

Your Job ID is 1627484904, the files will be deleted in **7 days**

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Download (results_all.zip) all tables and plots

Dataset Name: seflPastQ.zip

Data Summary:

#	Files	K	Individuals	Populations(Groups)
	400	8	36	5

Puechmaille Method

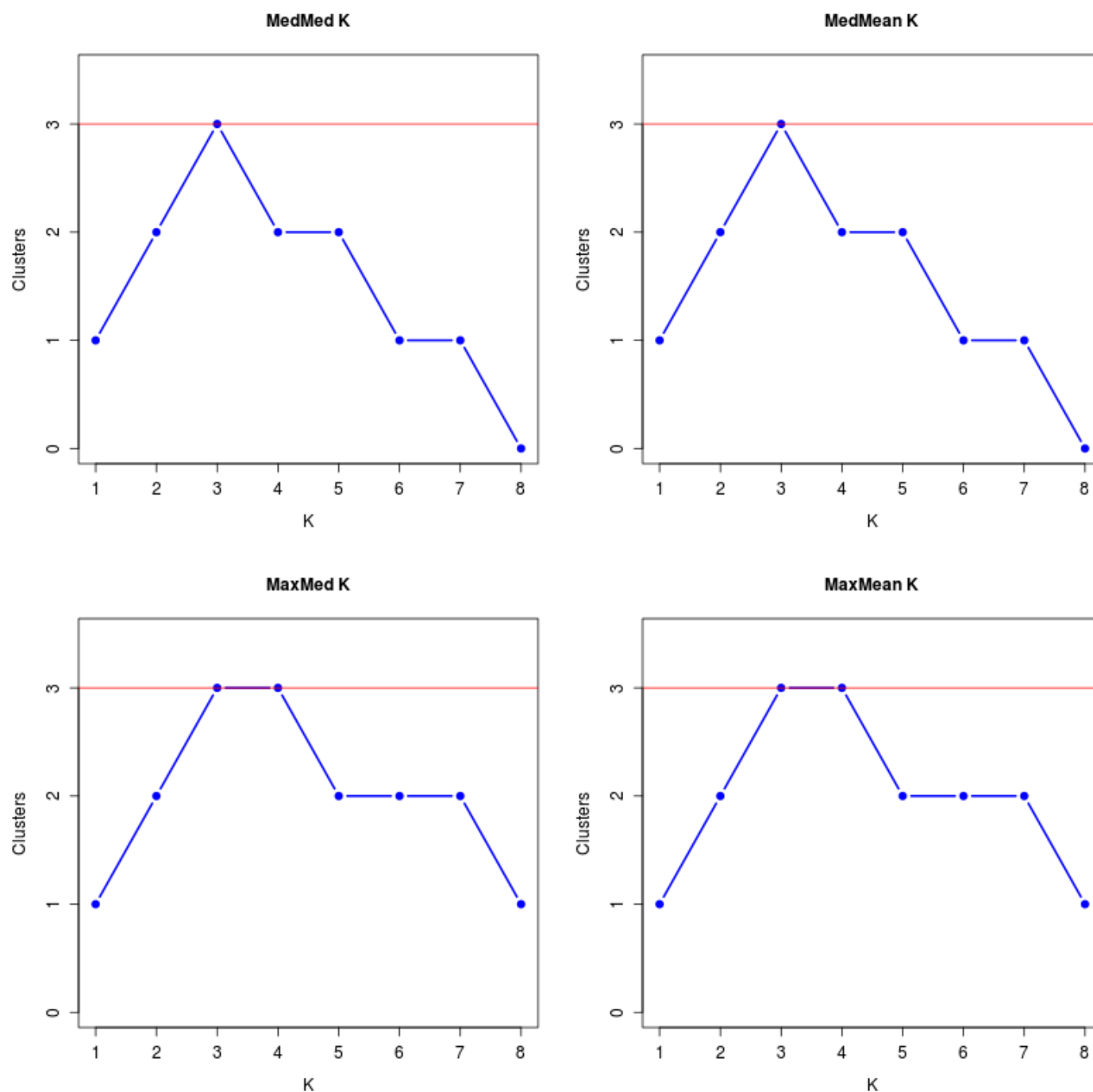
— Puechmaille SJ (2016) The program structure does not reliably recover the correct population structure when sampling is uneven: subsampling and new estimators alleviate the problem. *Molecular Ecology Resources*, 16:608–627. [link (<http://dx.doi.org/10.1111/1755-0998.12512>)]

MedMeaK, MaxMeaK, MedMedK, MaxMedK (Threshold=0.5):

The optimal K (Y-axis) after removing spurious clusters are indicated by red lines, i.e. the number of clusters (used to explain predefined 5 populations).

K	MedMed	MedMean	MaxMed	MaxMean	Reps
1	1	1	1	1	50
2	2	2	2	2	50
3	3	3	3	3	50
4	2	2	3	3	50
5	2	2	2	2	50
6	1	1	2	2	50
7	1	1	2	2	50
8	0	0	1	1	50
MedMedK		MedMeaK	MaxMedK	MaxMeaK	
3		3	3	3	

download table 1627484904.MedK.0.5.tsv (1627484904.MedK.0.5.tsv)



download plots 1627484904.MedK.0.5.pdf (1627484904.MedK.0.5.pdf)

Choose K Method

— Raj A, Stephens M, Pritchard JK (2014) fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. *Genetics*, 197:573-589. [link (<https://doi.org/10.1534/genetics.114.164350>)]

- Model components used to explain structure in data is 1

Select specific K =

1



to generate graphical representations

Advanced Options

Email: (Fill this if you want to run CLUMPAK on all K)

Run

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