

Intersector (Venn diagram)

Use Intersector to find genes in common or that differ amongst gene lists.

1

Grp1 Mean	Grp1 Stats	Gene Identifier	Other ID	Gene Name	UG Cluster	LocusLink	Gene ID
0.002766	0	X04663	94789_r_at	tubulin, beta	Mm.273538	22154	Tubb5
0.000263	0	M97516	99804_at		-	-	-
0.002503	0	AA867646	103553_at	minichromos	Mm.23828	70024	Mcm10
0.003688	0	U29678	99413_at	chemokine (Mm.274927	12768	Ccr1
0.003425	0	AI845999	97505_at	Transcribed	Mm.325753	-	-
0.001054	0	X82692	99421_at		-	-	-
0.004083	0	X59060	102265_at	myogenic fa	Mm.11	17878	Myf6
0.003688	0	X63004	98382_f_a	proline-rich p	Mm.3320	56272	Prpmp5
0.002766	0	X06406	97750_at	laminin recep	Mm.4071	16785	Lamr1
0.004083	0	AJ228865	99432_at		-	-	-
0.003161	0	AI528219	97184_at	cDNA seque	Mm.28904	223754	BC023106
0.002503	0	V00726	97180_f_at		-	-	-

1. Intersector accepts text files (*.txt) exported from GeneSifter.Net. The header line should start with **Grp1 Mean, Stats** or **ANOVA**. The header line also contains the following:

Gene Identifier: This is the primary ID for a gene, usually a Genbank Accession number or Image clone ID.

Other ID: This is another chief identifier for a gene. For example, an Affymetrix probe set ID or SGD IDs for yeast genes.

Gene Name/title: Typically the Unigene name given to a gene.

UG Cluster: The Unigene ID for a gene

Locuslink: The LocusLink ID

Gene ID: The Gene Symbol for a gene (e.g. BCL2)

2. Enter the number of files to be searched for common / different genes.

2

Intersector

number of files

Reset next

Intersector (Venn diagram)

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- Browse to file locations.
- By default, Intersector will perform the following:
Gene Identifier will be used as the identifier to find common/different genes.
For 2-3 files: Calculate intersections and unique genes amongst all files (see figures 1 and 2).
For 4+ files: Calculate genes that are common to all files and genes that are unique to each file (see figure 3).
- Search by a different identifier, for example, **Other ID**
- Find genes either common or different. If common, choose whether to find genes present in all or a sub set of the files.
- If different, choose whether to find genes unique to each file or compare each file to the first file uploaded (file 1) (see figure 4).

3

4

5

6

7

Intersector

load files

/home/daniel/test_files/intersector_file	Browse...	file 1
/home/daniel/test_files/intersector_file	Browse...	file 2
/home/daniel/test_files/intersector_file	Browse...	file 3

[advanced option](#) [close](#)

identifier

Gene ID

find genes

Common [find genes common in 3 out of 3 files]

Different

genes that differ

Unique to each file

Unique to File 1 [close](#)

Reset next

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- 8. A Venn diagram is returned with color-coded buttons corresponding to each section, and displays the number of genes present in that section. For example, there are 7 genes unique to the file "export2.txt".
- 9. To activate a section, click on it within the diagram and the corresponding colored button will appear in the bottom left-hand corner.
- 10. The gene list may be exported to a spreadsheet or may be viewed in another pop-up window.

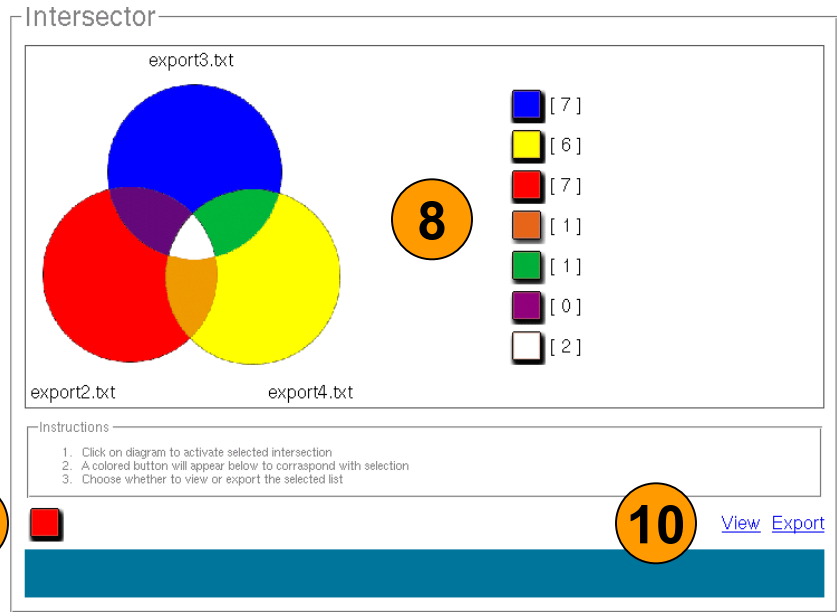


Figure 1: Find common/unique genes between 3 files

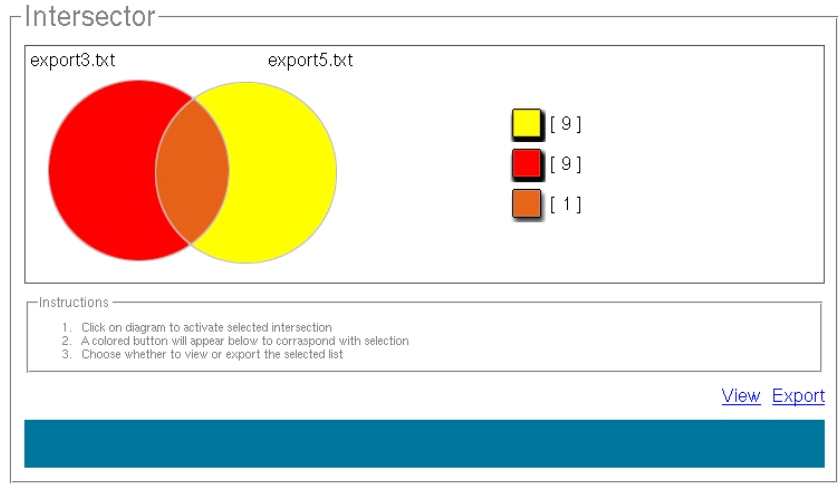


Figure 2: Find common/unique genes between 2 files

Intersector (Venn diagram)

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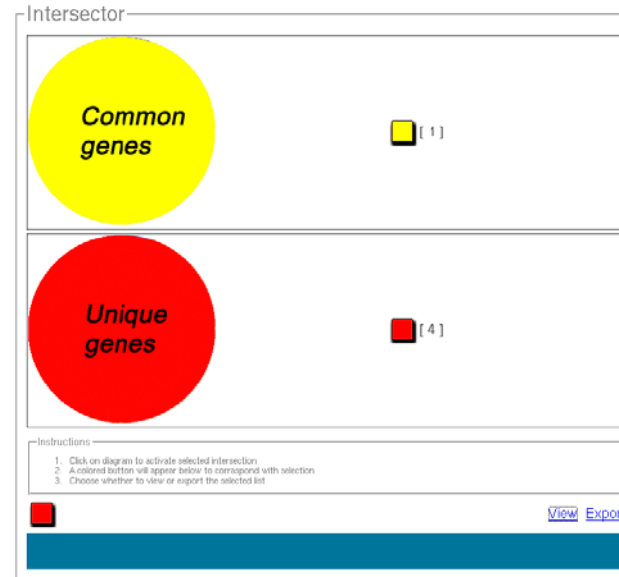


Figure 3: Find common/unique genes amongst more than 3 files

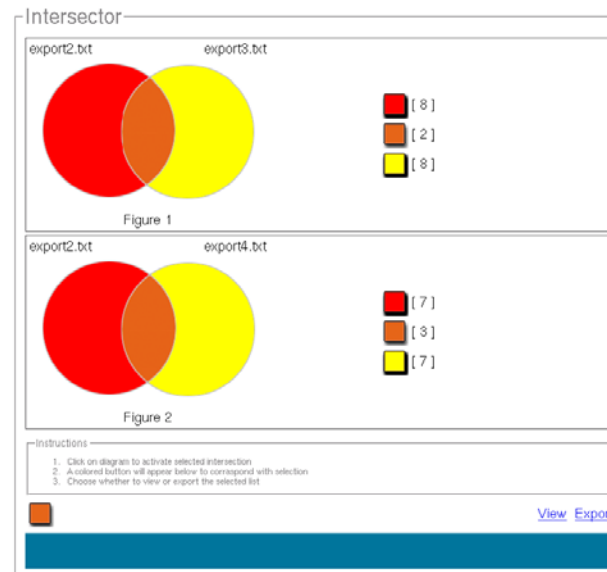


Figure 4: Find common/unique genes between file 1 and each of the remaining files