####### 5S-Eukaryota-aspralign #######

Method: single

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: complete

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: average

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

####### 5S-Eukaryota-pskorder #######

Reading 5S-Eukaryota-pskorder.csv ...

Method: single

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: complete

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: average

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

####### 5S-Eukaryota-genus #######

Reading 5S-Eukaryota-genus.csv ...

Method: single

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: complete

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: average

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

####### 5S-Eukaryota-psmalign #######

Method: single

Rand\_score 0.5686944634313056

Homogeneity\_score 0.26931300474761116

completeness\_score 0.7250175065750913

Method: complete

Rand\_score 0.9015721120984279

Homogeneity\_score 0.7839761640487695

completeness\_score 0.8709426418207984

Method: average

Rand\_score 0.7997265892002734

Homogeneity\_score 0.5761851827262697

completeness\_score 0.8405782170556084

####### 5S-Eukaryota-eigevalues #######

Method: single

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: complete

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

Method: average

Rand\_score 0.48564593301435405

Homogeneity\_score 0.09277817447592267

completeness\_score 0.32269299110875166

####### 16S-Eukaryota-aspralign #######

Method: single

Rand\_score 0.45709165386584744

Homogeneity\_score 0.2311863130870707

completeness\_score 0.5596395183633724

Method: complete

Rand\_score 0.7679723502304148

Homogeneity\_score 0.4741319447881433

completeness\_score 0.5203028676277968

Method: average

Rand\_score 0.7292882744495648

Homogeneity\_score 0.38029675035697125

completeness\_score 0.4834468514134316

####### 16S-Eukaryota-pskorder #######

Method: single

Rand\_score 0.23719918074756785

Homogeneity\_score 0.06567584408404563

completeness\_score 0.4083625431118507

Method: complete

Rand\_score 0.24841269841269842

Homogeneity\_score 0.07402549862093497

completeness\_score 0.4159410035996125

Method: average

Rand\_score 0.24841269841269842

Homogeneity\_score 0.07402549862093497

completeness\_score 0.4159410035996125

####### 16S-Eukaryota-genus #######

Method: single

Rand\_score 0.41036866359447005

Homogeneity\_score 0.10967638796566155

completeness\_score 0.2964705239885618

Method: complete

Rand\_score 0.4510752688172043

Homogeneity\_score 0.12360746570741526

completeness\_score 0.2975292034003028

Method: average

Rand\_score 0.4510752688172043

Homogeneity\_score 0.12360746570741526

completeness\_score 0.2975292034003028

####### 16S-Eukaryota-psmalign #######

Method: single

Rand\_score 0.4500768049155146

Homogeneity\_score 0.23376652928419736

completeness\_score 0.5910051155701137

Method: complete

Rand\_score 0.7337173579109063

Homogeneity\_score 0.45479835686182796

completeness\_score 0.4761965955775013

Method: average

Rand\_score 0.6882488479262673

Homogeneity\_score 0.33183770016110675

completeness\_score 0.49909585080568986

####### 16S-Eukaryota-eigevalues #######

Method: single

Rand\_score 0.6107270865335381

Homogeneity\_score 0.2227093950618926

completeness\_score 0.3184572562645185

Method: complete

Rand\_score 0.782642089093702

Homogeneity\_score 0.31016541990978125

completeness\_score 0.2802503676530229

Method: average

Rand\_score 0.7610343061955965

Homogeneity\_score 0.2947779338472894

completeness\_score 0.28168511173494487

####### 23S-Eukaryota-aspralign #######

Method: single

Rand\_score 0.8428571428571429

Homogeneity\_score 0.6760692642994329

completeness\_score 0.7261452444281522

Method: complete

Rand\_score 0.8571428571428571

Homogeneity\_score 0.6666666666666665

completeness\_score 0.6887679639802641

Method: average

Rand\_score 0.8428571428571429

Homogeneity\_score 0.6760692642994329

completeness\_score 0.7261452444281521

####### 23S-Eukaryota-pskorder #######

Method: single

Rand\_score 0.6952380952380952

Homogeneity\_score 0.4976874119776542

completeness\_score 0.5457941994445151

Method: complete

Rand\_score 0.6952380952380952

Homogeneity\_score 0.44469016737045663

completeness\_score 0.46739947063557424

Method: average

Rand\_score 0.6952380952380952

Homogeneity\_score 0.44469016737045663

completeness\_score 0.46739947063557424

####### 23S-Eukaryota-genus #######

Method: single

Rand\_score 0.7761904761904762

Homogeneity\_score 0.6009841443811977

completeness\_score 0.5512397406918308

Method: complete

Rand\_score 0.7761904761904762

Homogeneity\_score 0.6009841443811977

completeness\_score 0.5512397406918308

Method: average

Rand\_score 0.7761904761904762

Homogeneity\_score 0.6009841443811977

completeness\_score 0.5512397406918308

####### 23S-Eukaryota-psmalign #######

Method: single

Rand\_score 0.8285714285714286

Homogeneity\_score 0.5750832101247305

completeness\_score 0.6044513859461677

Method: complete

Rand\_score 0.8571428571428571

Homogeneity\_score 0.6501683300429656

completeness\_score 0.6833709301085988

Method: average

Rand\_score 0.8571428571428571

Homogeneity\_score 0.6501683300429656

completeness\_score 0.6833709301085988

####### 23S-Eukaryota-eigevalues #######

Method: single

Rand\_score 0.8

Homogeneity\_score 0.5712701511793005

completeness\_score 0.6547393905627992

Method: complete

Rand\_score 0.8095238095238095

Homogeneity\_score 0.5363371134725897

completeness\_score 0.5593001748419704

Method: average

Rand\_score 0.8095238095238095

Homogeneity\_score 0.5363371134725897

completeness\_score 0.5593001748419704