####### 5S-Archaea-**aspralign** #######

Method: single

Rand\_score 0.48

Homogeneity\_score 0.16445092468173897

completeness\_score 0.1304306764935216

Method: complete

Rand\_score 0.48

Homogeneity\_score 0.16445092468173897

completeness\_score 0.1304306764935216

Method: average

Rand\_score 0.48

Homogeneity\_score 0.16445092468173897

completeness\_score 0.1304306764935216

####### 5S-Archaea-**pskorder** #######

Method: single

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

Method: complete

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

Method: average

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

####### 5S-Archaea-**genus** #######

Method: single

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

Method: complete

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

Method: average

Rand\_score 0.6307692307692307

Homogeneity\_score 0.017149800160651887

completeness\_score 0.051500001379812754

####### 5S-Archaea-**psmalign** #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 5S-Archaea-eigevalues #######

Method: single

Rand\_score 0.676923076923077

Homogeneity\_score 0.04152823359566809

completeness\_score 0.07496689552225827

Method: complete

Rand\_score 0.676923076923077

Homogeneity\_score 0.04152823359566809

completeness\_score 0.07496689552225827

Method: average

Rand\_score 0.676923076923077

Homogeneity\_score 0.04152823359566809

completeness\_score 0.07496689552225827

####### 16S-Archaea-aspralign #######

Method: single

Rand\_score 0.9202898550724637

Homogeneity\_score 0.8331194079063331

completeness\_score 0.7775065845637619

Method: complete

Rand\_score 0.7463768115942029

Homogeneity\_score 0.8331194079063327

completeness\_score 0.5592776690565153

Method: average

Rand\_score 0.7463768115942029

Homogeneity\_score 0.8331194079063327

completeness\_score 0.5592776690565153

####### 16S-Archaea-pskorder #######

Method: single

Rand\_score 0.6014492753623188

Homogeneity\_score 0.11767594982769965

completeness\_score 0.23049559089177296

Method: complete

Rand\_score 0.6014492753623188

Homogeneity\_score 0.11767594982769965

completeness\_score 0.23049559089177296

Method: average

Rand\_score 0.6014492753623188

Homogeneity\_score 0.11767594982769965

completeness\_score 0.23049559089177296

####### 16S-Archaea-genus #######

Method: single

Rand\_score 0.5144927536231884

Homogeneity\_score 0.037352338210363656

completeness\_score 0.07316320182325417

Method: complete

Rand\_score 0.5652173913043478

Homogeneity\_score 0.1340194757177395

completeness\_score 0.19823149231282688

Method: average

Rand\_score 0.5652173913043478

Homogeneity\_score 0.1340194757177395

completeness\_score 0.19823149231282688

####### 16S-Archaea-psmalign #######

Method: single

Rand\_score 0.5942028985507246

Homogeneity\_score 0.2884702863250979

completeness\_score 0.42668347297946835

Method: complete

Rand\_score 0.7210144927536232

Homogeneity\_score 0.8331194079063324

completeness\_score 0.5408520829727549

Method: average

Rand\_score 0.4311594202898551

Homogeneity\_score 0.17969984895821217

completeness\_score 0.14720751150995967

####### 16S-Archaea-eigevalues #######

Rand\_score 0.5471014492753623

Homogeneity\_score 0.1277790936129017

completeness\_score 0.0994137925353896

Method: complete

Rand\_score 0.5471014492753623

Homogeneity\_score 0.1277790936129017

completeness\_score 0.0994137925353896

Method: average

Rand\_score 0.5471014492753623

Homogeneity\_score 0.1277790936129017

completeness\_score 0.0994137925353896

####### 23S-Archaea-aspralign #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 23S-Archaea-pskorder #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 23S-Archaea-genus #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 23S-Archaea-psmalign #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 23S-Archaea-eigevalues #######

Method: single

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: complete

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

Method: average

Rand\_score 1.0

Homogeneity\_score 1.0

completeness\_score 1.0

####### 5S-Bacteria-aspralign #######

Method: single

Rand\_score 0.5529175050301811

Homogeneity\_score 0.18073456660159648

completeness\_score 0.4626212981445627

Method: complete

Rand\_score 0.7090543259557344

Homogeneity\_score 0.4551692141619585

completeness\_score 0.602272969566192

Method: average

Rand\_score 0.7090543259557344

Homogeneity\_score 0.4551692141619584

completeness\_score 0.602272969566192

####### 5S-Bacteria-pskorder #######

Method: single

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: complete

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: average

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

####### 5S-Bacteria-genus #######

Method: single

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: complete

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: average

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

####### 5S-Bacteria-psmalign #######

Method: single

Rand\_score 0.7476861167002012

Homogeneity\_score 0.5569767655811528

completeness\_score 0.7196911632891175

Method: complete

Rand\_score 0.929979879275654

Homogeneity\_score 0.8542496297556706

completeness\_score 0.8156210364501525

Method: average

Rand\_score 0.8297786720321931

Homogeneity\_score 0.6999999890933517

completeness\_score 0.783776866149487

####### 5S-Bacteria-eigevalues #######

Method: single

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: complete

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

Method: average

Rand\_score 0.42334004024144867

Homogeneity\_score 0.030934202035020876

completeness\_score 0.07918142595297606

####### 16S-Bacteria-aspralign #######

Method: single

Rand\_score 0.46145728643216083

Homogeneity\_score 0.2764155680473436

completeness\_score 0.5641430868416992

Method: complete

Rand\_score 0.8179396984924623

Homogeneity\_score 0.6840400443629563

completeness\_score 0.5824012865799807

Method: average

Rand\_score 0.82321608040201

Homogeneity\_score 0.6605102152073611

completeness\_score 0.6131245192673109

####### 16S-Bacteria-pskorder #######

Method: single

Rand\_score 0.3024120603015075

Homogeneity\_score 0.07355571504234057

completeness\_score 0.2792971795181419

Method: complete

Rand\_score 0.3024120603015075

Homogeneity\_score 0.07355571504234057

completeness\_score 0.2792971795181419

Method: average

Rand\_score 0.3024120603015075

Homogeneity\_score 0.07355571504234057

completeness\_score 0.2792971795181419

####### 16S-Bacteria-genus #######

Method: single

Rand\_score 0.40733668341708545

Homogeneity\_score 0.09983866588126618

completeness\_score 0.20620720537595327

Method: complete

Rand\_score 0.45256281407035176

Homogeneity\_score 0.14574744915515345

completeness\_score 0.27164905133901884

Method: average

Rand\_score 0.45256281407035176

Homogeneity\_score 0.14574744915515345

completeness\_score 0.27164905133901884

####### 16S-Bacteria-psmalign #######

Method: single

Rand\_score 0.4949246231155779

Homogeneity\_score 0.35739359443662366

completeness\_score 0.8432382514557765

Method: complete

Rand\_score 0.8466834170854272

Homogeneity\_score 0.8112186885235896

completeness\_score 0.6308516270110918

Method: average

Rand\_score 0.7587437185929649

Homogeneity\_score 0.6181210851619614

completeness\_score 0.713472058488121

####### 16S-Bacteria-eigevalues #######

Method: single

Rand\_score 0.6959296482412061

Homogeneity\_score 0.23968606779491505

completeness\_score 0.2146656835458438

Method: complete

Rand\_score 0.7071356783919598

Homogeneity\_score 0.2530677233226602

completeness\_score 0.21255168157892046

Method: average

Rand\_score 0.7042211055276382

Homogeneity\_score 0.24660149248078836

completeness\_score 0.2101892688874817

####### 23S-Bacteriaa-aspralign #######

Method: single

Rand\_score 0.4274640088593577

Homogeneity\_score 0.21003750295377194

completeness\_score 0.4710271908025647

Method: complete

Rand\_score 0.8349944629014396

Homogeneity\_score 0.6598700951203536

completeness\_score 0.6849792905216411

Method: average

Rand\_score 0.5016611295681063

Homogeneity\_score 0.30311087712860973

completeness\_score 0.553847399495723

####### 23S-Bacteria-pskorder #######

Method: single

Rand\_score 0.44518272425249167

Homogeneity\_score 0.19082713831329973

completeness\_score 0.42794629351687336

Method: complete

Rand\_score 0.44739756367663347

Homogeneity\_score 0.16238125298649841

completeness\_score 0.30127111475474533

Method: average

Rand\_score 0.44739756367663347

Homogeneity\_score 0.16238125298649841

completeness\_score 0.30127111475474533

####### 23S-Bacteria-genus #######

Method: single

Rand\_score 0.4318936877076412

Homogeneity\_score 0.18416826200382552

completeness\_score 0.4130131898670756

Method: complete

Rand\_score 0.44629014396456257

Homogeneity\_score 0.18050545157965572

completeness\_score 0.3633229175084606

Method: average

Rand\_score 0.44629014396456257

Homogeneity\_score 0.18050545157965572

completeness\_score 0.3633229175084606

####### 23S-Bacteria-psmalign #######

Method: single

Rand\_score 0.8084163898117387

Homogeneity\_score 0.6749791744423378

completeness\_score 0.7464723008145635

Method: complete

Rand\_score 0.8970099667774086

Homogeneity\_score 0.8709633725236959

completeness\_score 0.8140322805751424

Method: average

Rand\_score 0.8504983388704319

Homogeneity\_score 0.7780514248683934

completeness\_score 0.7963473497294369

####### 23S-Bacteria-eigevalues #######

Method: single

Rand\_score 0.583610188261351

Homogeneity\_score 0.2161933823099246

completeness\_score 0.22963103460946435

Method: complete

Rand\_score 0.5913621262458472

Homogeneity\_score 0.22339298193595716

completeness\_score 0.22007585490161516

Method: average

Rand\_score 0.5913621262458472

Homogeneity\_score 0.2233929819359571

completeness\_score 0.22007585490161516

####### 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