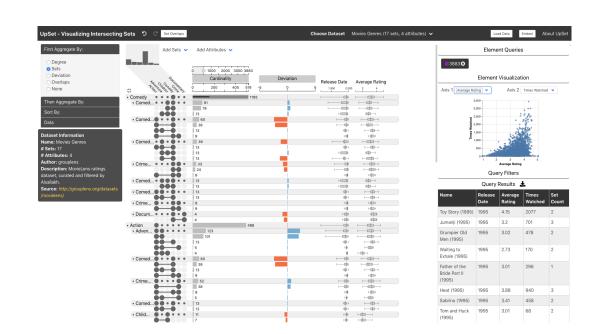


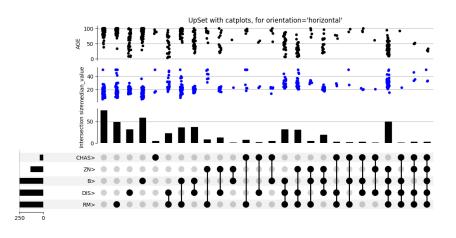


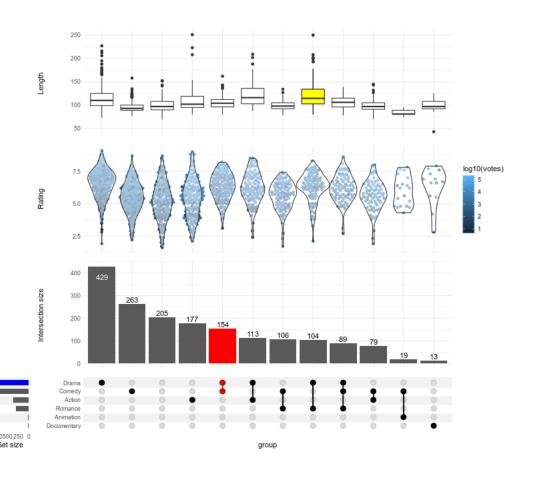


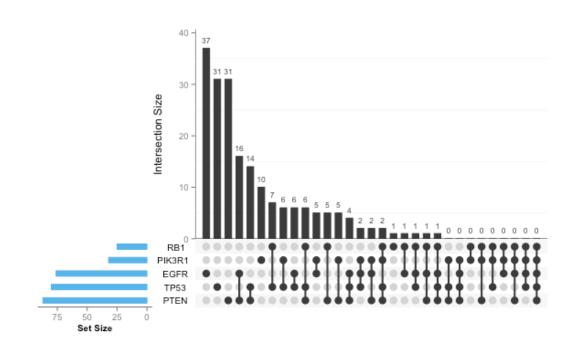
Approved Pesticide Use in Four Regions











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

Other Options

