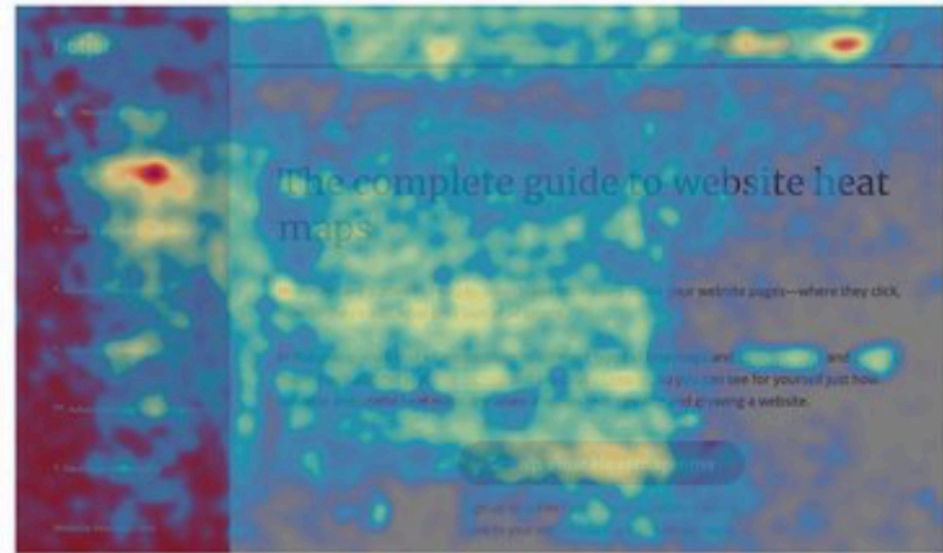


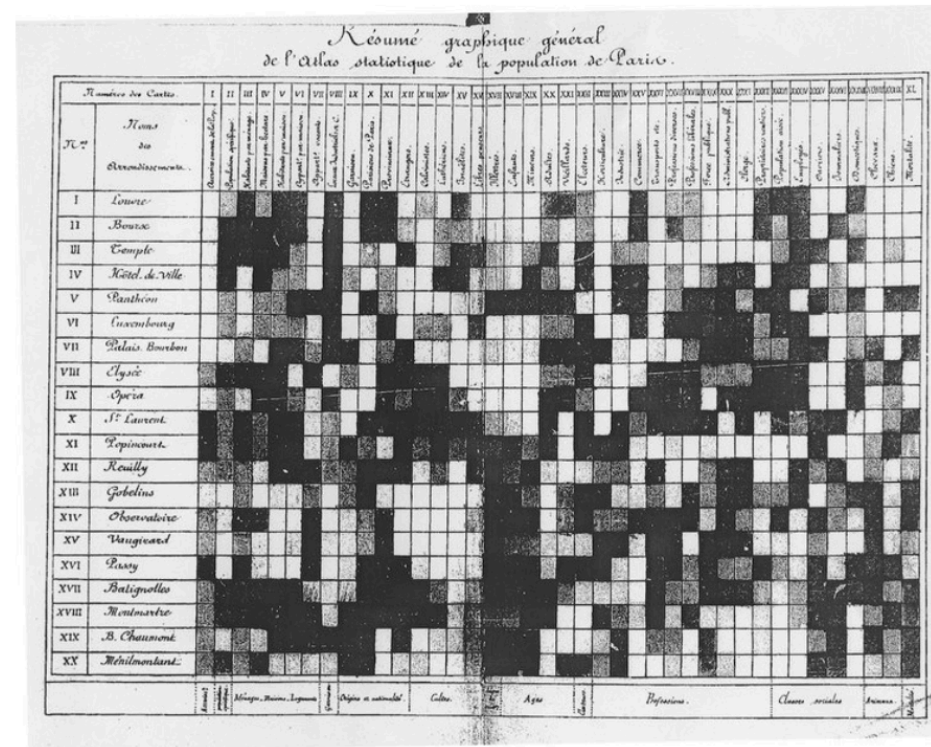
What are Heat Maps?

ELEMENT	VISIBLE	INTERACTION POINTS	% OF TOTAL
#hs_cos_wrapper_Main_Content	Yes	4,982	5.3%
...-content-column>div.hub-intro-section-content-text>]	Yes	3,987	4.2%
...n-content-column>div.hub-intro-section-content-text	Yes	3,051	3.2%
...olumn-wrapper>div.hub-intro-section-content-column	Yes	2,959	3.1%
...ow-normal.hub-content-image-row>div.image-row-ima	Yes	2,456	2.6%
div#hs_menu_wrapper_module_14701478960212019>ul (1	Yes	2,280	2.4%
...content-column>div.hub-intro-section-content-image	Yes	2,268	2.4%
#hub-content	Yes	2,081	2.2%
...553172750295>div.hub-content-row.hub-content-row-r	Yes	2,007	2.1%



THE DATA ON THE LEFT IS THE SAME AS THAT ON THE RIGHT—BUT ONE IS MUCH EASIER TO UNDERSTAND

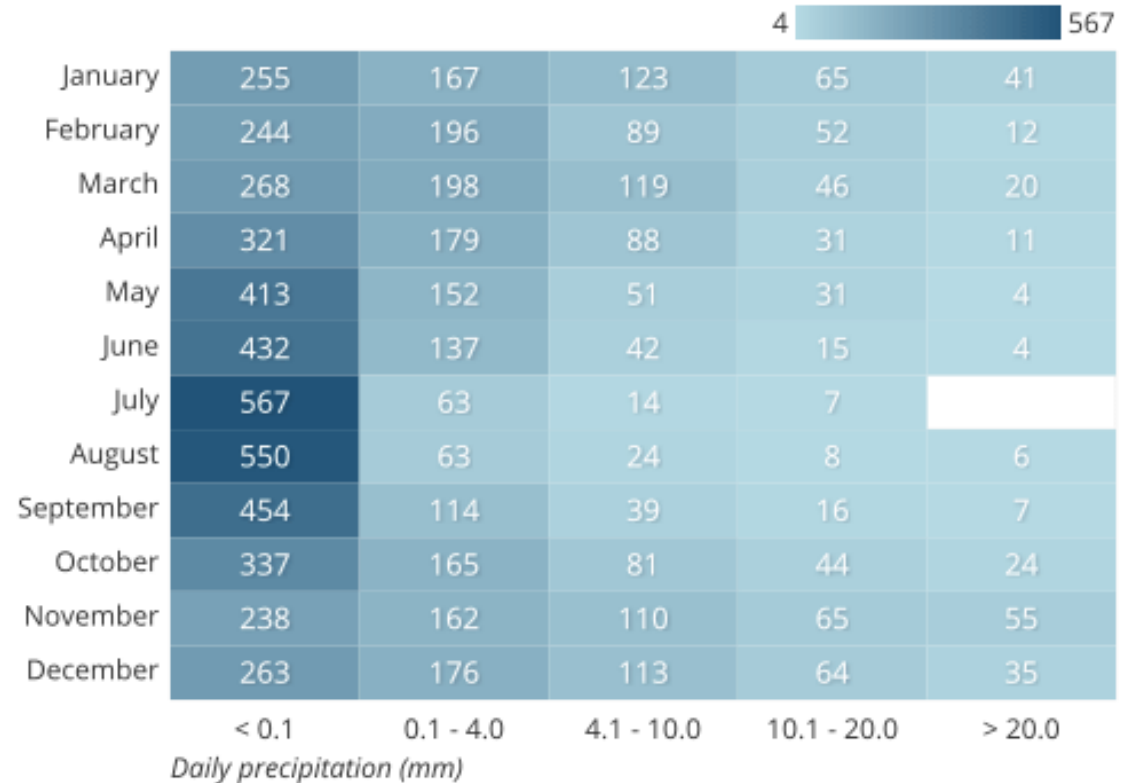
Heat maps is thought to have originated in the 19th century, where manual gray-scale shading was used to depict data patterns in matrices and tables



AN EARLY HEAT MAP SHOWING POPULATION DENSITY IN 19TH CENTURY PARIS DISTRICTS.

The example heatmap depicts the daily precipitation distribution, grouped by month, and recorded over eleven years in Seattle, Washington*.

Seattle precipitation by month, 1998-2018



Best practices for using a heatmap

Choose an appropriate color palette

Sequential Palette (continuous values)



Diverging Palette (meaningful central value)

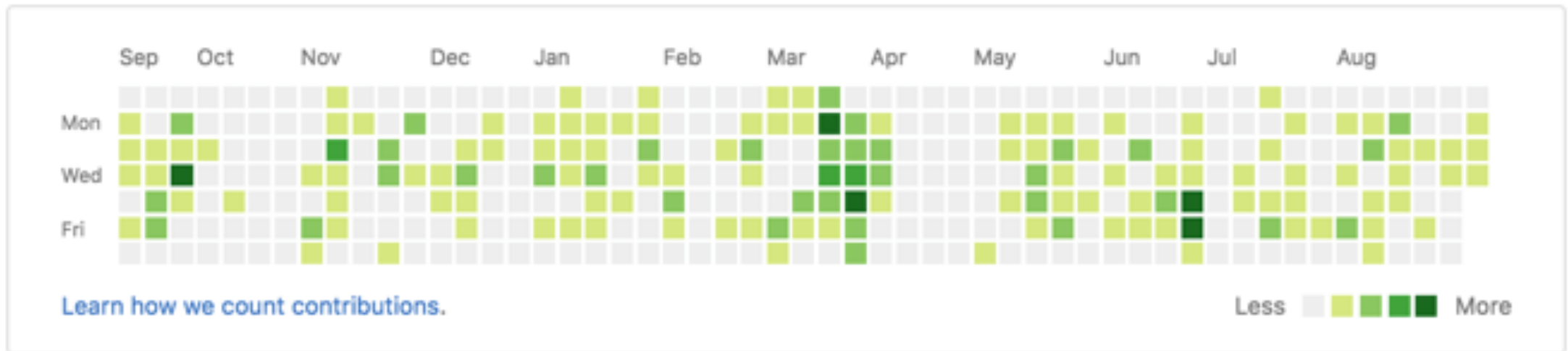


Best practices for using a heatmap

Include a legend

2,298 contributions in the last year

Contribution settings ▾

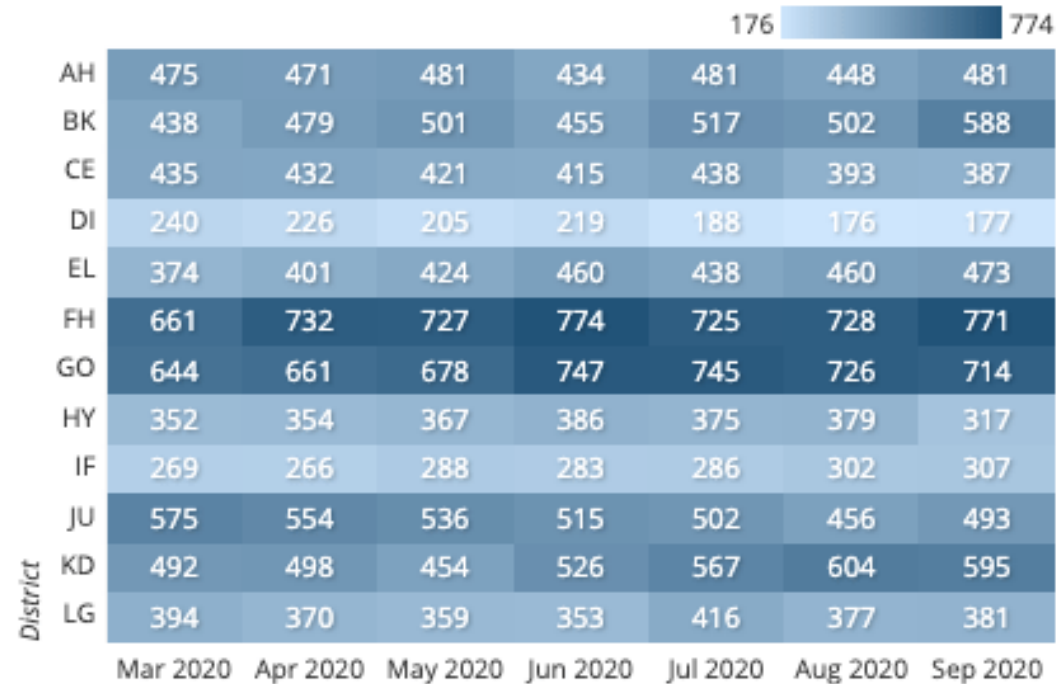


Show values in cell

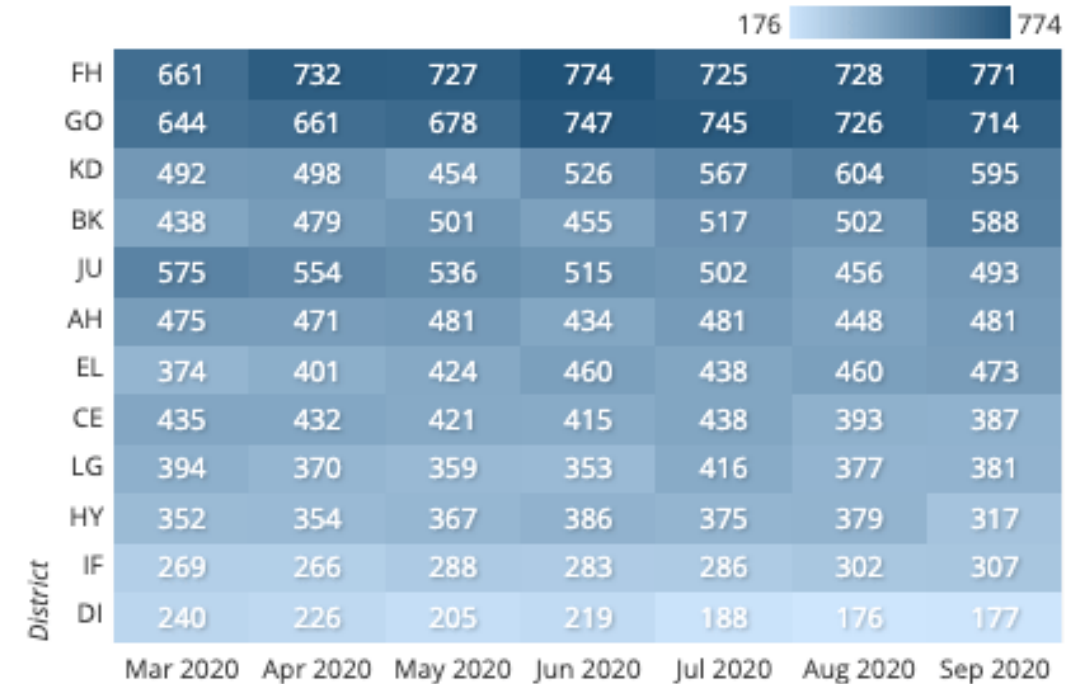
- There is a lack of precision for mapping color to value, especially compared to other encodings like position or length. Where possible, it is a good idea to add cell value annotations to the heatmap as a double encoding of value.

Sort levels by similarity or value

Active Users by Month



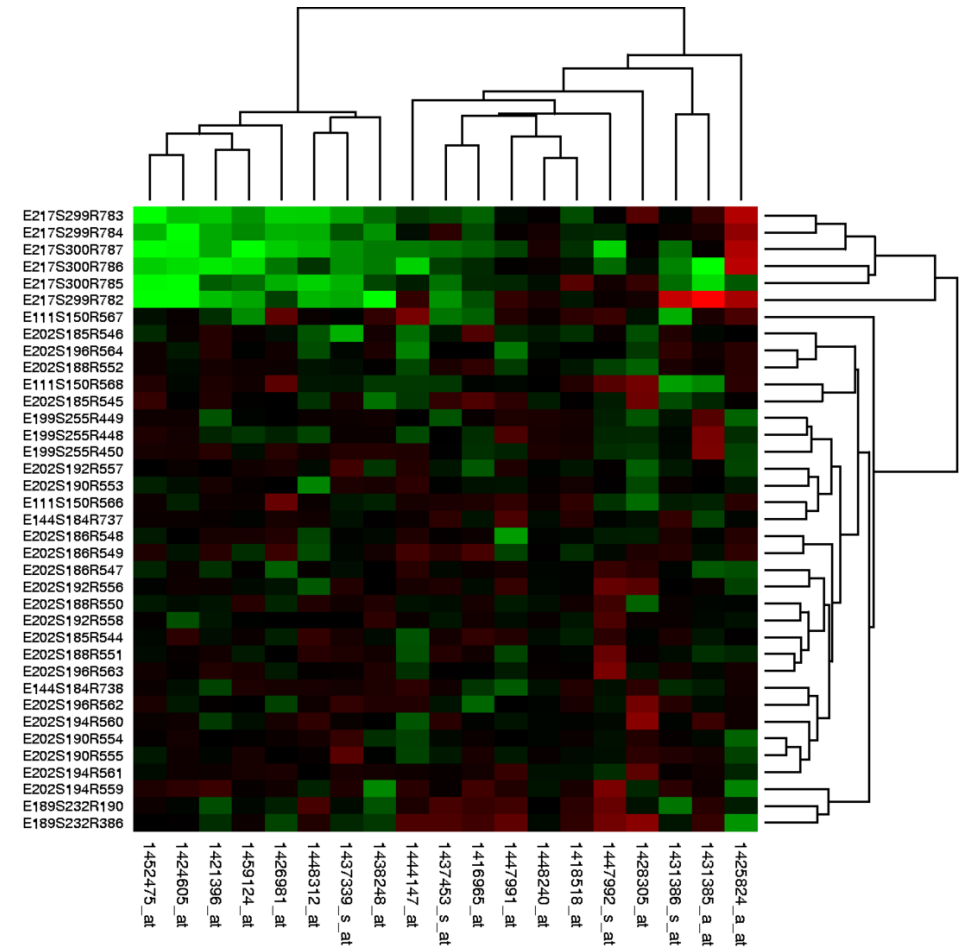
Active Users by Month



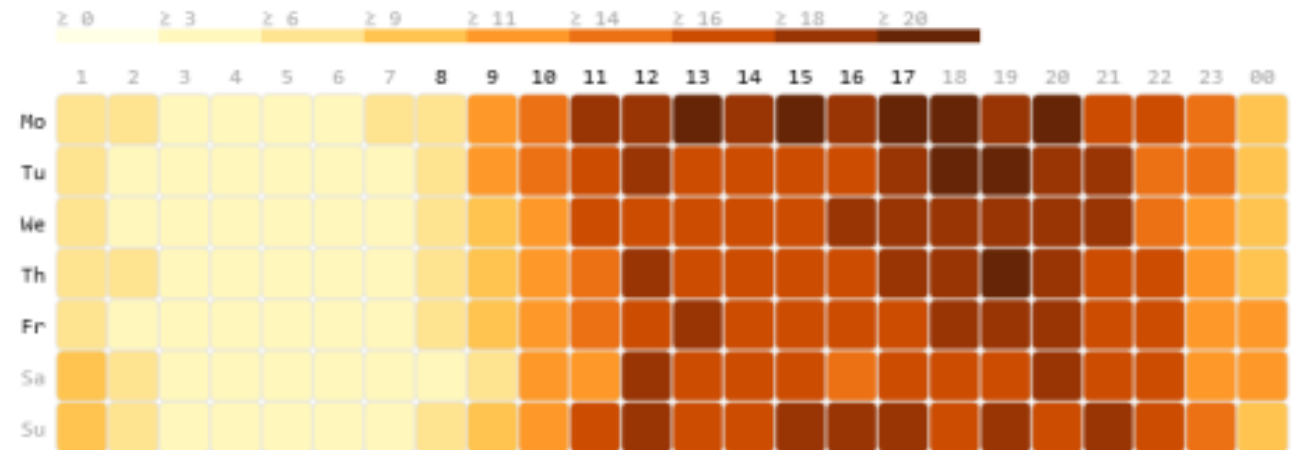
The right-side heatmap is sorted by the last column value.

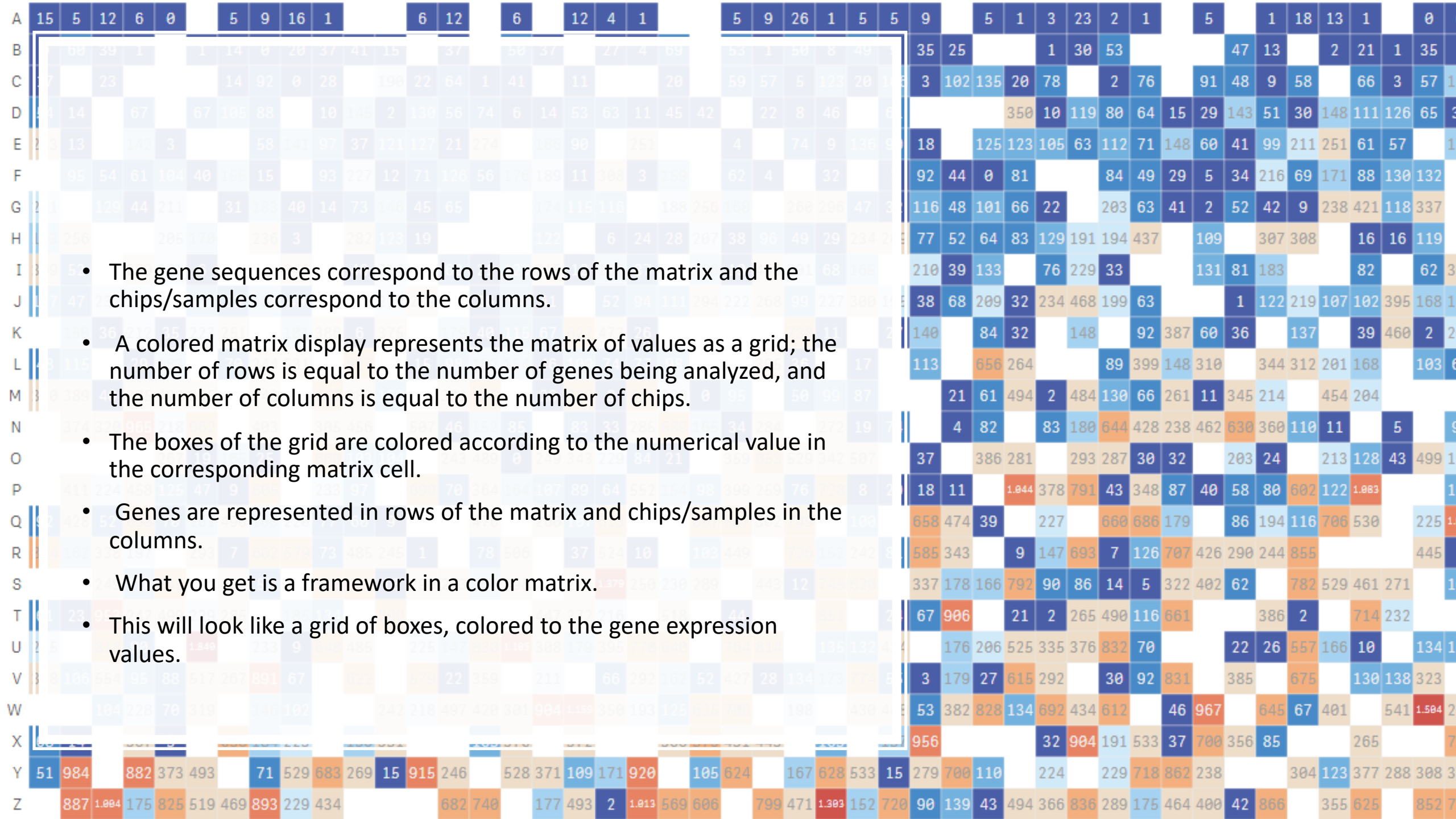
Illustration of gene expression data

- A heat map is a well-received approach to illustrate gene expression data.
- It is an impressive visual exhibit that addresses explosive amounts of **NGS** data.
- It's packed with closely set patches in shades of colors, pumping the gene expression data of multifarious high-throughput tryouts.



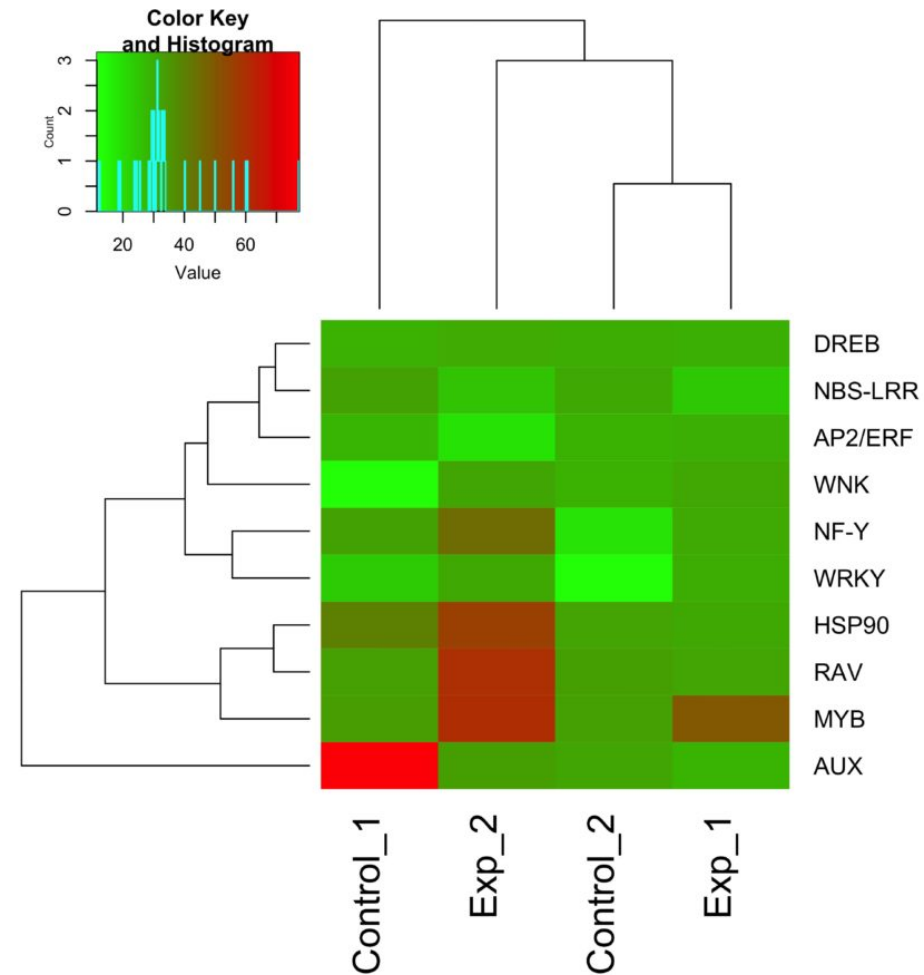
- The individual tiles or rectangles in a heat map are scaled with a range of colors proportionate to gene expression values.
- The outcome makes a pitch to check upon the rows, columns, and joint structural patterns. It's a tool used widely by the statisticians and bioinformatics scientists to make sense of large multi-dimensional datasets. It helps one to pry out groups among the genes and the samples handled by setting up associations.





- The gene sequences correspond to the rows of the matrix and the chips/samples correspond to the columns.
- A colored matrix display represents the matrix of values as a grid; the number of rows is equal to the number of genes being analyzed, and the number of columns is equal to the number of chips.
- The boxes of the grid are colored according to the numerical value in the corresponding matrix cell.
- Genes are represented in rows of the matrix and chips/samples in the columns.
- What you get is a framework in a color matrix.
- This will look like a grid of boxes, colored to the gene expression values.

- You will be able to pick genes based on their expression levels under different conditions.
- Many do not change, either because they are not on or are need to be on all the time.
- Those that do change are of the most interest. These represent the signature tune of gene expression affiliated to a particular condition.



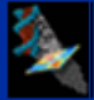
Online Tools

- CIMminer
- HeatmapGenerator
- MultiExperiment Viewer
- Bioconductor
- Morpheus
- MeV
- GenePatterns
- ExpressionProfiler
- geWorkbench
- DAVID
- Babelomics
- GoMiner
- ConceptGen
- GSEA
- EXPANDER
- ClustVis

Databases

- GEO
- ArrayExpress
- Expression Atlas

<https://discover.nci.nih.gov/cimminer/home.do>



CIMminer

Genomics and Pharmacology Facility

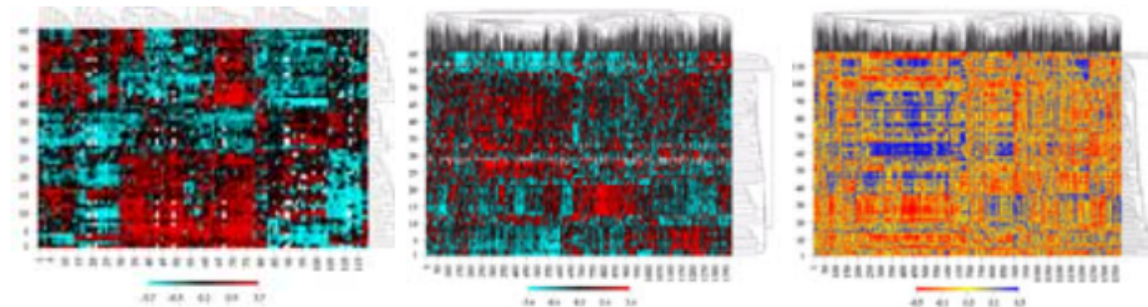
DTB, CCR, National Cancer Institute

Home

One Matrix CIM

Two Matrix CIM

Help



Drugs x Cells

Genes x Cells

Genes x Drugs

CIMminer generates color-coded Clustered Image Maps (CIMs) ("heat maps") to represent "high-dimensional" data sets such as gene expression profiles. We introduced CIMs in the mid-1990's for data on drug activity, target expression, gene expression, and proteomic profiles. Clustering of the axes brings like together with like to create patterns of color. (Weinstein, et al., Science 1997; 275:343-349). To learn more details, look at the following articles.



[Home](#)

[One Matrix CIM](#)

[Two Matrix CIM](#)

[Help](#)

Step 1: Select input file

(Detailed description of the [input file](#) is available.)

Dosya seçilmedi

Input should be a text file with '.txt' extension ([example file](#)). CIMminer only accepts tab delimited text files.
(limit 1000 rows)

Step 2: Your E-mail Address

Step 3: Fine tune image

Use defaults Advanced options

CIMminer Success Result - RefId 1219264670 Gelen Kutusu x



webadmin@discover.nci.nih.gov

18:

Alıcı: ben ▾

CIMminer processing is completed. Your Reference Id is :1219264670 .

To view your CIM,click this: <https://discover.nci.nih.gov/cimminer/cimMinerResultLoad.do?Id=1219264670&Dir=cimminerdata> .

To download your CIM,click this: <https://discover.nci.nih.gov/cimminerdata/1219264670/download.zip> .

Your result will be available for next one week. After that it will be deleted from our system.

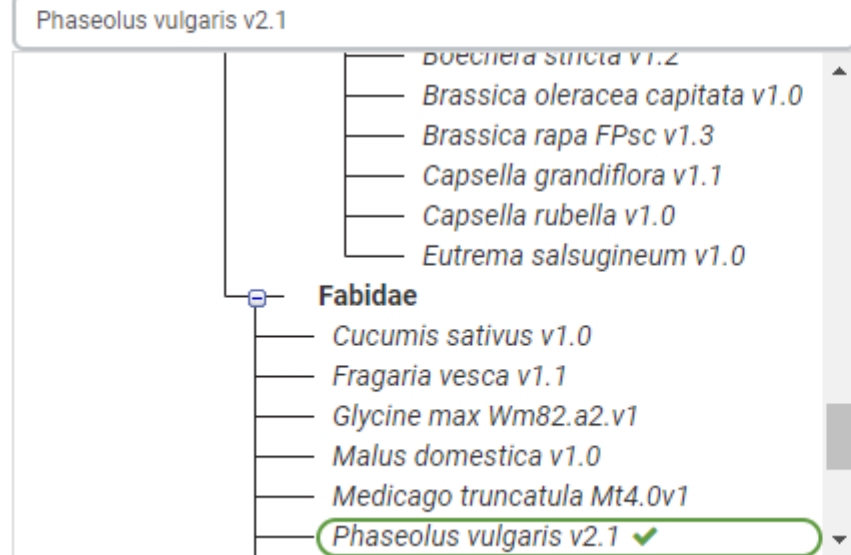
Search for genes, families and sequences

1. Select a Target 1 species selected ✕

Target set: Phytozome 12.1 Pre-release species

Target type: Ancestor nodes Species

Phaseolus vulgaris v2.1



- *Boechera stricta* v1.2
- *Brassica oleracea capitata* v1.0
- *Brassica rapa* FPsc v1.3
- *Capsella grandiflora* v1.1
- *Capsella rubella* v1.0
- *Eutrema salsugineum* v1.0
- Fabidae**
 - *Cucumis sativus* v1.0
 - *Fragaria vesca* v1.1
 - *Glycine max* Wm82.a2.v1
 - *Malus domestica* v1.0
 - *Medicago truncatula* Mt4.0v1
 - **Phaseolus vulgaris v2.1 ✓**

2. Build your query GO

Search type: Keyword BLAST

Phvul.002G116000.1 ⬇ ✕

Algorithm parameters

Add trailing wildcard:

Use family settings:

Genes		Ontologies
<input type="checkbox"/>	Views	Description
<input type="checkbox"/>	G B	Phvul.002G116000.1.p - (1 of 1) PTHR32002:SF13 - PROTEIN RKD5

Organism Phaseolus vulgaris

Transcript Name Phvul.002G116000.1 (primary)

Location: Chr02:24790146..24795421 reverse

Alias Phvul.002G116000.v1.0 Phvul.002G116000.1.v1.0

Description (1 of 1) PTHR32002:SF13 - PROTEIN RKD5

Links [B](#) [M](#)

Functional Annotation

Genomic

Sequences

Protein Homologs

Gene Ancestry

Expression

Show:

Expression

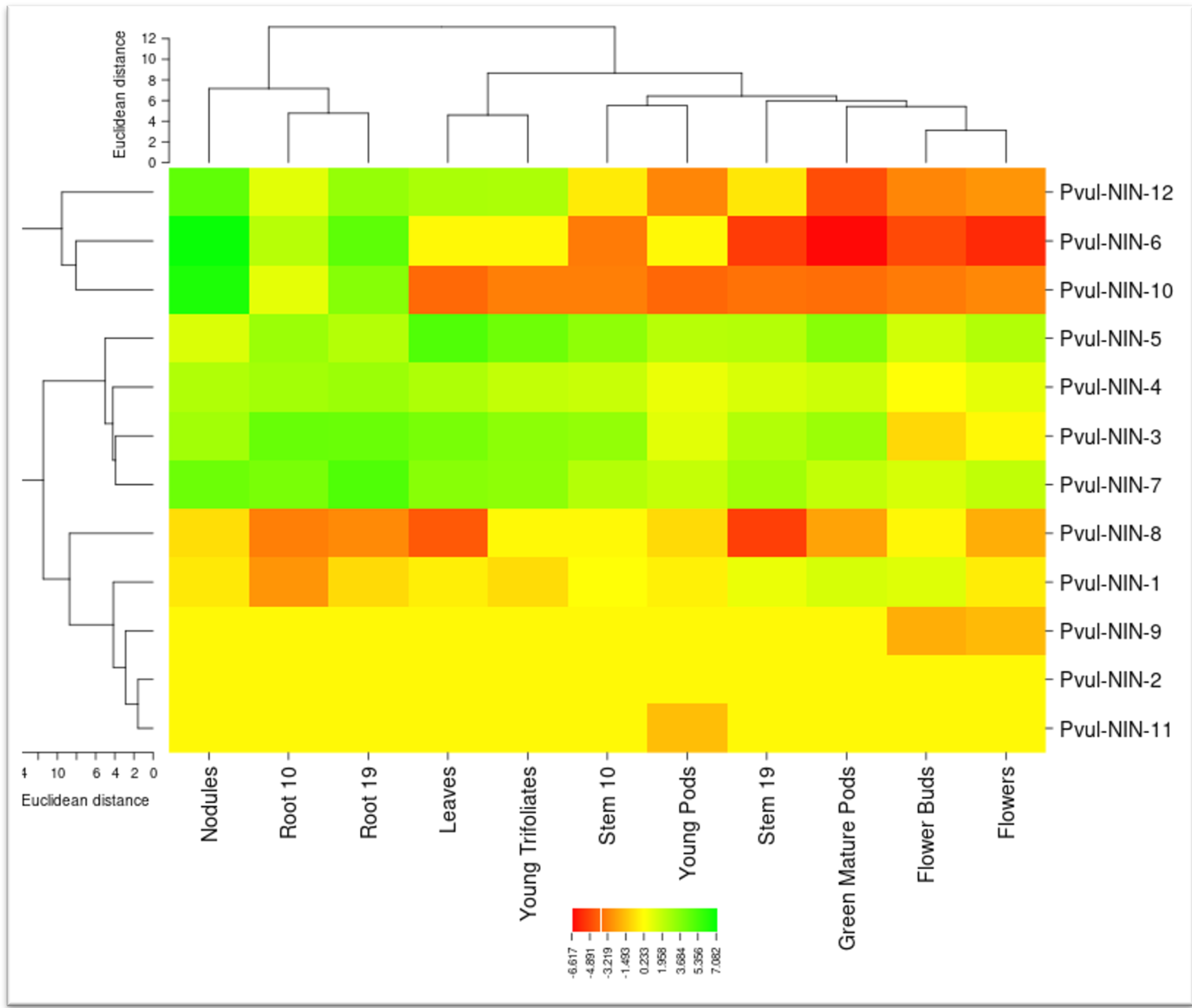
Coexpression

Experiment Group	Experiment Name	FPKM	Locus DE
Tissue Sample	Leaves	0.844	
Tissue Sample	Nodules	0.744	

Contact Disclaimer

Accessibility / Section 508 Statement

	Flower Buds	Flowers	Green Mature Pods	Leaves	Nodules	Root 10	Root 19	Stem 10	Stem 19	Young Pods	Young Trifoliate
Pvul-NIN-1	2.299	0.797	2.722	0.844	0.744	0.153	0.549	1.135	1.743	0.872	0.578
Pvul-NIN-2	0	0	0	0	0	0	0	0	0	0	0
Pvul-NIN-3	0.538	1	8.228	16.309	7.296	21.864	20.884	9.509	5.328	2.134	11.124
Pvul-NIN-4	1.149	1.999	3.249	5.66	5.54	7.094	8.128	3.462	2.562	1.773	3.904
Pvul-NIN-5	3.026	5.318	11.77	34.005	2.476	8.216	4.978	10.214	4.981	4.866	19.242
Pvul-NIN-6	0.035	0.019	0.01	0	138.043	4.776	26.901	0.093	0.027	0	0
Pvul-NIN-7	2.677	3.971	3.894	12.031	19.81	15.72	35.487	4.969	7.22	3.681	10.813
Pvul-NIN-8	0.959	0.248	0.198	0.048	0.602	0.101	0.121	0	0.029	0.555	0
Pvul-NIN-9	0.241	0.304	0	0	0	0	0	0	0	0	0
Pvul-NIN-10	0.092	0.117	0.072	0.067	92.671	2.003	12.352	0.098	0.077	0.063	0.098
Pvul-NIN-11	0	0	0	0	0	0	0	0	0	0.335	0
Pvul-NIN-12	0.111	0.153	0.038	6.161	26.073	2.172	9.041	0.767	0.733	0.11	5.813





Thanks for listening