

Appendix 6 to:

Measures of Genetic Diversity

Applying the simple matching coefficient for morphological characters (categorical variables)

We have three characters:

- Leaf hairiness: rare (1), common (2), abundant (3)
- Petal colour: white (1), yellow (2), red (3)
- Petiole length: short (1), medium (2), long (3)

We first transform the measurement data to binary data. Note that the three original characters are transformed into 9 binary characters. This could overweight these characters in detriment to others used in the analysis.

	Character 1			Character 2			Character 3		
OTU 1	2			1			2		
OTU 2	2			3			3		
OTU 3	1			2			1		
OTU 4	3			3			1		
	Character 1 (binary code)			Character 2 (binary code)			Character 3 (binary code)		
	Rare	Common	Abundant	White	Yellow	Red	Short	Medium	Long
OTU 1	0	1	0	1	0	0	0	1	0
OTU 2	0	1	0	0	0	1	0	0	1
OTU 3	1	0	0	0	1	0	1	0	0
OTU 4	0	0	1	0	0	1	1	0	0

We then apply the simple matching coefficient to calculate the pairwise distances between individuals:

Pairwise comparisons for all characters									
OTU 1 vs. 2	1	0	OTU 1 vs. 3	1	0	OTU 1 vs. 4	1	0	
1	a = 1	b = 2	1	a = 0	b = 3	1	a = 0	b = 3	
0	c = 2	d = 4	0	c = 3	d = 3	0	c = 3	d = 3	
OTU 2 vs. 3	1	0	OTU 2 vs. 4	1	0	OTU 3 vs. 4	1	0	
1	a = 0	b = 3	1	a = 1	b = 2	1	a = 1	b = 2	
0	c = 3	d = 3	0	c = 2	d = 4	0	c = 2	d = 4	

Now we can proceed with the methodology to find groups and draw the corresponding phenogram:

	O1	O2	O3	O4
O1	0			
O2	0.56	0		
O3	0.33	0.33	0	
O4	0.33	0.56	0.56	0

