Harvard Forest Data Archive HF239-03

Data File:

Name = hf239-03-estimate-s.csv
Description = estimate-s output
Rows = 744 Columns = 49
MD5 checksum = 2f651a31c82b5cd9877129f3a2c10f5a

Variables:

samples = number of sampling units accumulated (number)
individuals = [t/T]*N, where T is the number of sampling units in the reference sample and N is the total number of individuals in all T samples (makes sense for sample-based abundance date only) (number)
s.est = expected number of species in t pooled samples, given the reference sample (analytical) (number)
s.est.95ci.lower.bound = lower bound of 95% Confidence Interval for S(est) (dimensionless)
s.est.95ci.upper.bound = upper bound of 95% Confidence Interval for S(est) (dimensionless)
s.est.sd = standard deviation of S(est) (analytical) (SD = SE) (dimensionless)
s.mean = number of species in t pooled samples, given the reference sample (mean among runs) (dimensionless)
singletons.mean = number of singletons (species with only one individual) in t pooled samples or among m individuals (mean among runs) (number)
singletons.sd = standard deviation of Singletons, among randomizations of sample order (dimensionless)
doubletons.mean = number of doubletons (species with only two individuals) in t pooled samples or among m individuals (mean among runs) (number)
doubletons.sd = standard deviation of doubletons, among randomizations of sample order (dimensionless)
uniques.mean = number of uniques (species that occur in a only one sample) in t pooled samples (mean among runs) (number)
uniques.sd = standard deviation of Uniques, among randomizations of sample order (dimensionless)
duplicates.mean = number of duplicates (species that occur in a only two samples) in t pooled samples (mean among runs) (number)
duplicates.sd = standard deviation of duplicates, among randomizations of sample order (dimensionless)
ace.mean = abundance coverage-based estimator of species richness (mean among runs) (dimensionless)
ace.sd = Standard deviation of ACE, among randomizations of sample order or individual order (dimensionless)
ice.mean = incidence coverage-based estimator of species richness (mean among runs) (dimensionless)
ice.sd = standard deviation of ICE, among randomizations of sample order (dimensionless)

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chao1.mean = chao 1 richness estimator (mean among runs)
   (dimensionless)
chao1.95ci.lower.bound = chao 1 log-linear confidence interval lower
   bound (mean among
 runs) (dimensionless)
chao1.95ci.upper.bound = chao 1 log-linear confidence interval upper
   bound (mean among
 runs) (dimensionless)
chao1.sd = chao 1 standard deviation (by Chao's formulas)
   (dimensionless)
chao2.mean = chao 2 richness estimator (mean among runs)
   (dimensionless)
chao2.95ci.lower.bound = chao 2 log-linear confidence interval lower
   bound (mean among
 runs) (dimensionless)
chao2.95ci.upper.bound = chao 2 log-linear confidence interval upper
   bound (mean among
 runs) (dimensionless)
chao2.sd = chao 2 standard deviation (by Chao's formula)
   (dimensionless)
jack.1.mean = first-order Jackknife richness estimator (mean among

   runs) (dimensionless)
jack1.sd = first-order Jackknife standard deviation (dimensionless)
jack2.mean = second-order Jackknife richness estimator (mean among

   runs) (dimensionless)
jack2.sd = standard deviation of Jack2, among randomizations of
   sample
 order (dimensionless)
bootstrap.mean = bootstrap richness estimator (mean among runs)
   (dimensionless)
bootstrap.sd = standard deviation of Bootstrap, among randomizations
   of sample
 order (dimensionless)
mmruns.mean = michaelis-Menten richness estimator: estimators
   averaged over
 randomizations (mean among runs) (dimensionless)
mmmeans = michaelis-Menten richness estimator: estimators computed
   once for
 analytica rarefaction curve, computed by Eq. 5 in Colwell et
   al. (2004) (dimensionless)
cole.rarefaction = coleman rarefaction (number of species expected
   in t pooled samples,
 assuming individuals distributed at random
   among samples) (number)
cole.sd = coleman standard deviation (analytical) (dimensionless)
alpha.mean = fisher's alpha diversity index (dimensionless)
alpha.sd = fisher's alpha standard deviation (dimensionless)
shannon.mean = shannon diversity index (mean among runs), natural

   logarithms (dimensionless)
shannon.sd = standard deviation of Shannon index among
   randomizations of sample
 order (dimensionless)
shannon.exp.mean = exponential Shannon diversity index (mean among

   runs) (dimensionless)
shannon.exp.sd = standard deviation of Exponential Shannon index
   among randomizations of
 sample order (dimensionless)
simpson.inv.mean = simpson (inverse) diversity index (mean among
   runs) (dimensionless)
simpson.inv.sd = standard deviation of Simpson (inverse) index among
   randomizations of
 sample order (dimensionless)
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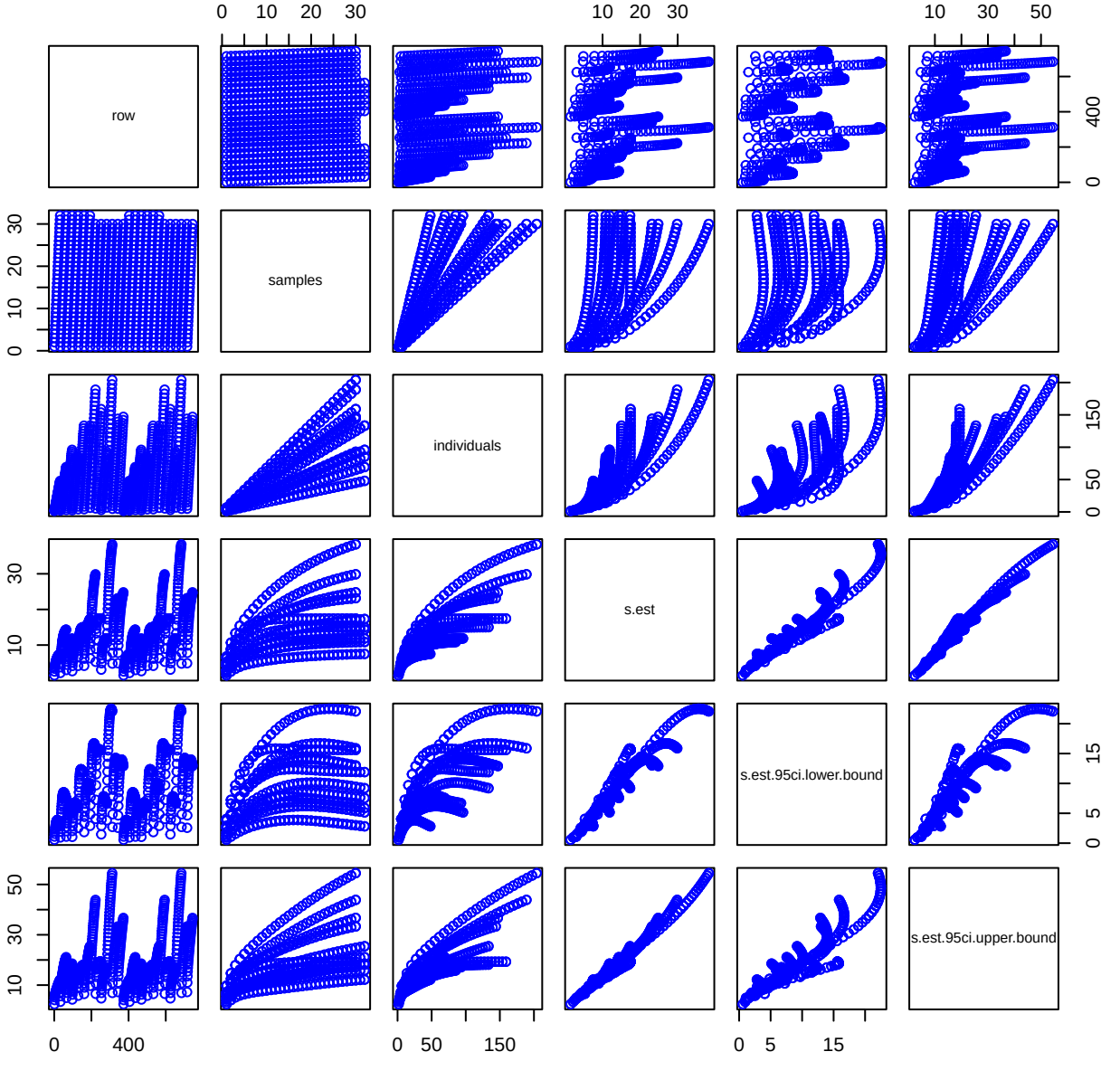
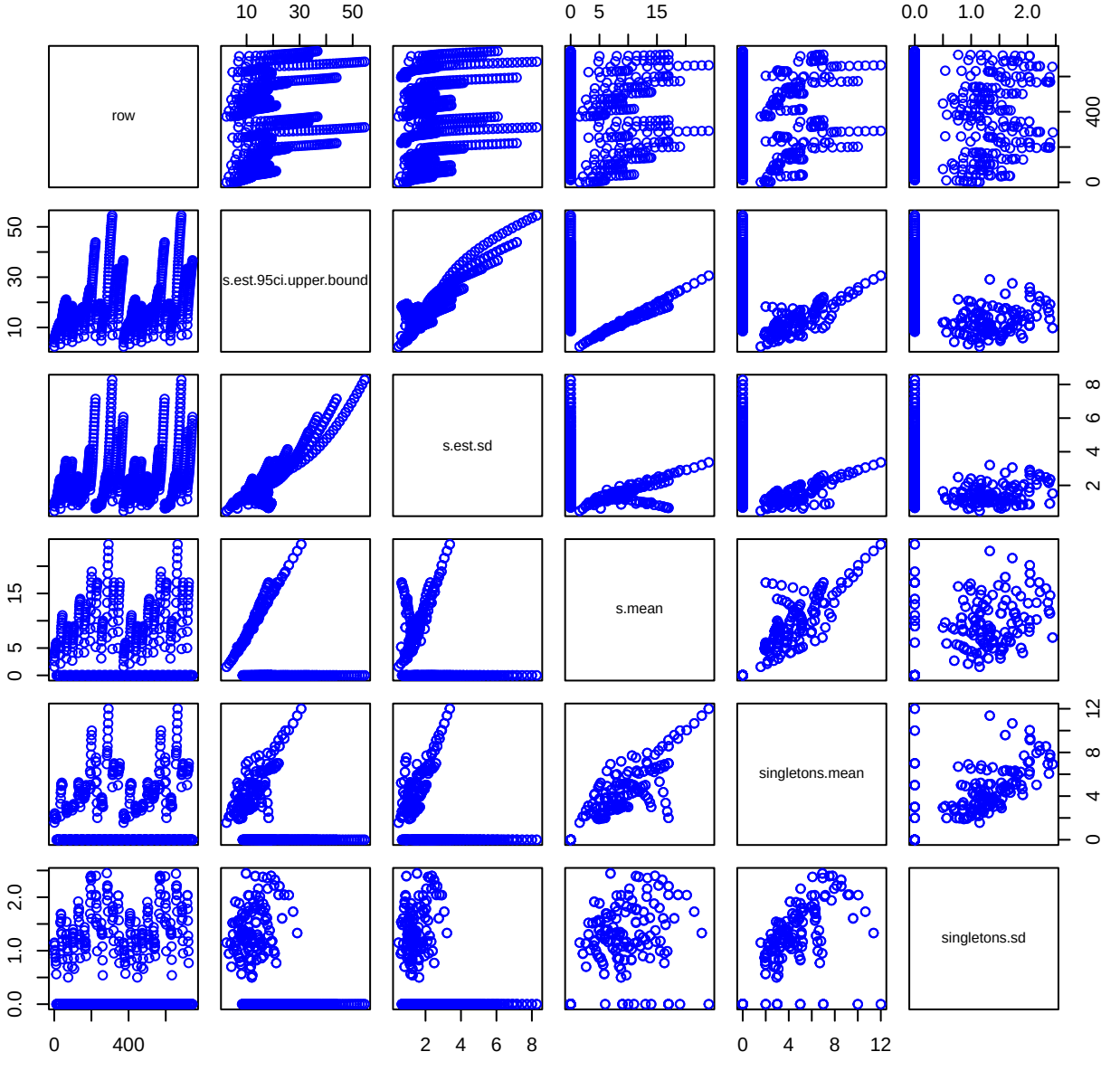
Variable	Min	Median	Mean	Max	NAs
samples	1.000	16.000	16.016	32.000	0
individuals	1.500	55.100	64.075	204.000	0
s.est	1.500	13.220	14.424	38.270	0
s.est.95ci.l	0.570	8.505	9.682	22.500	0
s.est.95ci.u	2.430	17.000	19.165	54.490	0
s.est.sd	0.480	2.010	2.419	8.270	0
s.mean	0.000	0.000	3.540	24.000	0
singletons.m	0.000	0.000	1.694	12.000	0
singletons.s	0.000	0.000	0.453	2.450	0
doubletons.m	0.000	0.000	0.720	5.780	0
doubletons.s	0.000	0.000	0.305	2.070	0
uniques.mean	0.000	0.000	1.694	12.000	0
uniques.sd	0.000	0.000	0.453	2.450	0
duplicates.m	0.000	0.000	0.720	5.780	0
duplicates.s	0.000	0.000	0.305	2.070	0
ace.mean	0.000	0.000	5.688	39.180	0
ace.sd	0.000	0.000	1.553	18.870	0
ice.mean	0.000	0.000	6.088	44.860	0
ice.sd	0.000	0.000	1.843	30.800	0
chao1.mean	0.000	0.000	5.727	49.040	0
chao1.95ci.l	0.000	0.000	3.937	29.630	0
chao1.95ci.u	0.000	0.000	15.921	177.540	0
chao1.sd	0.000	0.000	2.354	30.920	0
chao2.mean	0.000	0.000	5.174	46.430	0
chao2.95ci.l	0.000	0.000	3.850	29.130	0
chao2.95ci.u	0.000	0.000	13.161	157.980	0
chao2.sd	0.000	0.000	1.818	27.170	0
jack.1.mean	0.000	0.000	4.787	34.800	0
jack1.sd	0.000	0.000	0.543	3.790	0
jack2.mean	0.000	0.000	5.229	42.270	0
jack2.sd	0.000	0.000	0.881	5.730	0
bootstrap.me	0.000	0.000	4.114	28.550	0
bootstrap.sd	0.000	0.000	0.508	2.950	0
mmruns.mean	0.000	0.000	7.260	115.630	0
mmmeans	0.000	0.000	5.342	31.770	0
cole.rarefac	0.000	0.000	3.458	24.000	0
cole.sd	0.000	0.000	0.407	2.110	0
alpha.mean	0.000	0.000	0.000	0.000	0
alpha.sd	0.000	0.000	0.000	0.000	0
shannon.mean	0.000	0.000	0.000	0.000	0
shannon.sd	0.000	0.000	0.000	0.000	0
shannon.exp.	0.000	0.000	0.000	0.000	0
shannon.exp.	0.000	0.000	0.000	0.000	0
simpson.inv.	0.000	0.000	0.000	0.000	0
simpson.inv.	0.000	0.000	0.000	0.000	0

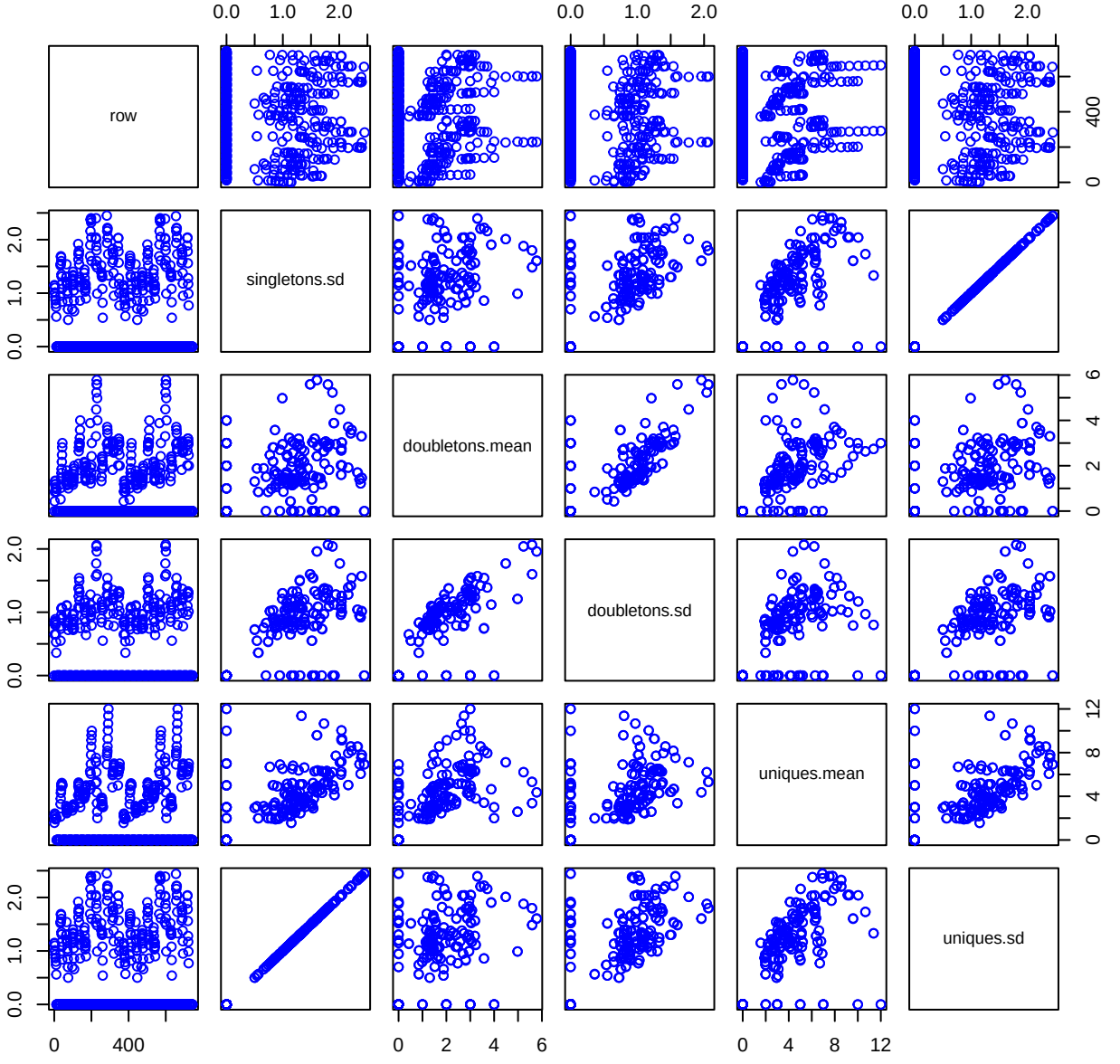
HF239−03 Plot 1



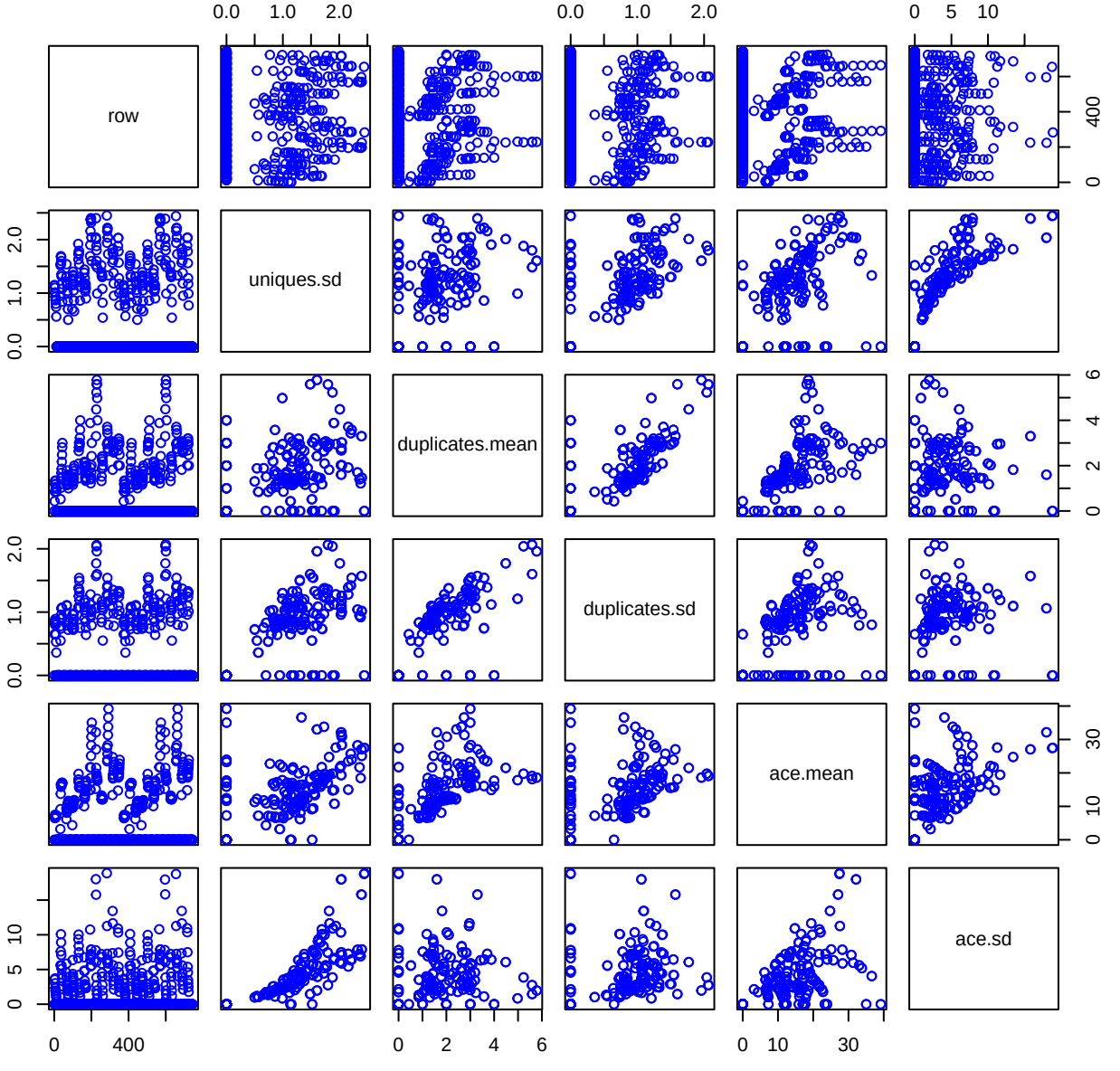
HF239−03 Plot 2



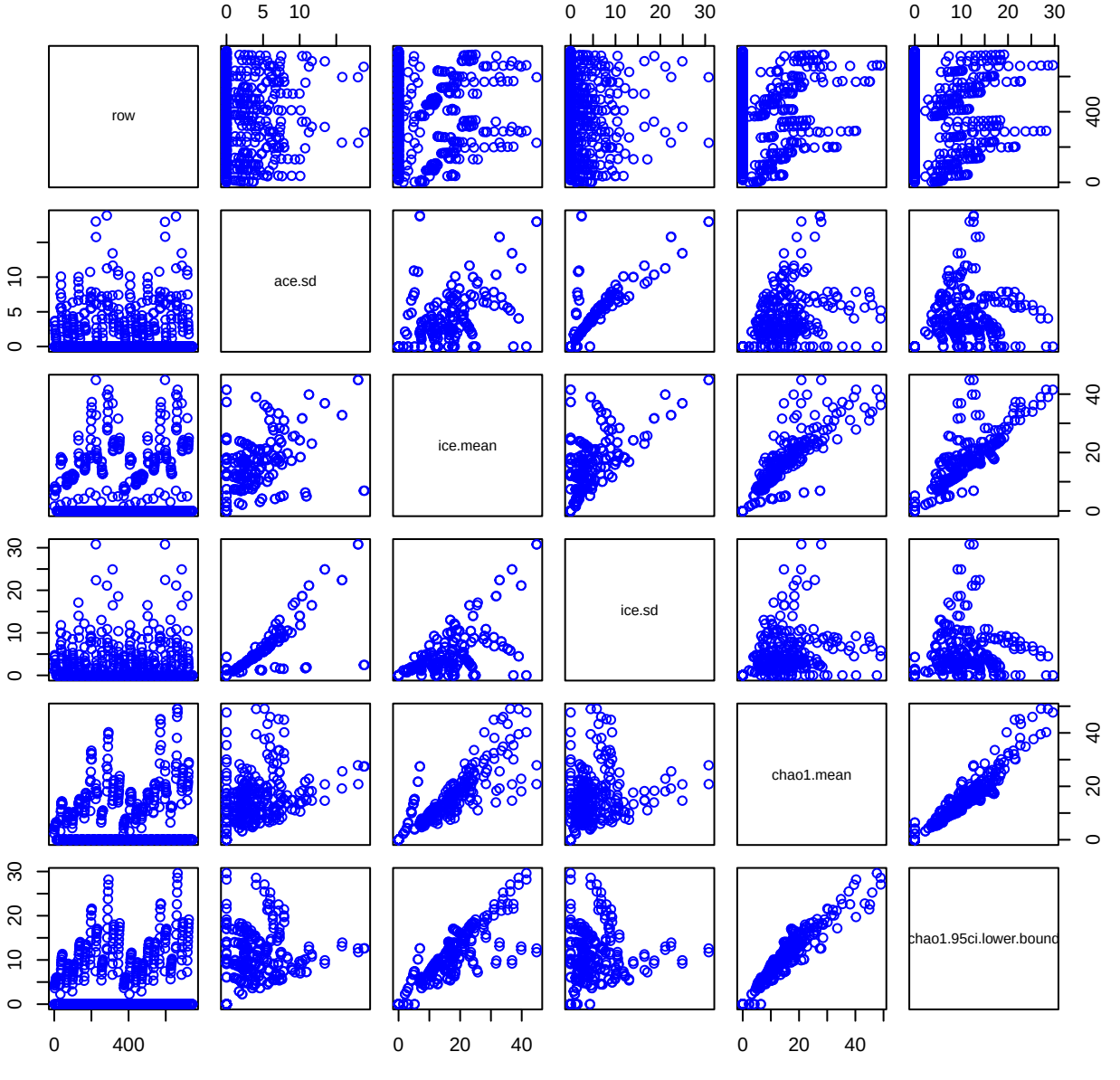
HF239−03 Plot 3



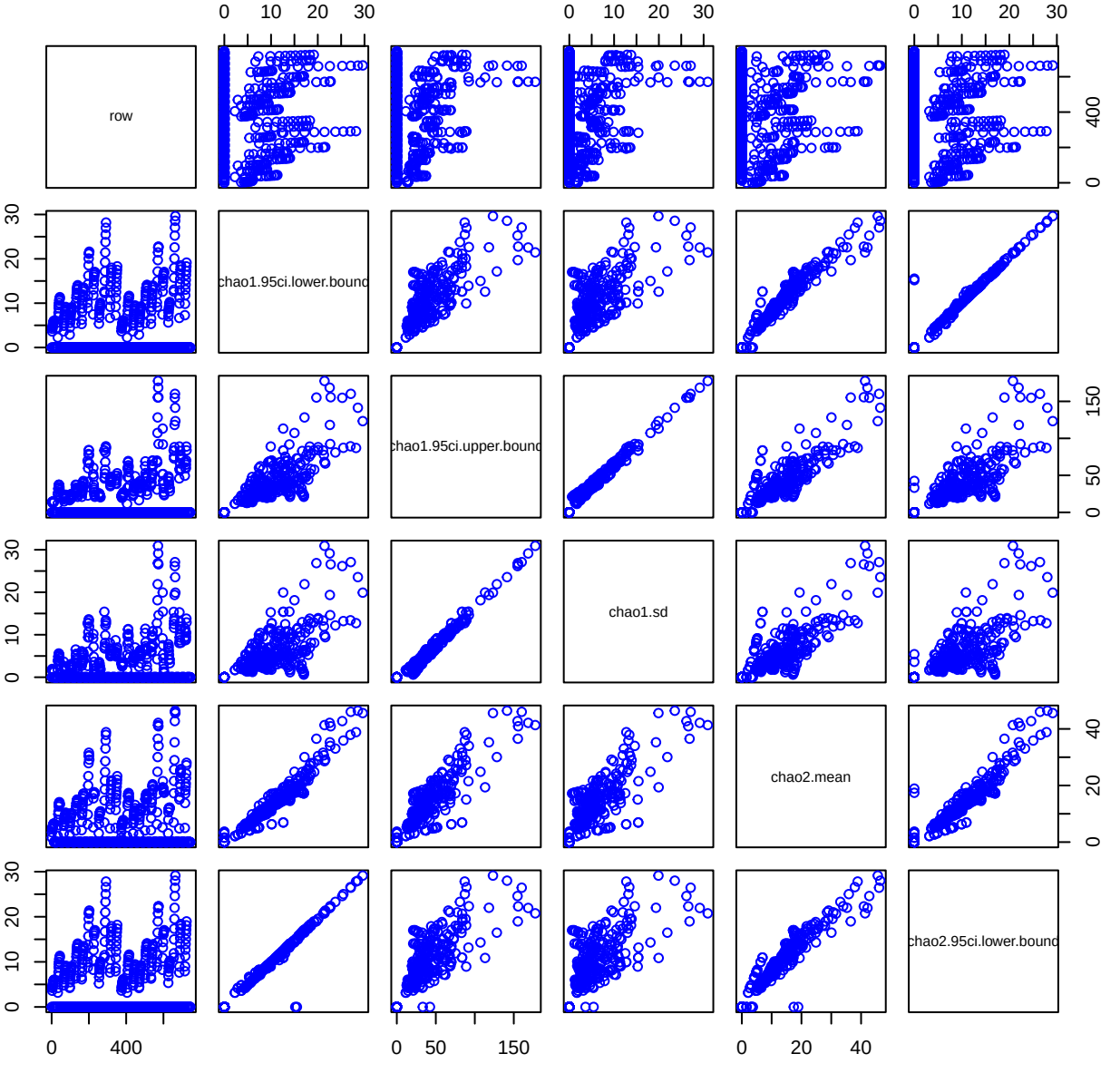
HF239−03 Plot 4



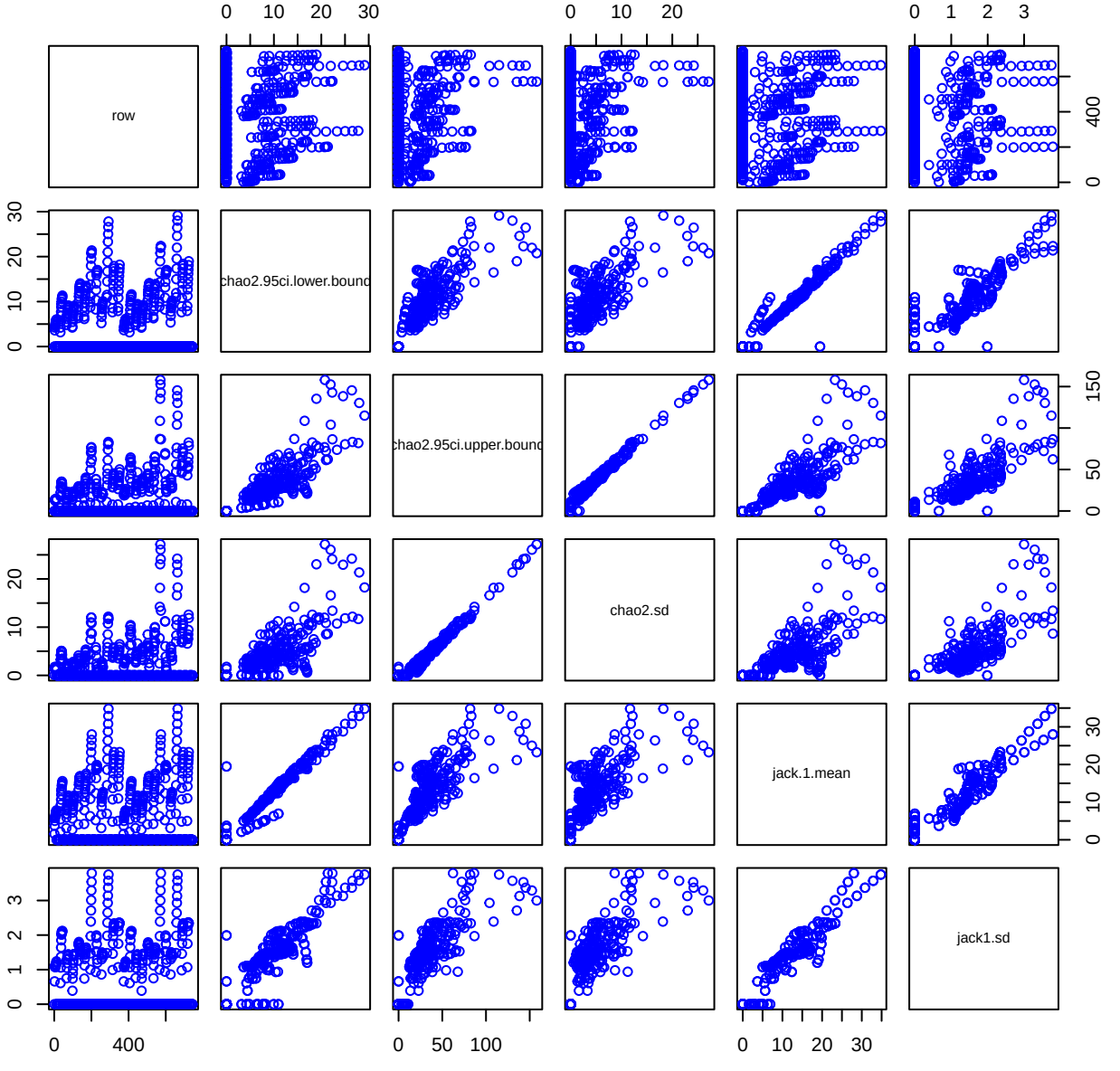
HF239−03 Plot 5



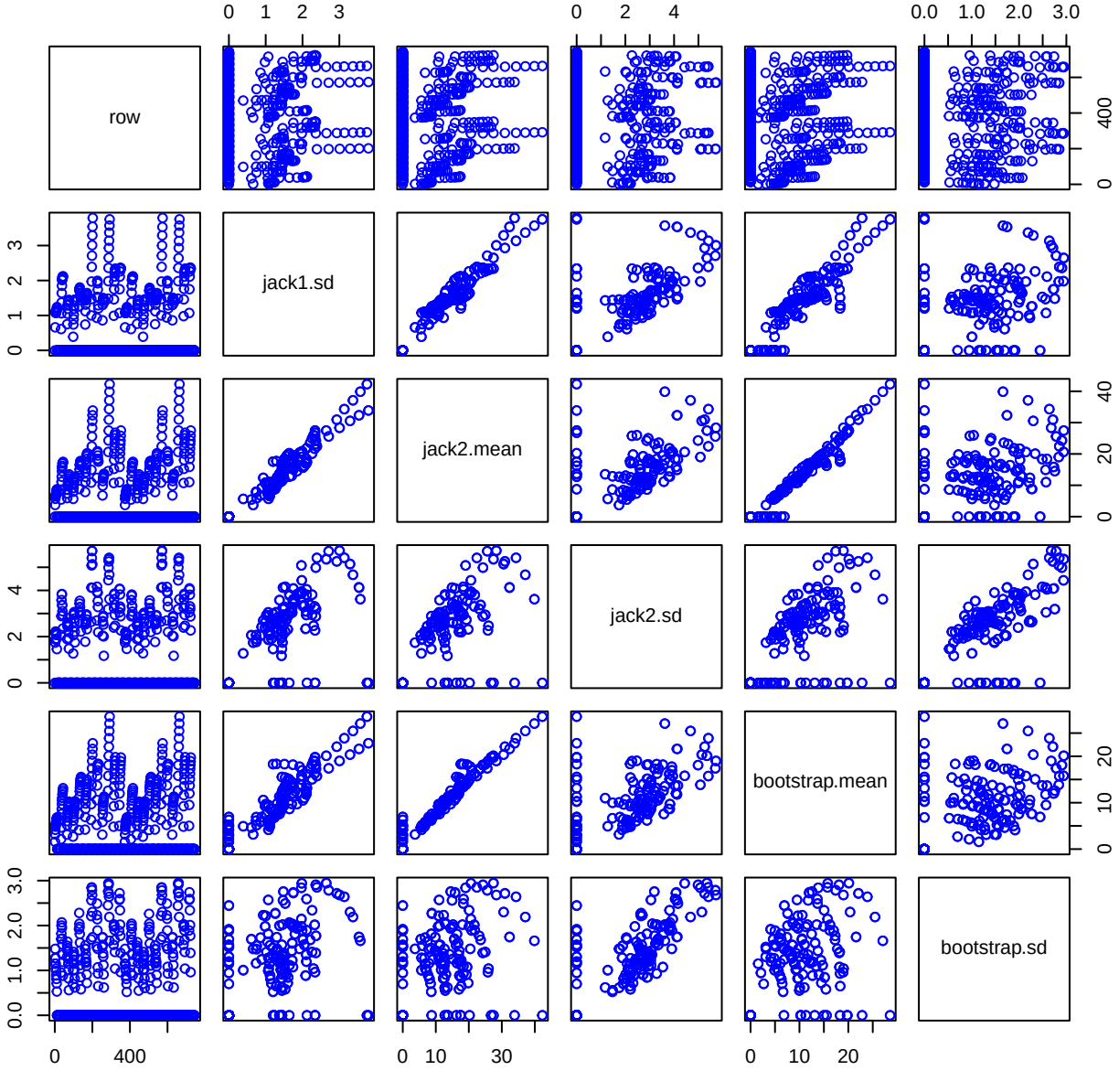
HF239−03 Plot 6



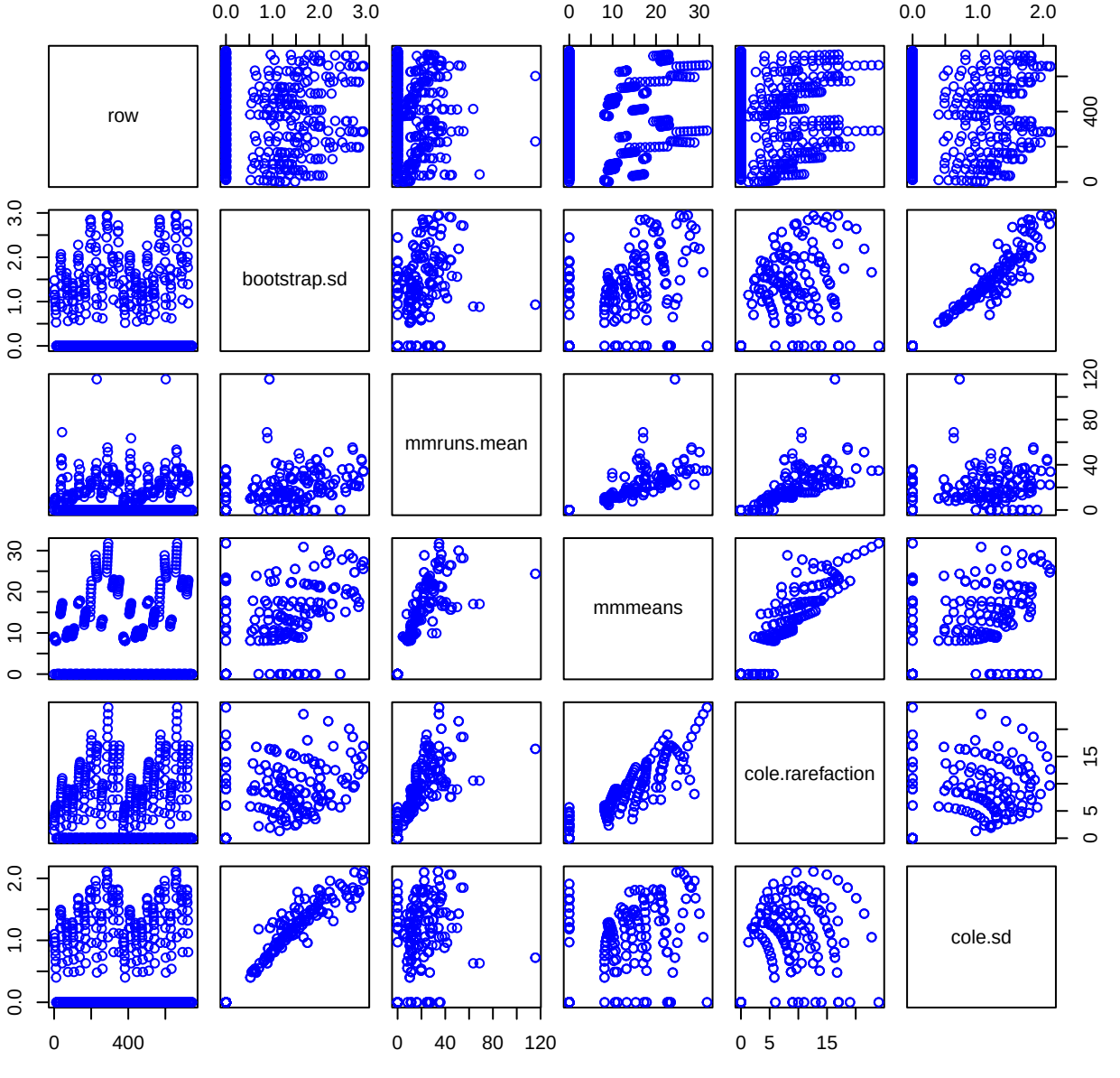
HF239−03 Plot 7



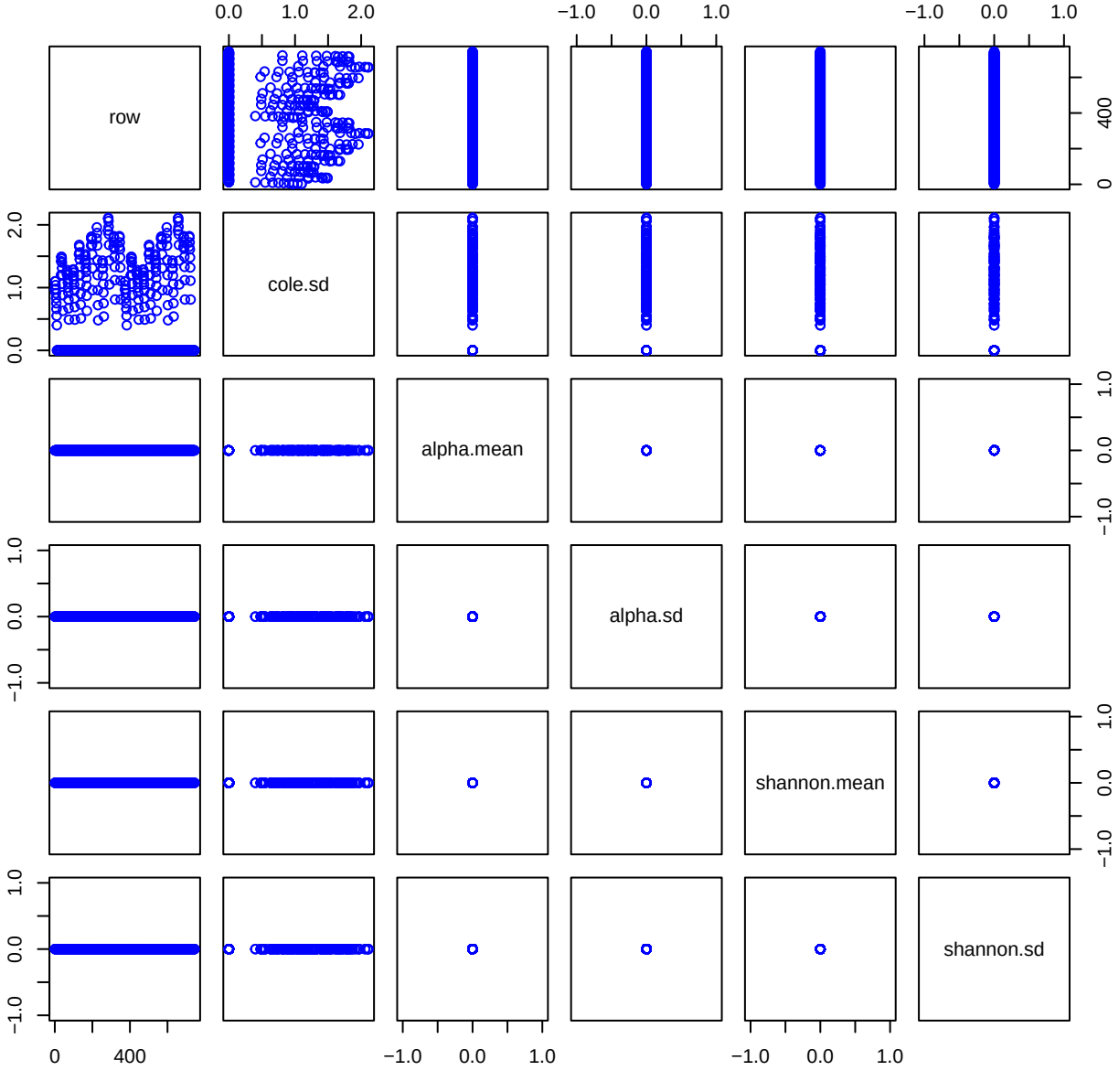
HF239−03 Plot 8



HF239−03 Plot 9



HF239−03 Plot 10



HF239−03 Plot 11