Confidence Regions and Averaging for Trees Examples

Susan Holmes

Statistics Department, Stanford

and INRA- Biométrie, Montpellier,France

susan@stat.stanford.edu

`http://www-stat.stanford.edu/~susan/`

$\longrightarrow$

Phylogenetic Tree Example

Family trees or phylogenetic trees whose leaves are different evolutionary entities (species, genes, populations).

DNA Data for 12 species of primates

Mitochondria, 898 characters on 12 species.
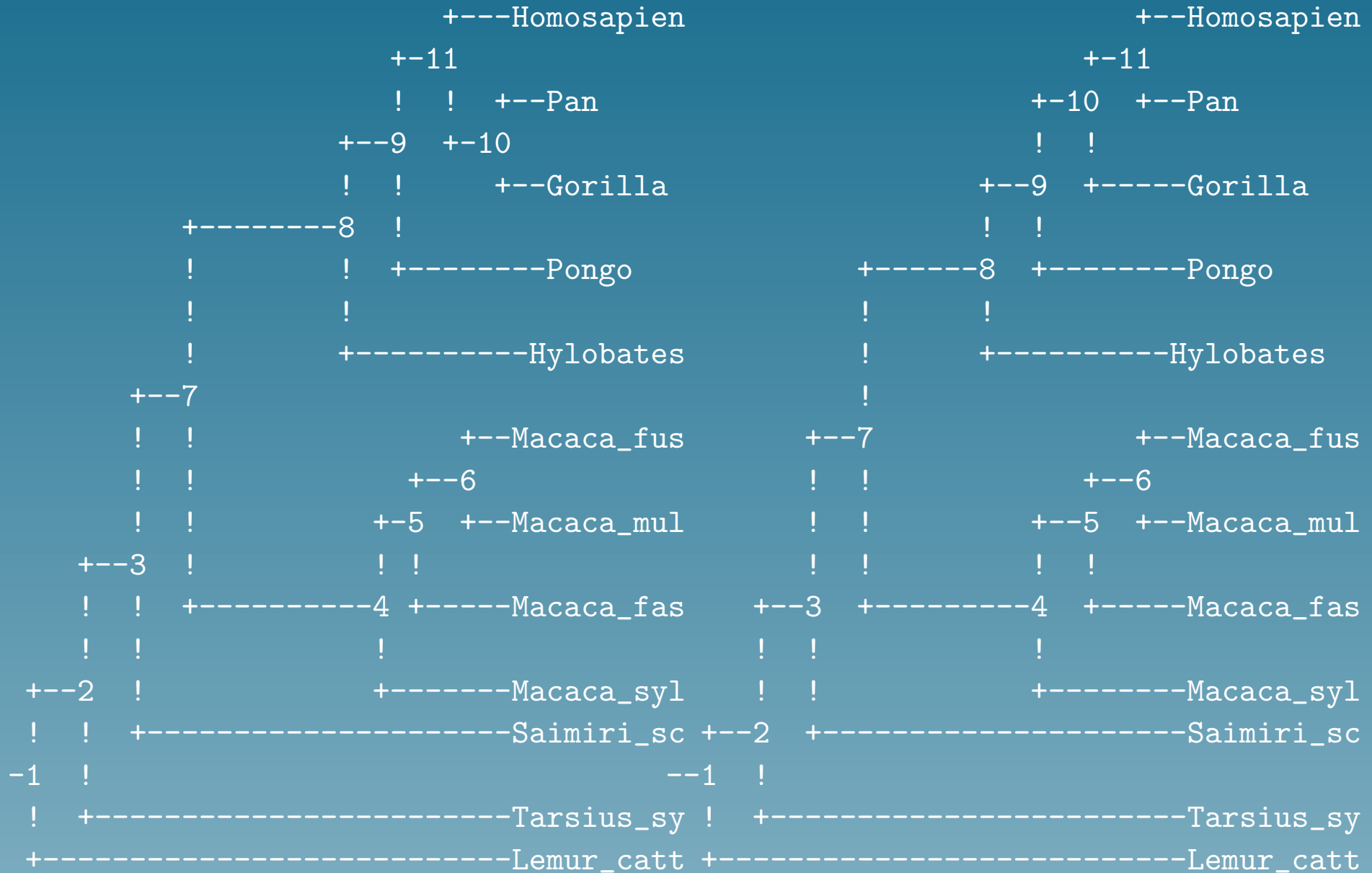
Hayasaka, K., T. Gojobori, and S. Horai. 1988.

Trees are built from DNA data such as the following:

```
  12   60
Lemur_cat AAGCTTCATA GGAGCAACCA TTCTAATAAT CGCACATGGC CTTACATCAT CCATATTATT
Tarsius_s AAGTTTCATT GGAGCCACCA CTCTTATAAT TGCCCATGGC CTCACCTCCT CCCTATTATT
Saimiri_s AAGCTTCACC GGCGCAATGA TCCTAATAAT CGCTCACGGG TTTACTTCGT CTATGCTATT
Macaca_sy AAGCTTCTCC GGTGCAACTA TCCTTATAGT TGCCCATGGA CTCACCTCTT CCATATACTT
Macaca_fa AAGCTTCTCC GGCGCAACCA CCCTTATAAT CGCCCACGGG CTCACCTCTT CCATGTATTT
Macaca_mu AAGCTTTTCT GGCGCAACCA TCCTCATGAT TGCTCACGGA CTCACCTCTT CCATATATTT
Macaca_fu AAGCTTTTCC GGCGCAACCA TCCTTATGAT CGCTCACGGA CTCACCTCTT CCATATATTT
 Hylobate AAGCTTTACA GGTGCAACCG TCCTCATAAT CGCCCACGGA CTAACCTCTT CCCTGCTATT
Pongo     AAGCTTCACC GGCGCAACCA CCCTCATGAT TGCCCATGGA CTCACATCCT CCCTACTGTT
Gorilla   AAGCTTCACC GGCGCAGTTG TTCTTATAAT TGCCCACGGA CTTACATCAT CATTATTATT
Pan       AAGCTTCACC GGCGCAATTA TCCTCATAAT CGCCCACGGA CTTACATCCT CATTATTATT
Homosapie AAGCTTCACC GGCGCAGTCA TTCTCATAAT CGCCCACGGG CTTACATCCT CATTACTATT
```
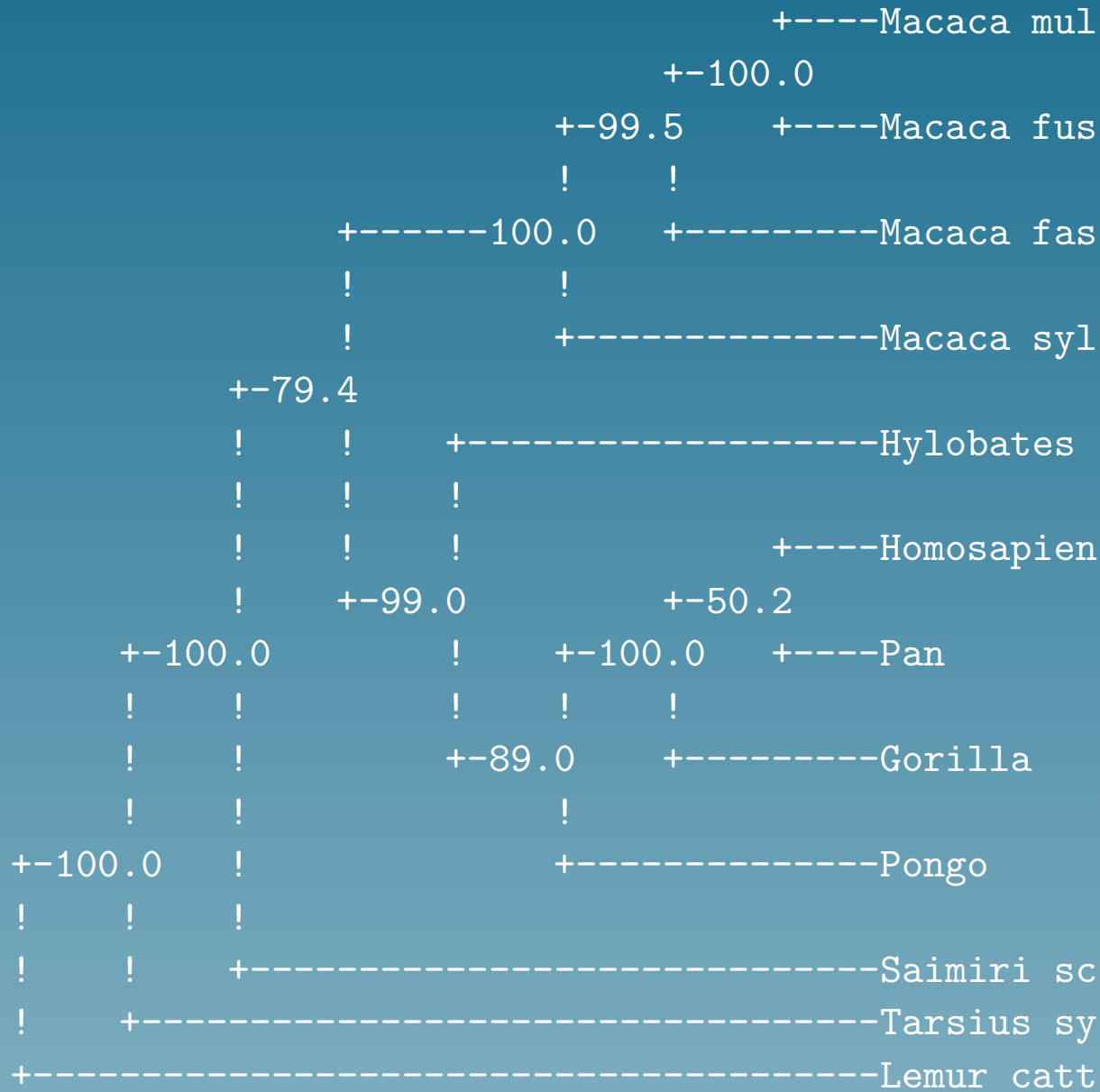
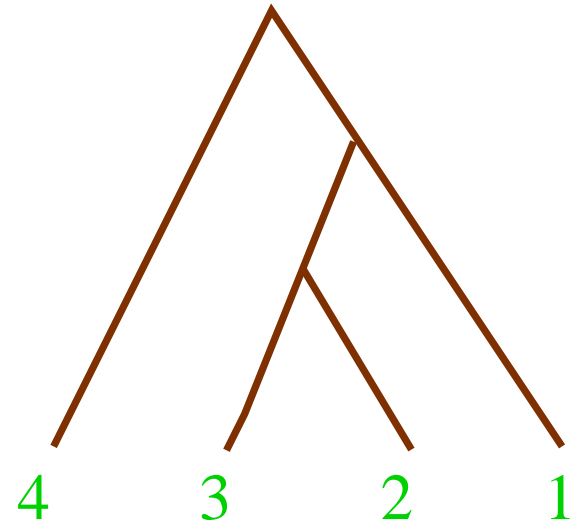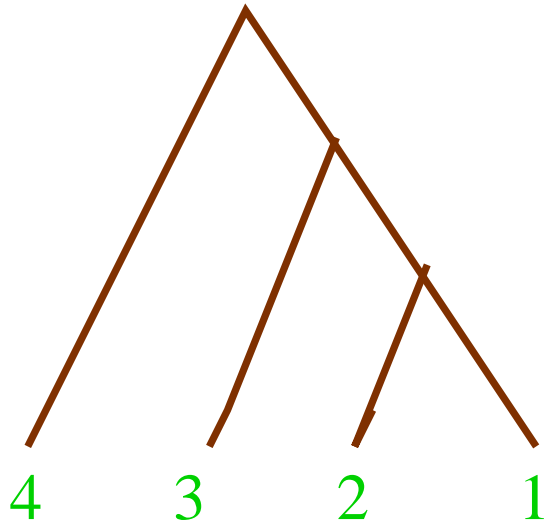# Color Coded version of the data, after alignment

TwoTrees Built with this data by parsimony

```
                    +---Homosapien                              +--Homosapien
               +-11                                        +-11
               !   !  +--Pan                          +-10  +--Pan
          +--9  +-10                                  !   !
          !   !     +--Gorilla                   +--9  +-----Gorilla
    +--------8  !                                !   !
    !          !  +--------Pongo            +------8  +--------Pongo
    !          !  !                         !        !
    !          +---------Hylobates          !        +---------Hylobates
  +--7                                       !
    !  !              +--Macaca_fus        +--7              +--Macaca_fus
    !  !            +--6                      !  !          +--6
    !  !            +-5  +--Macaca_mul        !  !          +-5  +--Macaca_mul
  +--3  !              ! !                    !  !              ! !
    !  !  +---------4 +-----Macaca_fas     +--3  +---------4  +-----Macaca_fas
    !  !            !                        !  !            !
  +--2  !            +-------Macaca_syl      !  !            +-------Macaca_syl
  !  !  +-------------------Saimiri_sc    +--2  +------------------------Saimiri_sc
 -1  !                                     --1  !
  !  +-----------------------Tarsius_sy !  +------------------------Tarsius_sy
  +-----------------------Lemur_catt  +------------------------Lemur_catt
```

With the Bootstrap "Confidence" Values

```
                                        +----Macaca mul
                               +-100.0
                      +-99.5      +----Macaca fus
                      !       !
             +------100.0    +---------Macaca fas
             !          !
             !          +-------------Macaca syl
        +-79.4
        !    !   +------------------Hylobates
        !    !   !
        !    !   !              +----Homosapien
        !    +-99.0            +-50.2
    +-100.0          !    +-100.0   +----Pan
    !    !          !    !    !
    !    !      +-89.0    +---------Gorilla
    !    !          !
+-100.0   !              +-------------Pongo
!    !    !
!    !    +--------------------------Saimiri sc
!    +----------------------------------Tarsius sy
+--------------------------------------Lemur catt
```

Using the geometry

4   3   2   1 4   3   2   14   3   2   1

Using the geometry

4   3   2   1 4   3   2   14   3   2   1
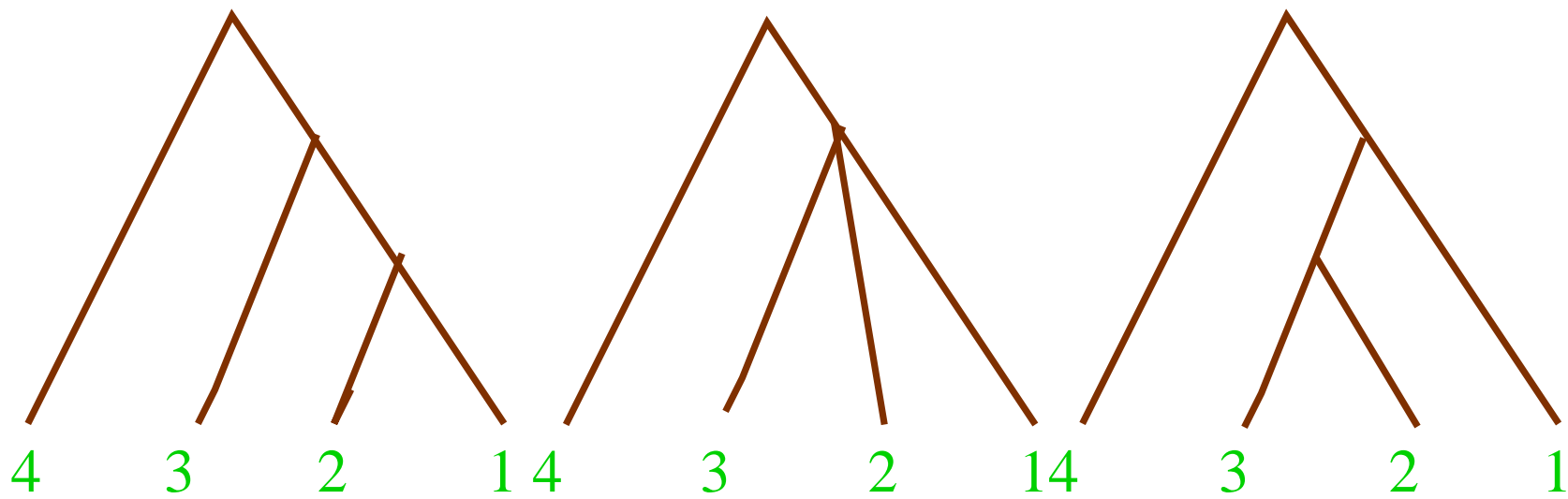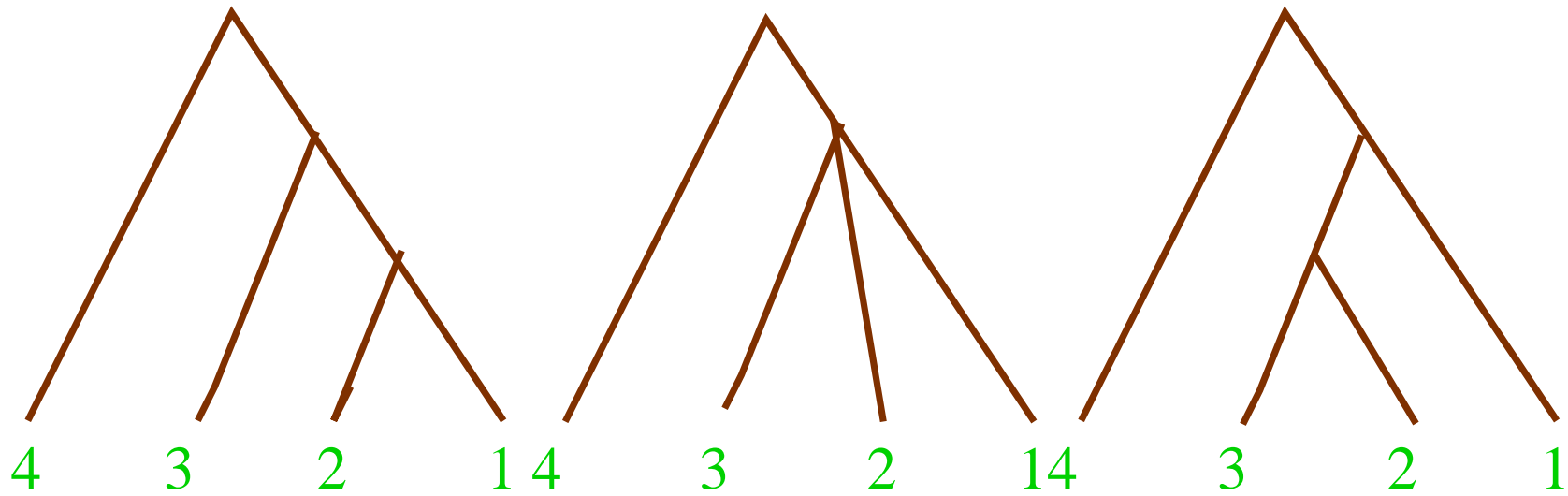
Already used by biolgists to indicate 'unresolved' branchings.

The Wine Data

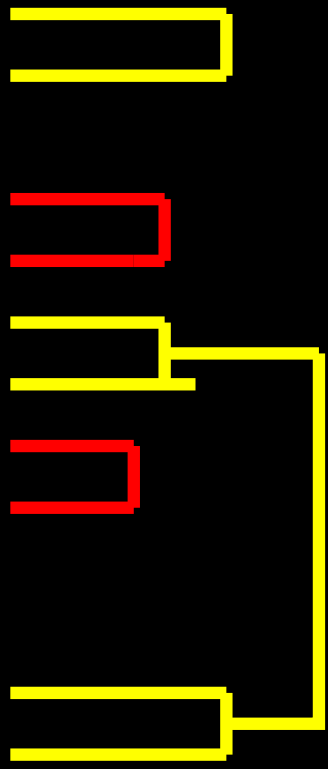| wine	D28	TAN	IGEL	IHCL	COL	JAU	RGE	BLE	DFLV	TNT	ANT	PVP	ION	PH	cepag
1	1.09	2.09	45	13	1.06	64	52	14	54	0.64	413	40	26	3.80	Syrah
2	0.61	1.27	35	20	0.65	40	45	16	38	0.89	220	48	22	3.80	Syrah
3	0.90	1.68	38	29	0.84	36	49	15	48	0.74	422	46	22	3.84	Syrah
4	1.11	2.00	28	26	0.74	37	51	12	51	0.74	527	27	11	3.83	Syrah
5	0.85	1.50	37	40	0.66	39	49	12	48	0.80	369	38	17	3.78	Syrah
6	0.98	2.00	41	26	0.99	36	51	13	51	0.72	316	67	16	3.75	Syrah
7	1.24	2.41	58	27	0.83	38	50	12	49	0.77	316	44	16	3.69	Syrah
8	0.92	1.63	50	18	0.58	40	47	12	45	0.85	229	15	15	3.70	Syrah
9	1.18	2.00	59	30	0.84	39	48	13	46	0.80	316	39	15	3.80	Syrah
10	1.13	2.32	62	25	0.84	40	48	12	46	0.82	281	41	9	3.82	Syrah
11	1.04	2.36	61	30	0.69	40	47	13	44	0.85	299	53	7	3.84	Syrah
12	1.27	2.69	69	38	0.91	40	47	13	43	0.85	352	68	11	3.85	Syrah
13	1.23	3.09	62	22	0.88	42	46	12	41	0.92	255	62	10	3.82	Syrah
14	1.34	3.00	64	28	0.89	42	46	12	42	0.91	141	44	11	3.76	Syrah
15	1.28	3.00	75	33	1.00	42	46	12	41	0.91	202	83	18	3.82	Syrah
16	1.17	2.23	68	20	1.06	42	45	13	39	0.92	105	83	57	3.76	Syrah
17	1.31	2.81	65	58	1.00	42	45	13	39	0.94	123	71	43	3.71	Syrah
18	0.91	1.63	39	21	0.59	47	42	11	32	1.10	132	73	25	3.76	Syrah
19	0.93	1.63	64	12	0.62	46	42	12	32	1.08	149	76	19	3.88	Syrah
20	1.08	2.01	44	30	0.79	44	43	13	35	1.02	141	38	21	3.90	Syrah
21	1.11	2.27	30	9	0.69	46	42	12	30	1.09	229	46	13	4.08	Syrah
22	0.90	1.76	54	23	0.80	46	41	13	29	1.11	88	70	37	4.08	Syrah
23	1.09	2.06	55	26	1.21	43	42	15	31	1.03	158	94	27	4.28	Syrah
24	0.80	1.76	35	19	0.62	47	41	12	28	1.15	62	86	36	3.94	Syrah
25	0.76	1.62	31	24	0.55	47	42	11	31	1.13	202	78	12	4.04	Syrah
26	0.86	1.71	39	20	0.67	47	41	12	28	1.14	44	40	16	4.13	Syrah
27	0.63	1.41	33	26	0.59	39	49	12	47	0.80	290	45	6	3.66	Carign
28	0.65	2.11	48	26	0.66	37	50	13	49	0.75	387	55	3	3.63	Carign
29	0.69	1.34	22	27	0.60	38	51	11	51	0.74	308	40	7	3.65	Carign
30	0.70	1.25	33	16	0.59	43	45	13	38	0.96	185	19	14	3.85	Carign
31	0.69	1.27	33	19	0.44	43	44	13	37	0.97	246	39	9	3.78	Carign
32	0.78	1.68	39	17	0.65	41	46	13	40	0.91	229	46	15	3.87	Carign
33	0.59	1.47	29	20	0.45	42	44	14	38	0.94	123	71	16	3.72	Carign
34	0.58	1.24	33	34	0.41	41	47	12	43	0.89	141	63	13	3.69	Carign
35	0.66	1.45	19	10	0.31	44	46	10	41	0.96	202	70	7	3.66	Carign
36	0.79	1.41	72	28	0.54	47	42	10	32	1.11	44	80	17	3.91	Carign

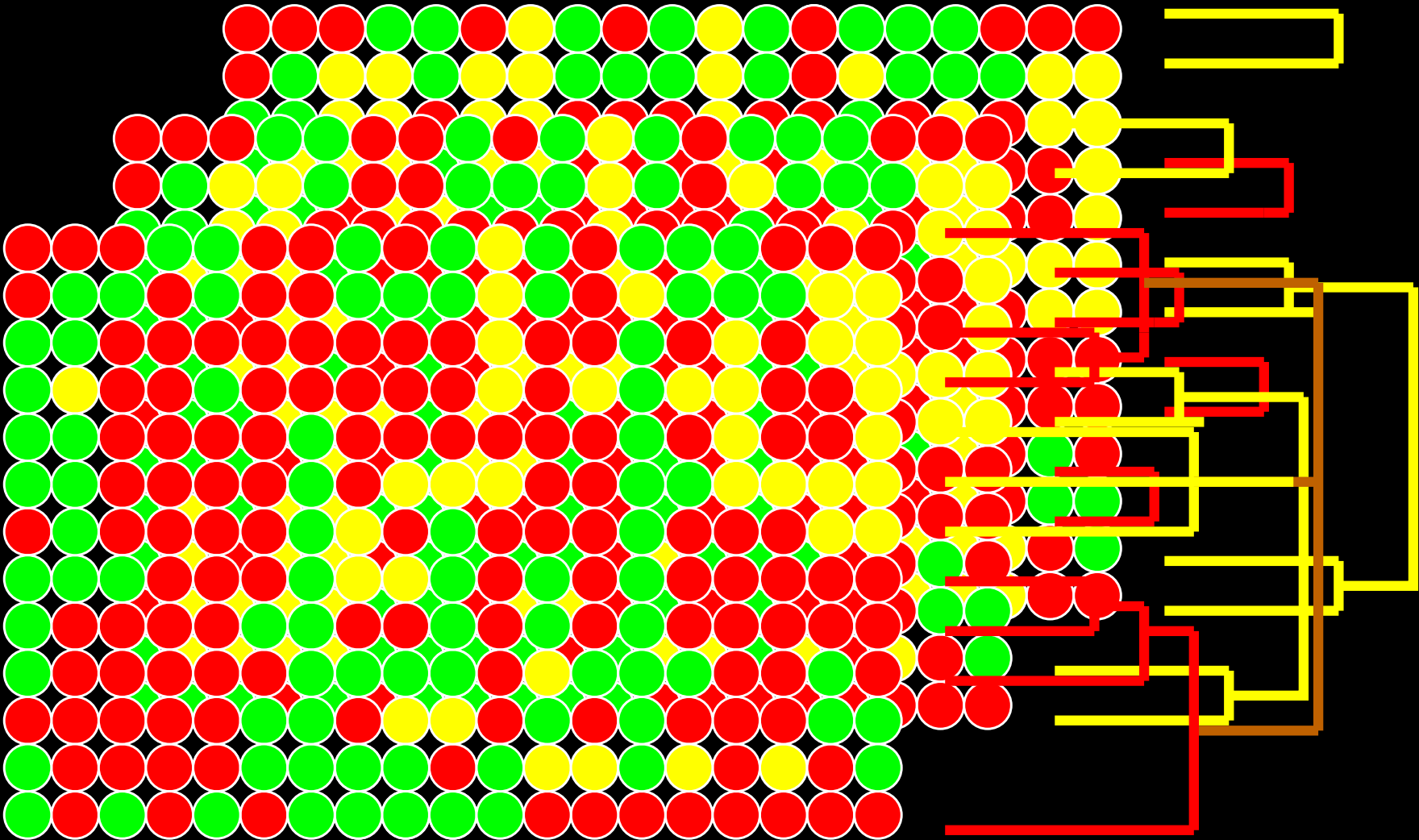# Classification And Regression Trees [3]

Syrah
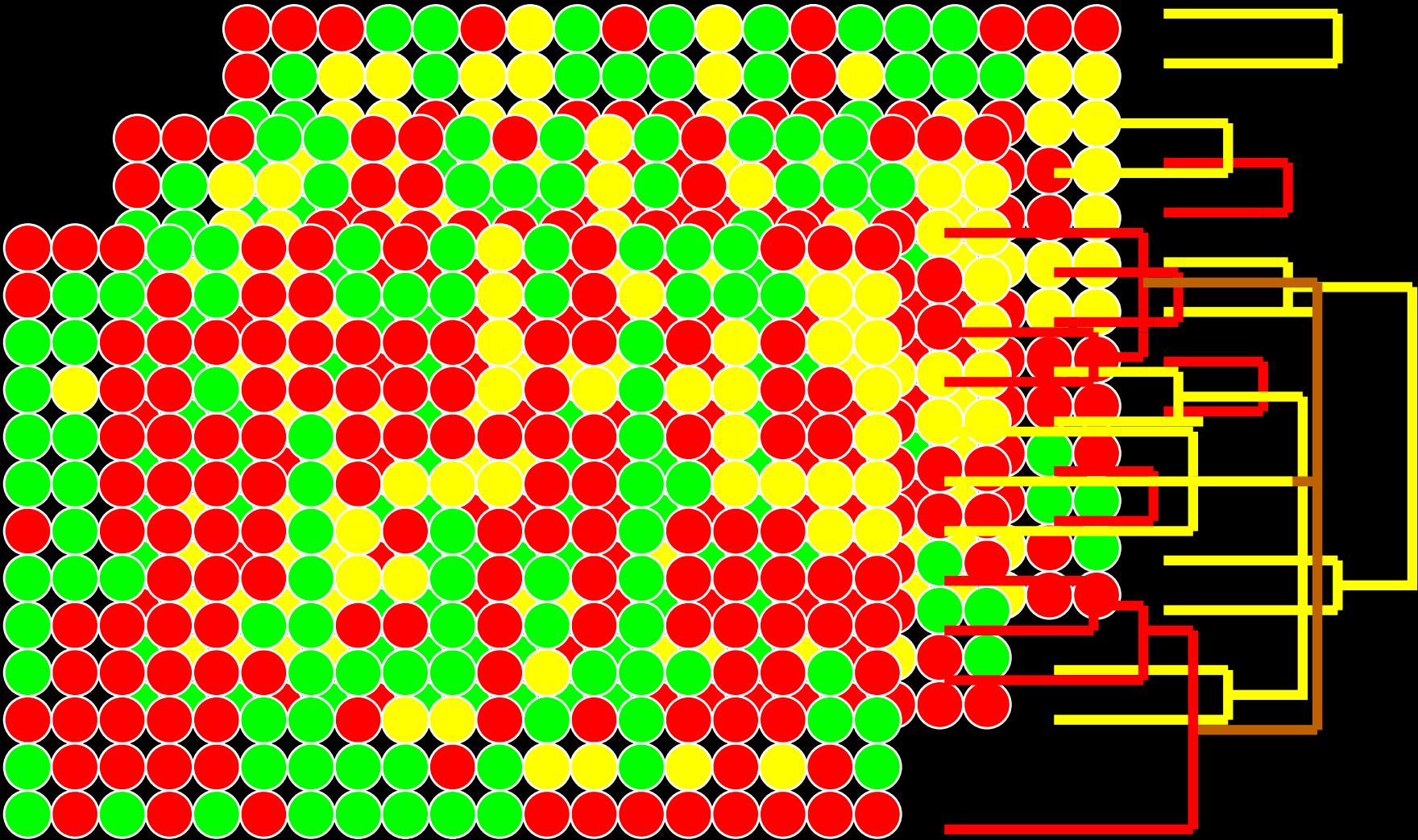52/78

Cinsault
8/34

Syrah
18/44

Cinsault
1/21

Carignan
6/13

Carignan
12/30

Syrah
0/14

Cinsault
0/20

Carignan
0/1

Cinsault
3/9

Carignan
0/4

Syrah
10/22

Carignan
0/8

Carignan
0/3

Cinsault
0/6

Carignan
0/4

Syrah
6/18

Syrah
0/6

Syrah
6/12

Carignan
2/8

Syrah
0/4

Carignan
0/4

Syrah
2/4

Syrah
0/2

Carignan
0/2

Syrah
52/78

Cinsault
8/34

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18/44

Cinsault
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0/14

Cinsault
1/5

Cinsault
0/16

Carignan
1/6

Cinsault
2/7

Syrah
10/22

Carignan
0/8

Syrah
5/16

Carignan
1/6

Carignan
2/7

Syrah
0/9

Clustering Trees - For micro-arrays [11]
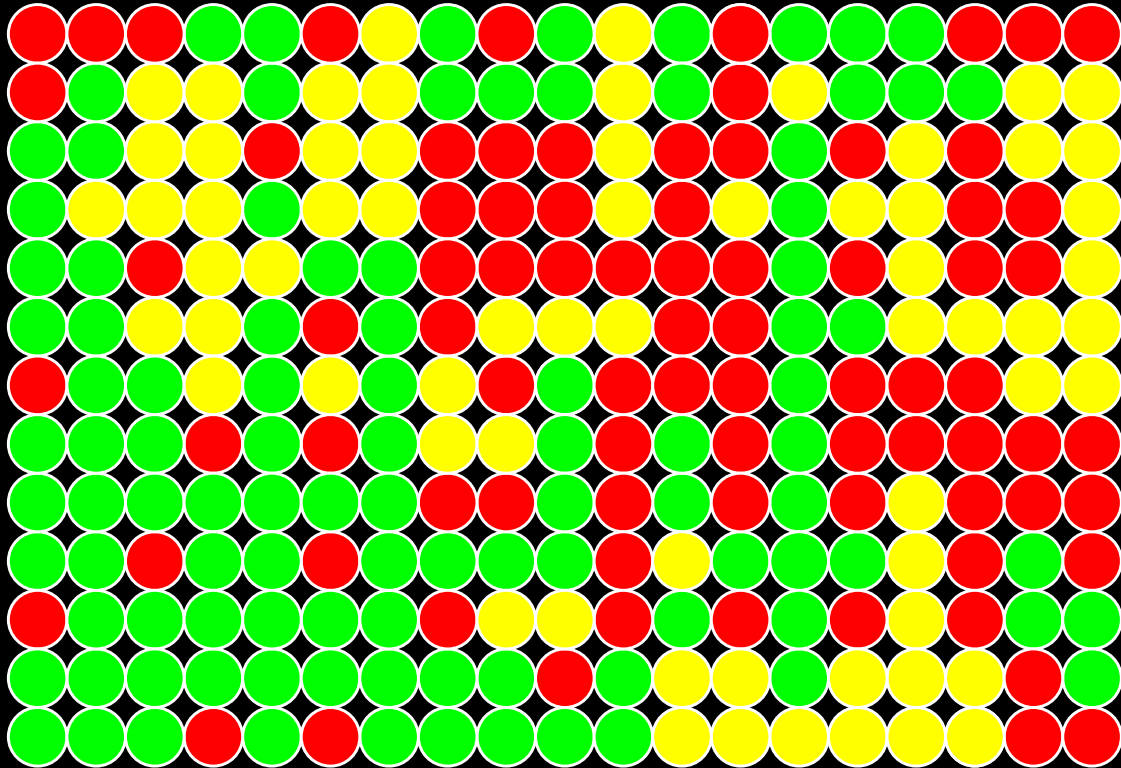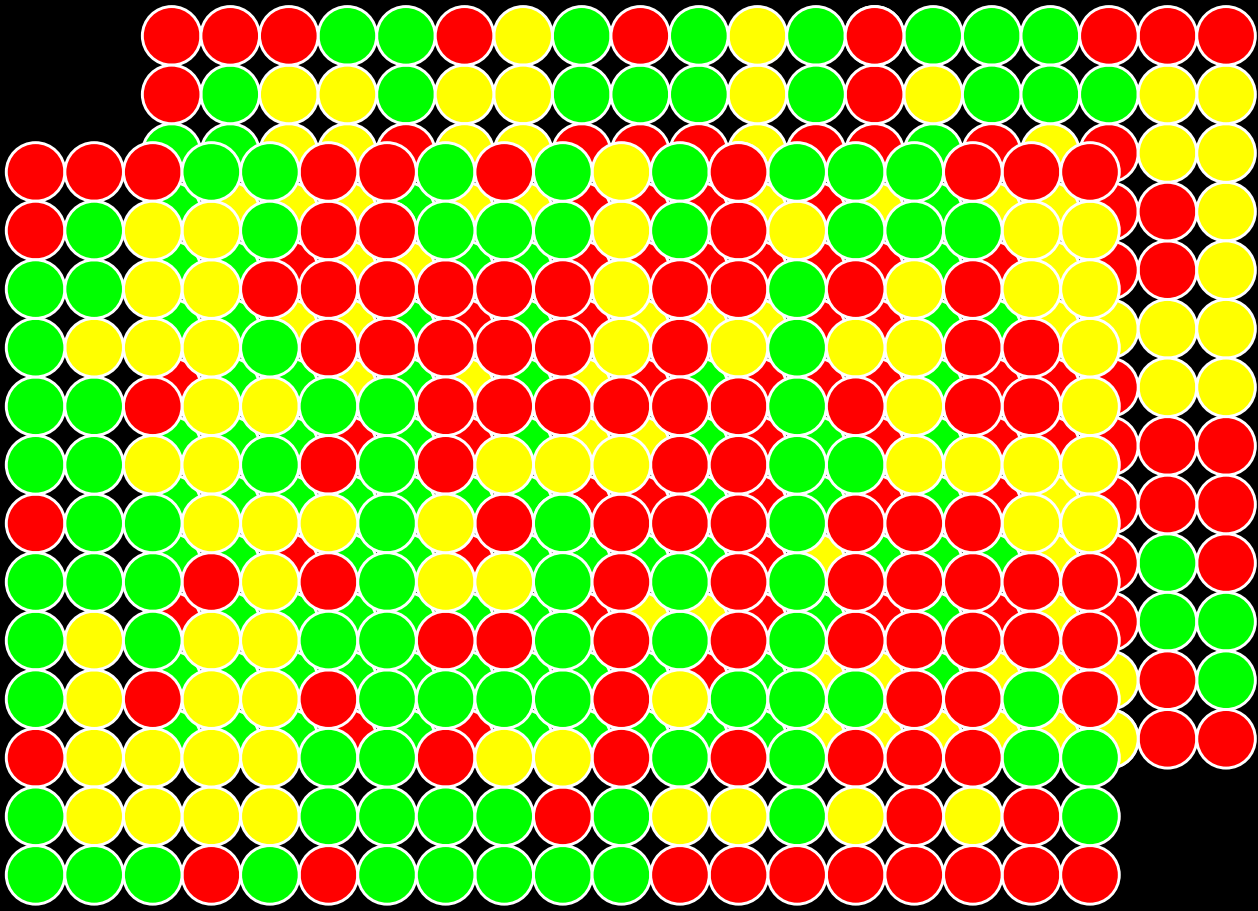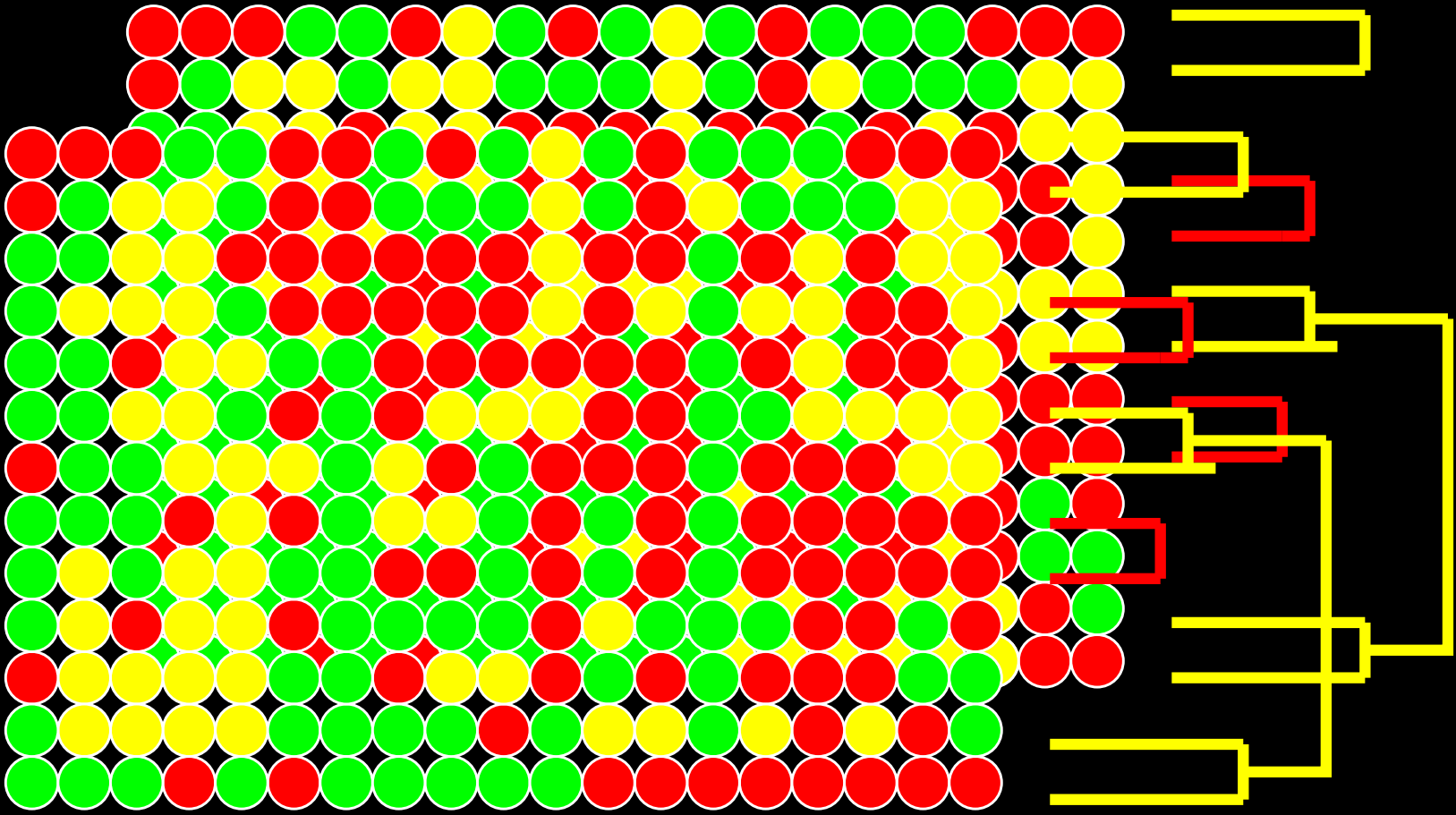
How can abstract mathematics help?

- Decompositions that can be generalisable.
- Geometric Picture of Tree Space
  - ⋆ A space for comparisons.
  - ⋆ Ways of *projecting*.
  - ⋆ *Follow* trees as they change, (paths of trees)
  - ⋆ Centroids of trees
  - ⋆ Neighborhoods (convex hulls of trees)....
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- Justification of commonsense, ground for generalizations.

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