

Harvard Forest Data Archive HF351-01

Data File:

Name = hf351-01-community\_transect.txt  
Description = community transect  
Rows = 20 Columns = 69  
MD5 checksum = 801c78591c015f2f5ddf45af7770fe5d

Variables:

num = number (number)  
Distance = median of the detection distance of all colonies recorded  
in  
transect (centimeter)  
Colony = observed ant colony number in each transect (number)  
Richness = observed ant species richness in each transect (number)  
Ap.pil = *Apterostigma* gr. *pilosum* - number of colonies recorded in  
transect (number)  
Az.s01 = *Azteca* sp. 01 - number of colonies recorded in transect  
(number)  
Bl.bra = *Blepharidatta brasiliensis* - number of colonies recorded in  
transect (number)  
Br.M02 = *Brachymyrmex* MPEG 02 - number of colonies recorded in  
transect (number)  
Br.M03 = *Brachymyrmex* MPEG 03 - number of colonies recorded in  
transect (number)  
Ce.opa = *Cephalotes opacus* - number of colonies recorded in transect  
(number)  
Cr.bra = *Crematogaster brasiliensis* - number of colonies recorded in  
transect (number)  
Cr.fla = *Crematogaster flavosensitiva* - number of colonies recorded  
in transect (number)  
Cr.lev = *Crematogaster levior* - number of colonies recorded in  
transect (number)  
Cr.lim = *Crematogaster limata* - number of colonies recorded in  
transect (number)  
Cr.sot = *Crematogaster sotobosque* - number of colonies recorded in  
transect (number)  
Do.bis = *Dolichoderus bispinosus* - number of colonies recorded in  
transect (number)  
Ec.ede = *Ectatomma edentatum* - number of colonies recorded in  
transect (number)  
Ec.tub = *Ectatomma tuberculatum* - number of colonies recorded in  
transect (number)  
Gn.hor = *Gnamptogenys horni* - number of colonies recorded in  
transect (number)  
Ma.con = *Mayaponera constricta* - number of colonies recorded in  
transect (number)  
Ne.api = *Neoponera apicalis* - number of colonies recorded in  
transect (number)  
Ne.cre = *Neoponera crenata* - number of colonies recorded in transect  
(number)

Ne.ver = Neoponera verenae - number of colonies recorded in transect  
(number)

Ny.M01 = Nylanderia MPEG 01 - number of colonies recorded in  
transect (number)

Ny.M02 = Nylanderia MPEG 02 - number of colonies recorded in  
transect (number)

Ny.M03 = Nylanderia MPEG 03 - number of colonies recorded in  
transect (number)

Oc.neo = Ochetomyrmex neopolitus - number of colonies recorded in  
transect (number)

Oc.sem = Ochetomyrmex semipolitus - number of colonies recorded in  
transect (number)

Od.cae = Odontomachus caelatus - number of colonies recorded in  
transect (number)

Od.hem = Odontomachus hematodus - number of colonies recorded in  
transect (number)

Pa.bug = Paratrachymyrmex nr. bugnioni - number of colonies recorded  
in transect (number)

Pa.str = Pachycondyla striata - number of colonies recorded in  
transect (number)

Ph.a\_l = Pheidole aff. laidlowi - number of colonies recorded in  
transect (number)

Ph.ade = Pheidole ademonia - number of colonies recorded in transect  
(number)

Ph.ast = Pheidole astur - number of colonies recorded in transect  
(number)

Ph.bic = Pheidole biconstricta - number of colonies recorded in  
transect (number)

Ph.car = Pheidole aff. caribbaea - number of colonies recorded in  
transect (number)

Ph.cur = Pheidole cursor - number of colonies recorded in transect  
(number)

Ph.dis = Pheidole distorta - number of colonies recorded in transect  
(number)

Ph.fow = Pheidole fowleri - number of colonies recorded in transect  
(number)

Ph.fra = Pheidole fracticeps - number of colonies recorded in  
transect (number)

Ph.gau = Pheidole aff. gauthieri - number of colonies recorded in  
transect (number)

Ph.hua = Pheidole huacana - number of colonies recorded in transect  
(number)

Ph.jea = Pheidole jeannei - number of colonies recorded in transect  
(number)

Ph.leo = Pheidole nr. leonina - number of colonies recorded in  
transect (number)

Ph.lon = Pheidole longiseta - number of colonies recorded in  
transect (number)

Ph.mei = Pheidole meinerti - number of colonies recorded in transect  
(number)

Ph.moo = Pheidole nr. mooreorum - number of colonies recorded in  
transect (number)

Ph.p\_1 = Pheidole nr. longiseta - number of colonies recorded in transect (number)

Ph.par = Pheidole paraensis - number of colonies recorded in transect (number)

Ph.ped = Pheidole nr. pedana - number of colonies recorded in transect (number)

Ph.pyg = Pheidole pygmaea - number of colonies recorded in transect (number)

Ph.s03 = Pheidole sp. 03 - number of colonies recorded in transect (number)

Ph.s14 = Pheidole sp. 14 - number of colonies recorded in transect (number)

Ph.s16 = Pheidole sp. 16 - number of colonies recorded in transect (number)

Ph.sch = Pheidole schwarzmaieri - number of colonies recorded in transect (number)

Ph.sco = Pheidole scolioceps - number of colonies recorded in transect (number)

Ph.sen = Pheidole sensitiva - number of colonies recorded in transect (number)

Ph.sub = Pheidole subarmata - number of colonies recorded in transect (number)

Ph.tri = Pheidole triconstricta - number of colonies recorded in transect (number)

Ps.ten = Pseudomyrmex tenuis - number of colonies recorded in transect (number)

So.M01 = Solenopsis MPEG 01 - number of colonies recorded in transect (number)

So.M02 = Solenopsis MPEG 02 - number of colonies recorded in transect (number)

So.M03 = Solenopsis MPEG 03 - number of colonies recorded in transect (number)

So.M07 = Solenopsis MPEG 07 - number of colonies recorded in transect (number)

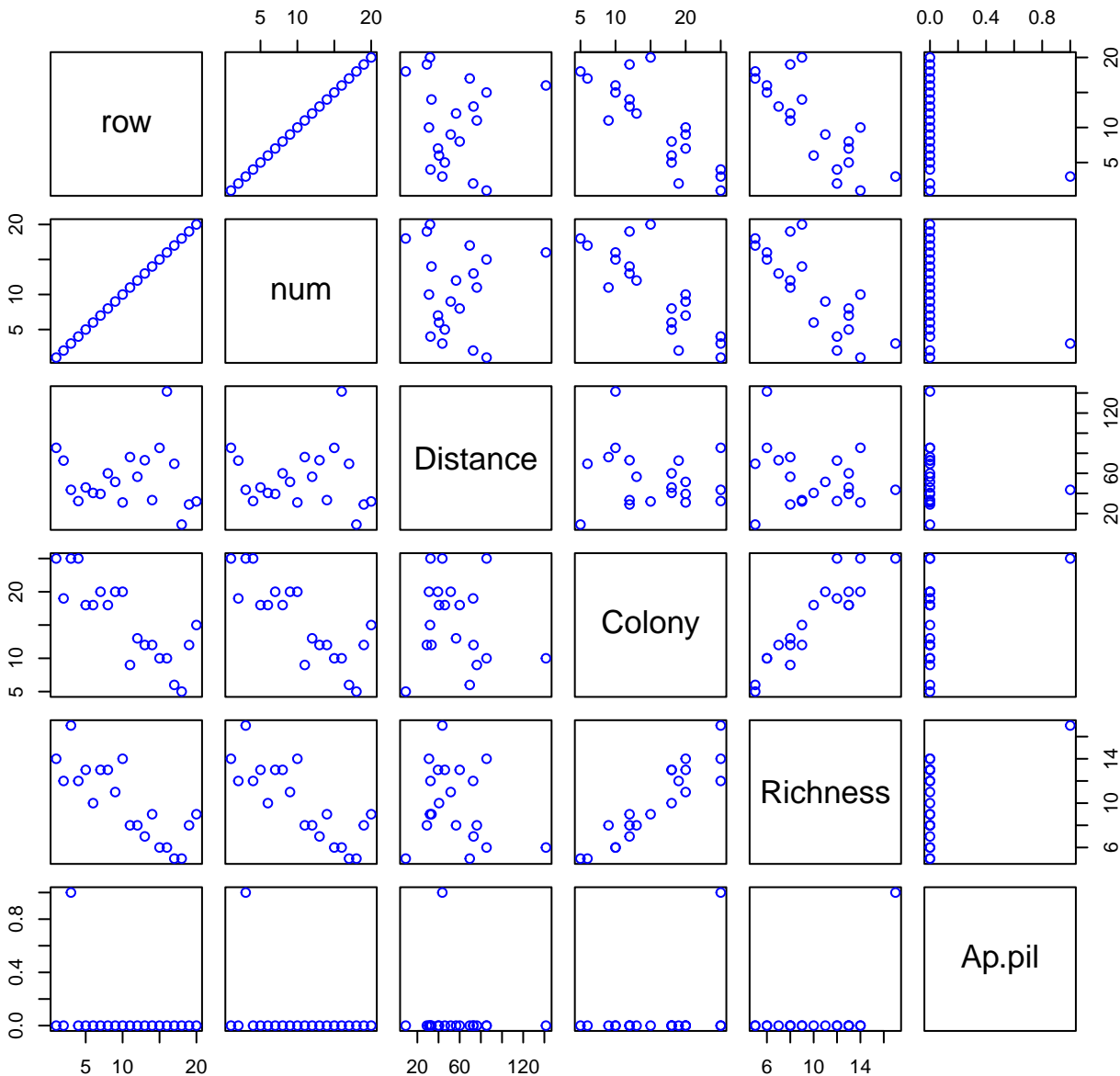
So.M08 = Solenopsis MPEG 08 - number of colonies recorded in transect (number)

Wa.aur = Wasmannia auropunctata - number of colonies recorded in transect (number)

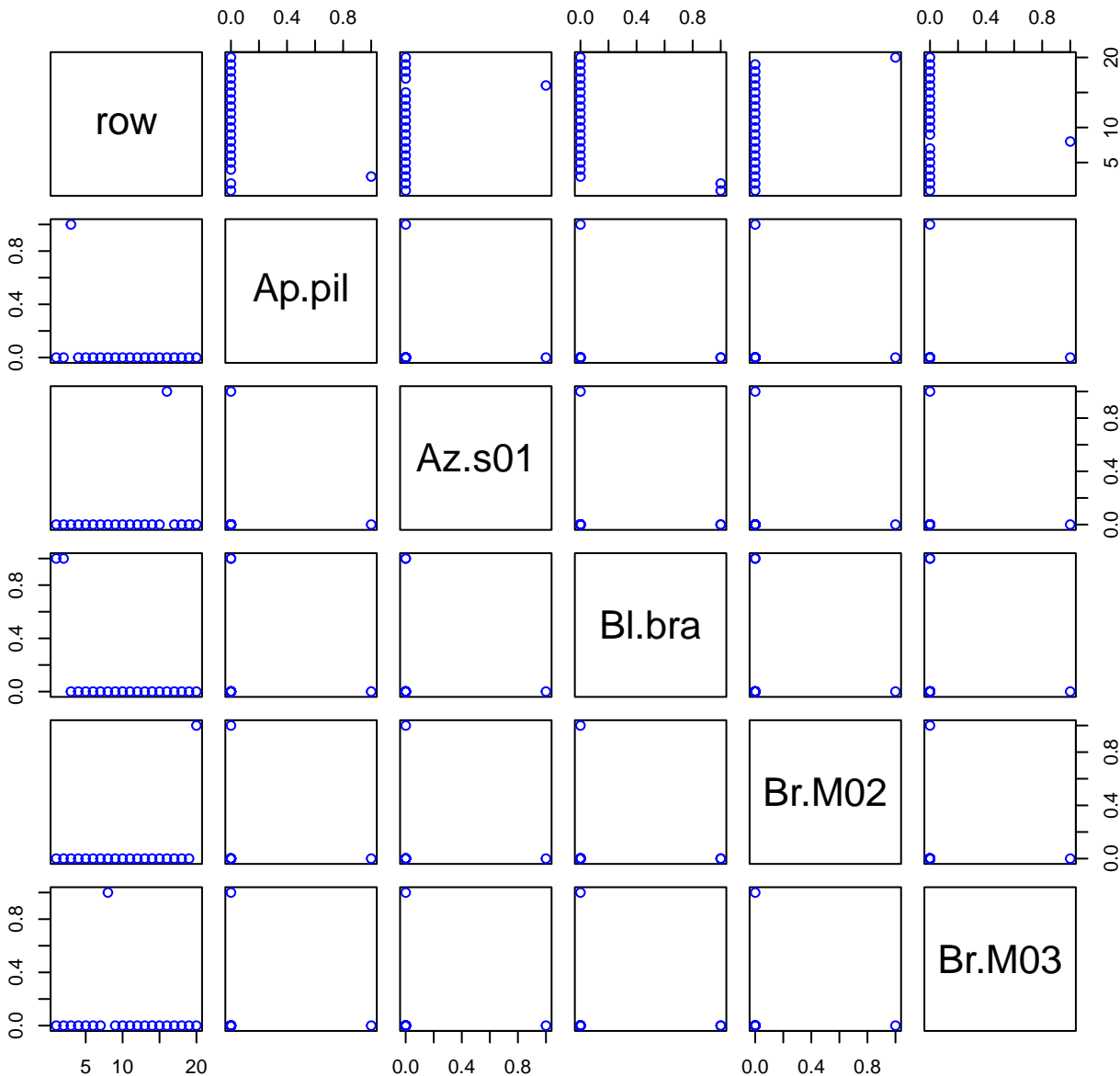
Variable	Min	Median	Mean	Max	NAs
num	1.000	10.500	10.500	20.000	0
Distance	9.000	48.725	55.405	141.500	0
Colony	5.000	16.500	15.600	25.000	0
Richness	5.000	9.500	10.000	17.000	0
Ap.pil	0.000	0.000	0.050	1.000	0
Az.s01	0.000	0.000	0.050	1.000	0
Bl.bra	0.000	0.000	0.100	1.000	0
Br.M02	0.000	0.000	0.050	1.000	0
Br.M03	0.000	0.000	0.050	1.000	0
Ce.opa	0.000	0.000	0.050	1.000	0
Cr.bra	0.000	0.000	0.100	1.000	0
Cr.fla	0.000	0.000	0.100	1.000	0
Cr.lev	0.000	0.000	1.100	4.000	0
Cr.lim	0.000	0.000	0.400	3.000	0
Cr.sot	0.000	0.000	0.400	3.000	0
Do.bis	0.000	0.000	0.100	1.000	0
Ec.ede	0.000	0.000	0.250	3.000	0
Ec.tub	0.000	0.000	0.200	2.000	0
Gn.hor	0.000	0.000	0.050	1.000	0
Ma.con	0.000	0.000	0.500	3.000	0
Ne.api	0.000	0.000	0.100	1.000	0
Ne.cre	0.000	0.000	0.050	1.000	0
Ne.ver	0.000	0.000	0.200	1.000	0
Ny.M01	0.000	0.000	0.100	2.000	0
Ny.M02	0.000	0.000	0.200	2.000	0
Ny.M03	0.000	0.000	0.100	1.000	0
Oc.neo	0.000	0.000	0.300	3.000	0
Oc.sem	0.000	0.000	0.200	2.000	0
Od.cae	0.000	0.000	0.050	1.000	0
Od.hem	0.000	0.000	0.200	2.000	0
Pa.bug	0.000	0.000	0.600	3.000	0
Pa.str	0.000	0.000	0.050	1.000	0
Ph.a_l	0.000	0.000	0.050	1.000	0
Ph.ade	0.000	0.000	0.050	1.000	0
Ph.ast	0.000	0.000	0.350	3.000	0
Ph.bic	0.000	0.500	1.150	5.000	0
Ph.car	0.000	0.000	0.050	1.000	0
Ph.cur	0.000	0.500	1.050	4.000	0
Ph.dis	0.000	0.000	0.100	1.000	0
Ph.fow	0.000	0.000	0.300	2.000	0
Ph.fra	0.000	1.000	1.550	4.000	0
Ph.gau	0.000	0.000	0.200	2.000	0
Ph.hua	0.000	0.000	0.100	1.000	0
Ph.jea	0.000	0.000	0.800	3.000	0
Ph.leo	0.000	0.000	0.050	1.000	0
Ph.lon	0.000	0.000	0.050	1.000	0
Ph.mei	0.000	0.000	0.100	1.000	0
Ph.moo	0.000	0.000	0.250	2.000	0
Ph.p_l	0.000	0.000	0.050	1.000	0

Variable	Min	Median	Mean	Max	NAs
Ph.par	0.000	0.000	0.200	2.000	0
Ph.ped	0.000	0.000	0.200	1.000	0
Ph.pyg	0.000	0.000	0.450	2.000	0
Ph.s03	0.000	0.000	0.050	1.000	0
Ph.s14	0.000	0.000	0.100	1.000	0
Ph.s16	0.000	0.000	0.050	1.000	0
Ph.sch	0.000	0.000	0.400	2.000	0
Ph.sco	0.000	0.000	0.400	3.000	0
Ph.sen	0.000	0.000	0.050	1.000	0
Ph.sub	0.000	0.000	0.250	2.000	0
Ph.tri	0.000	0.000	0.500	3.000	0
Ps.ten	0.000	0.000	0.050	1.000	0
So.M01	0.000	0.000	0.100	1.000	0
So.M02	0.000	0.000	0.050	1.000	0
So.M03	0.000	0.000	0.100	1.000	0
So.M07	0.000	0.000	0.250	2.000	0
So.M08	0.000	0.000	0.050	1.000	0
Wa.aur	0.000	0.000	0.400	3.000	0

# HF351-01 Plot 1

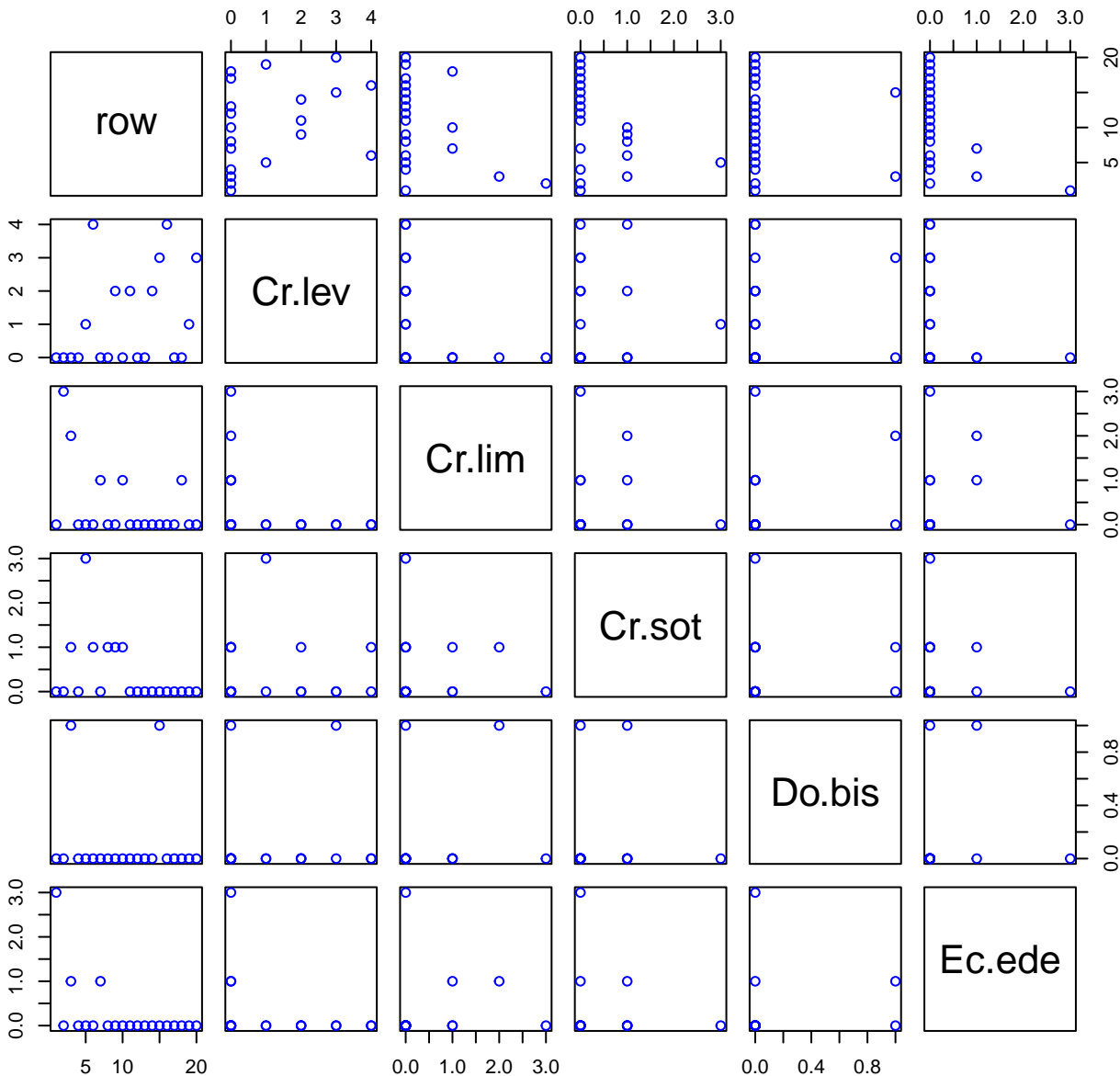


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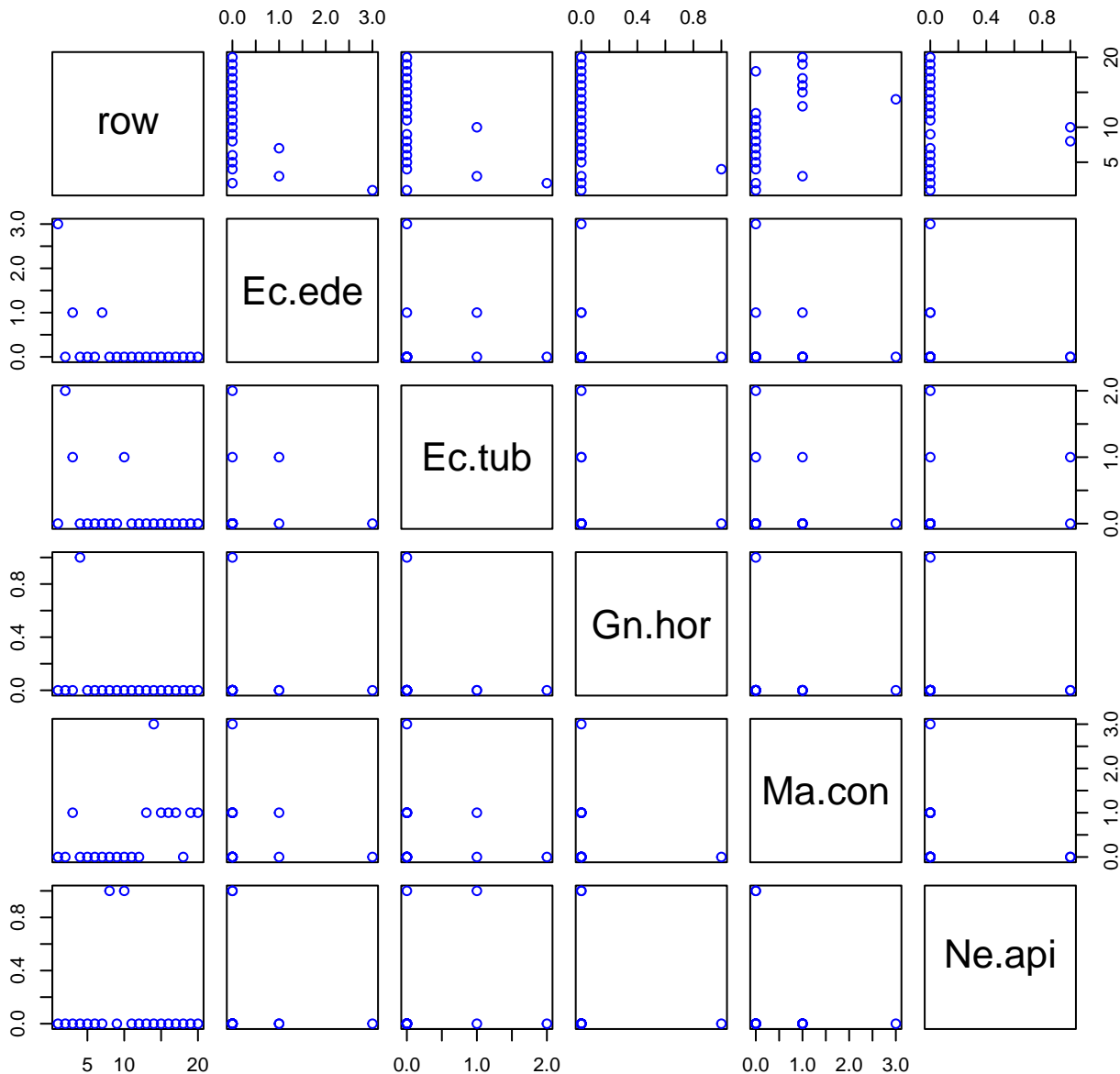




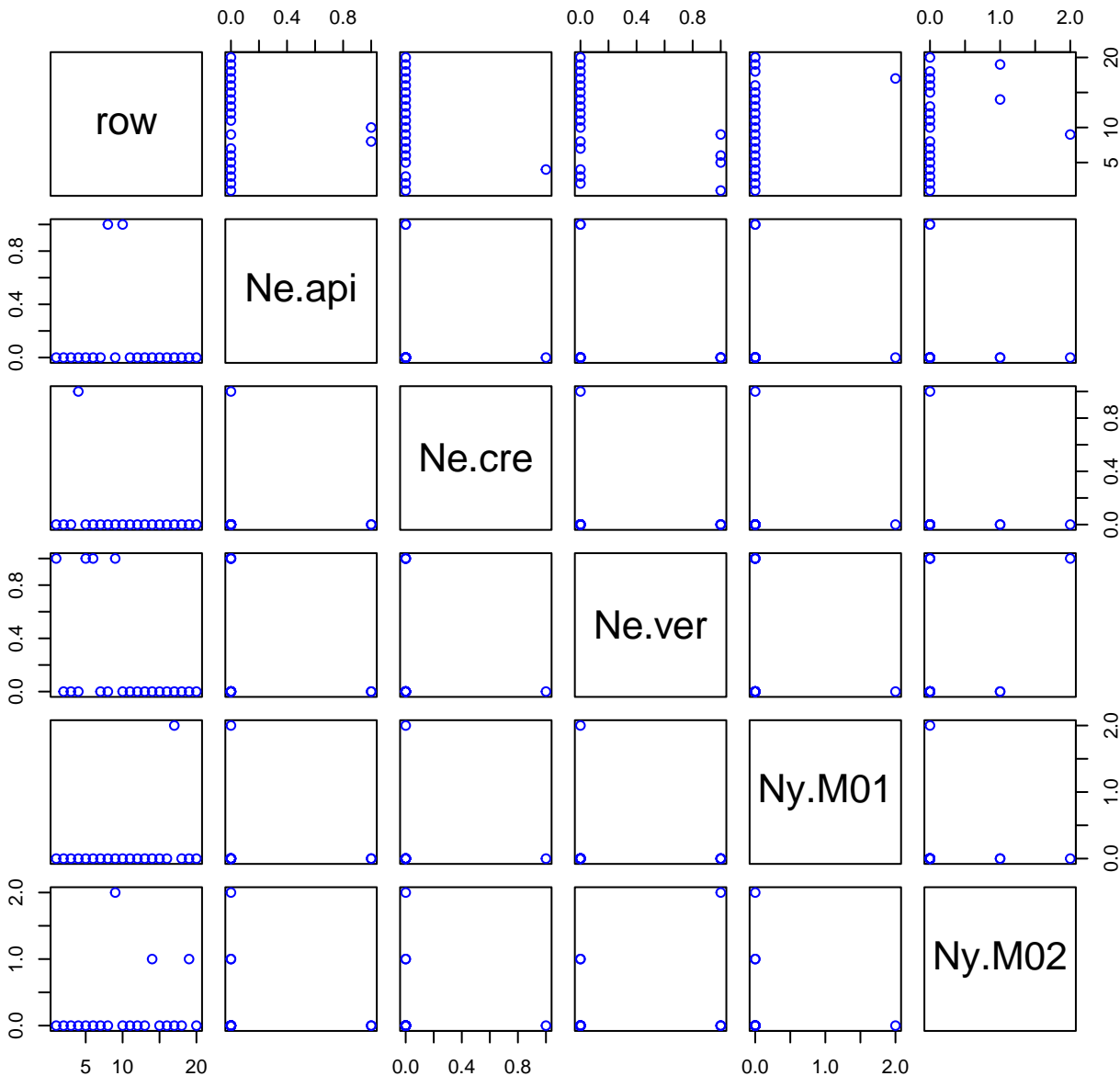
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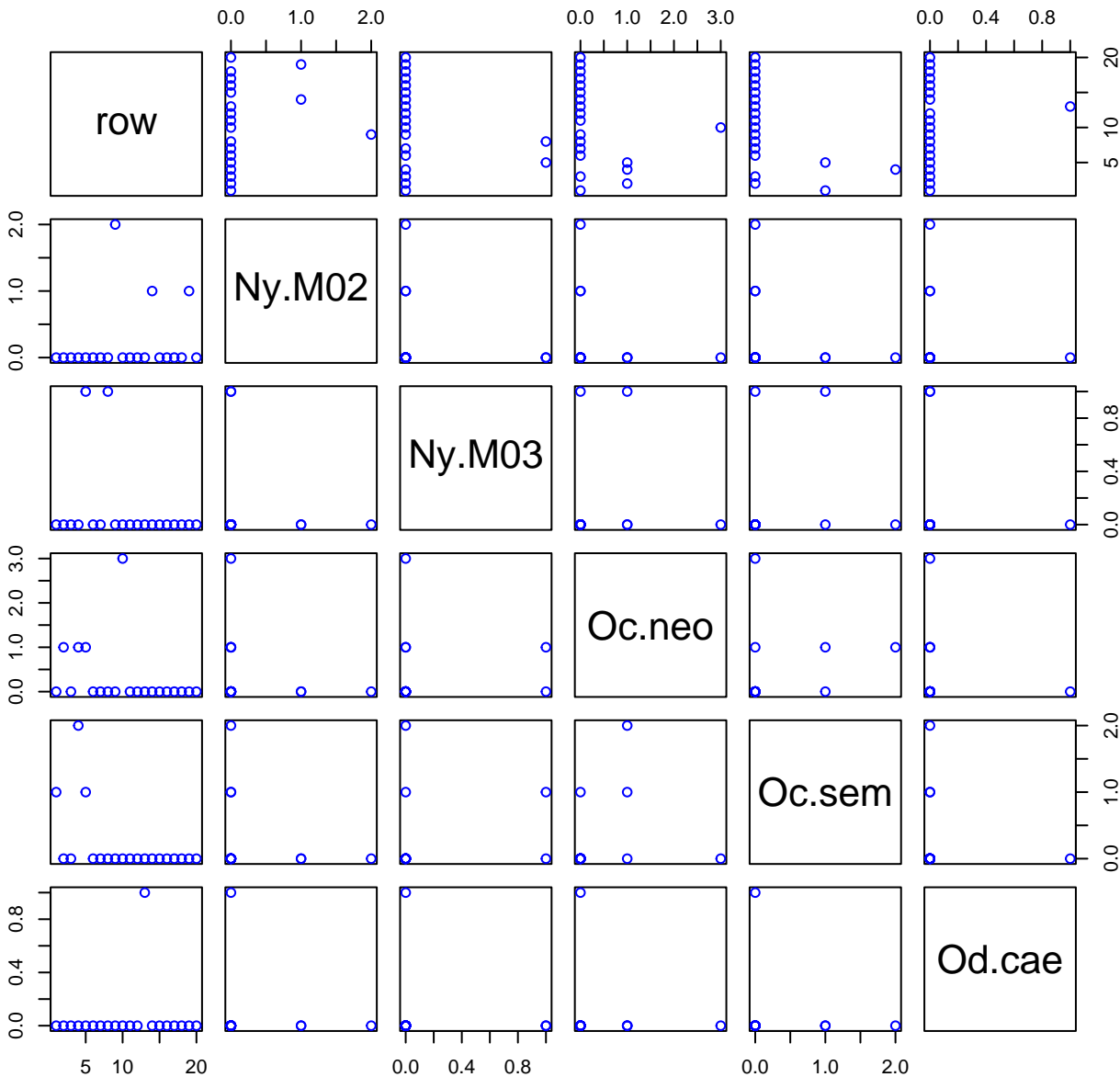
# HF351-01 Plot 5



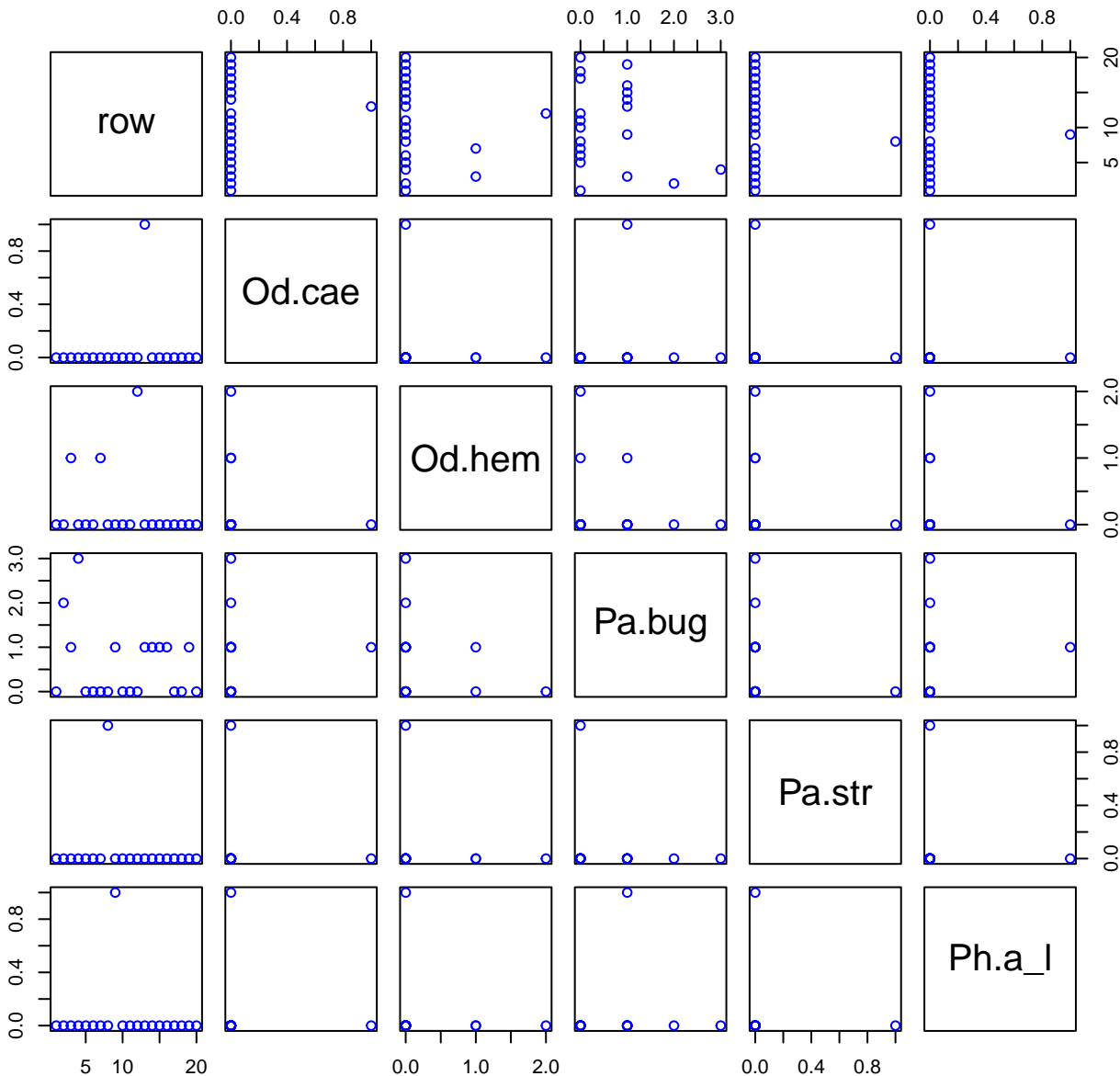
# HF351-01 Plot 6



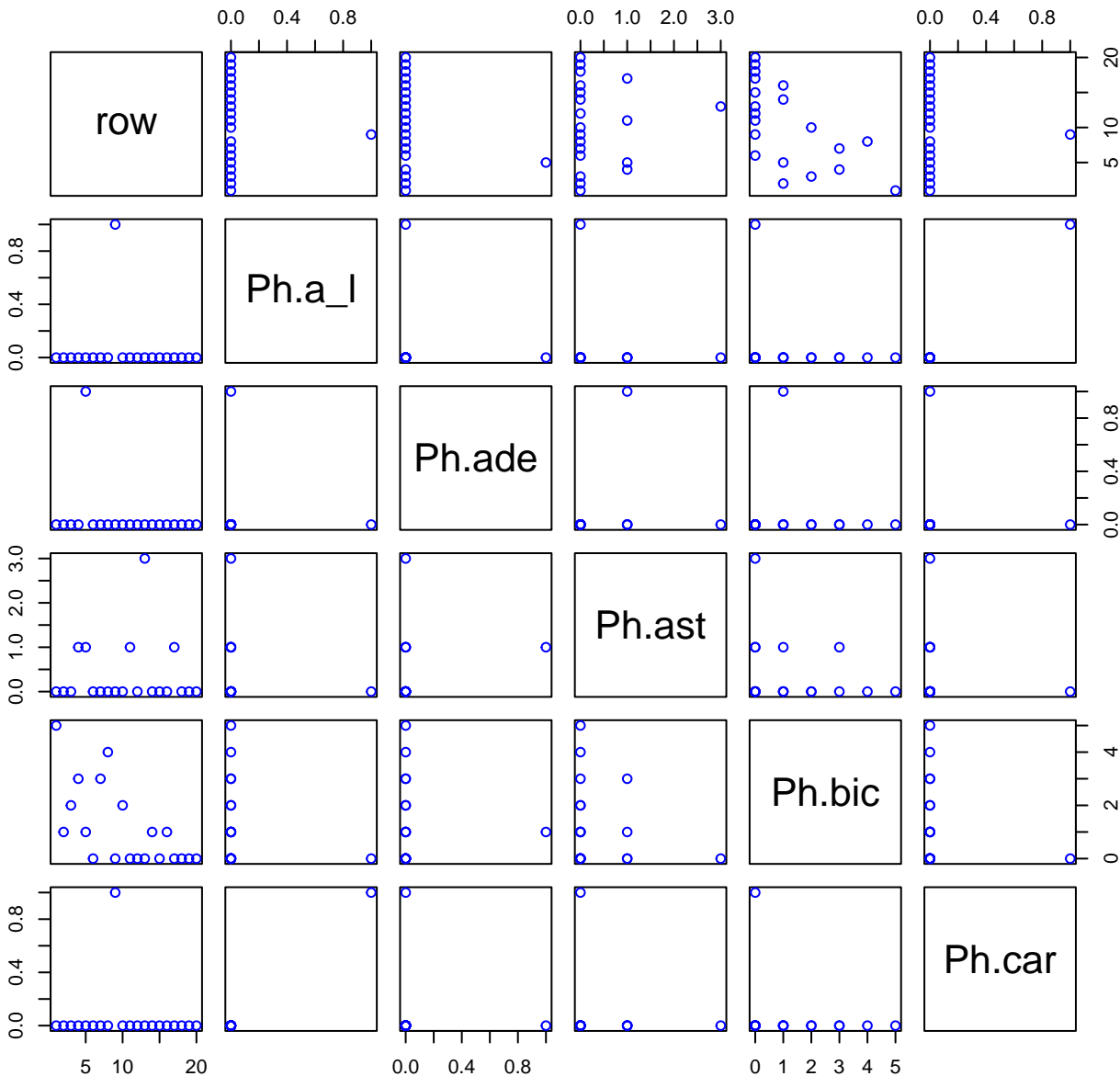
# HF351-01 Plot 7



# HF351-01 Plot 8

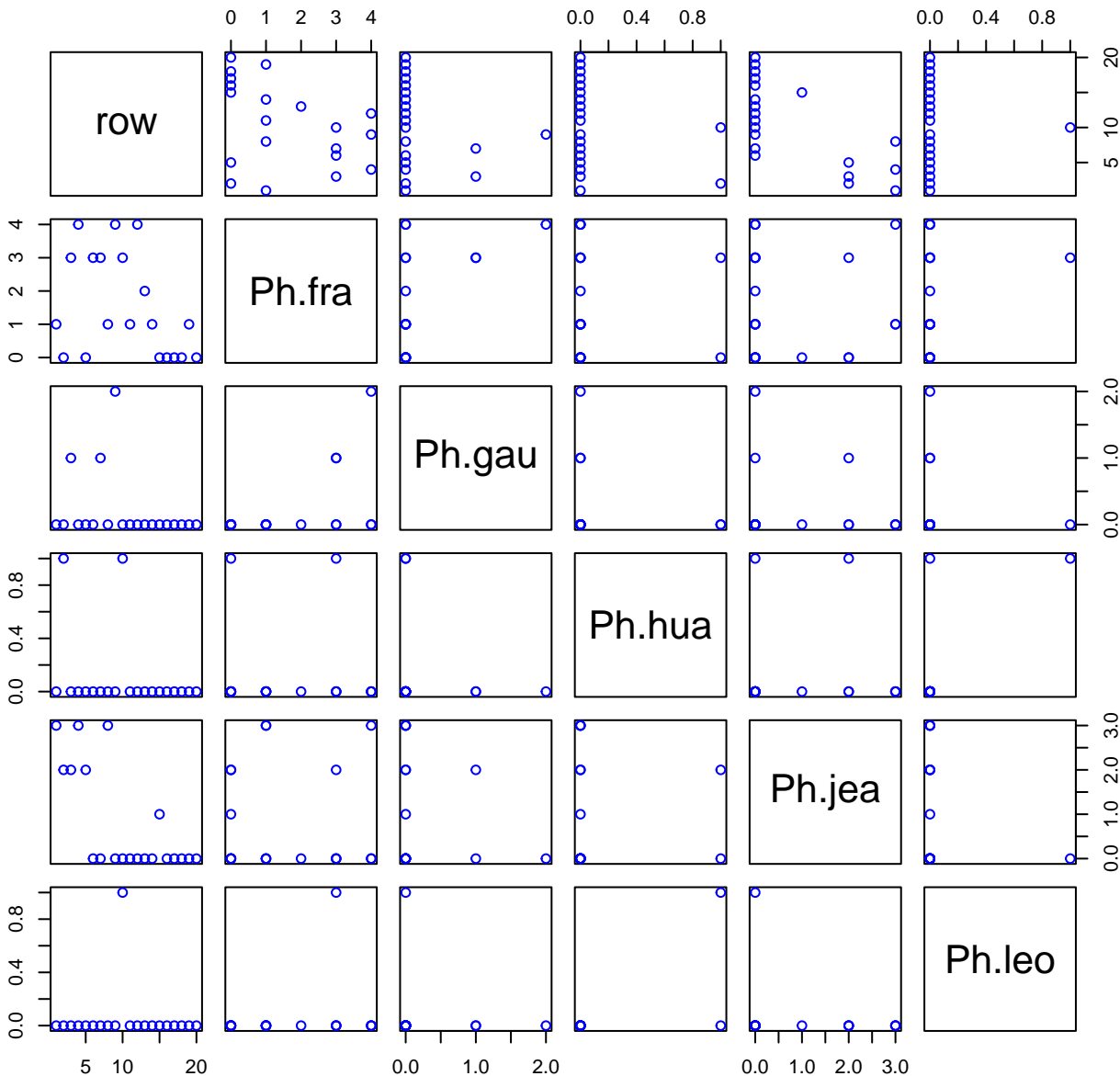


# HF351-01 Plot 9

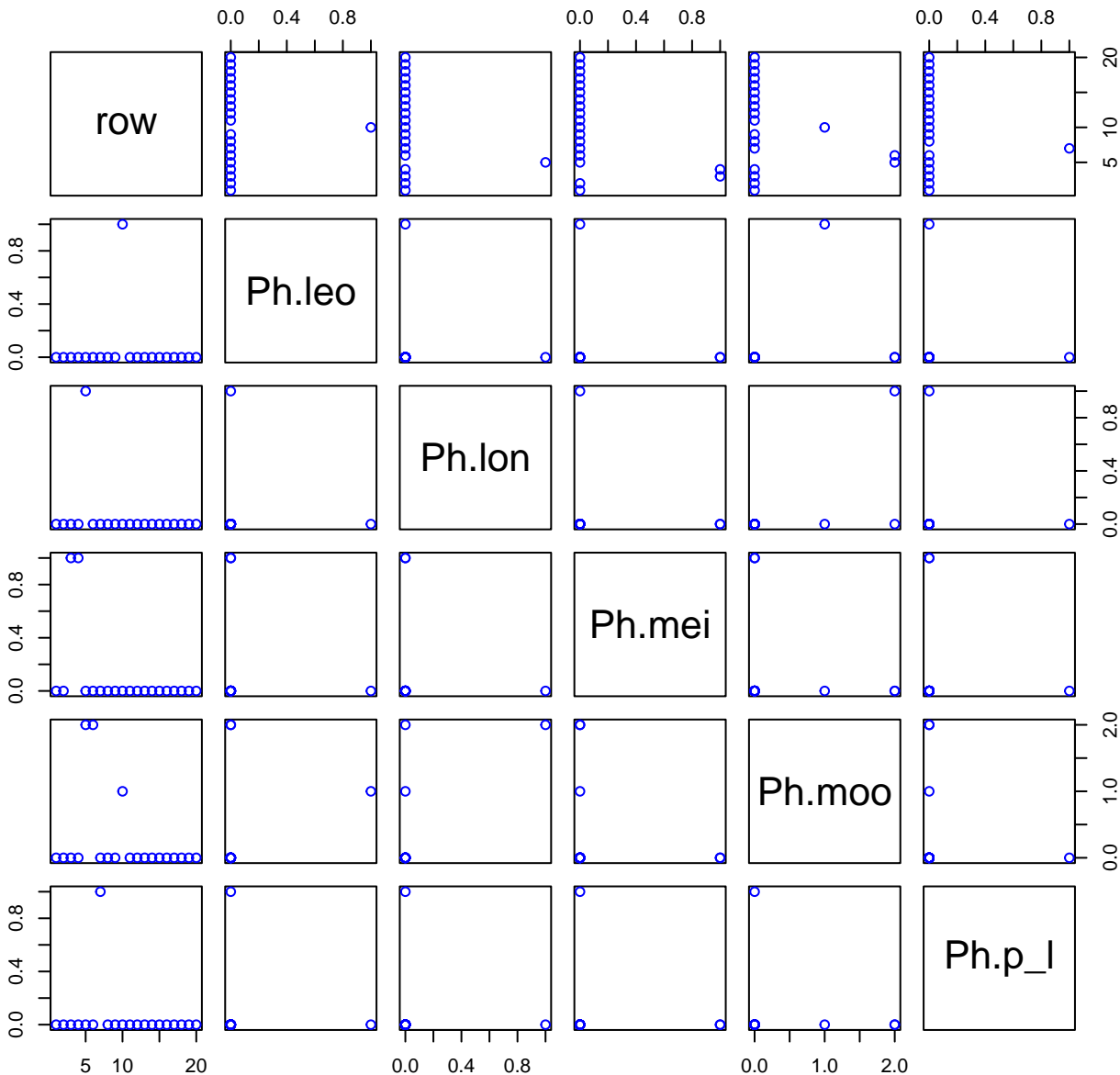




# HF351-01 Plot 11

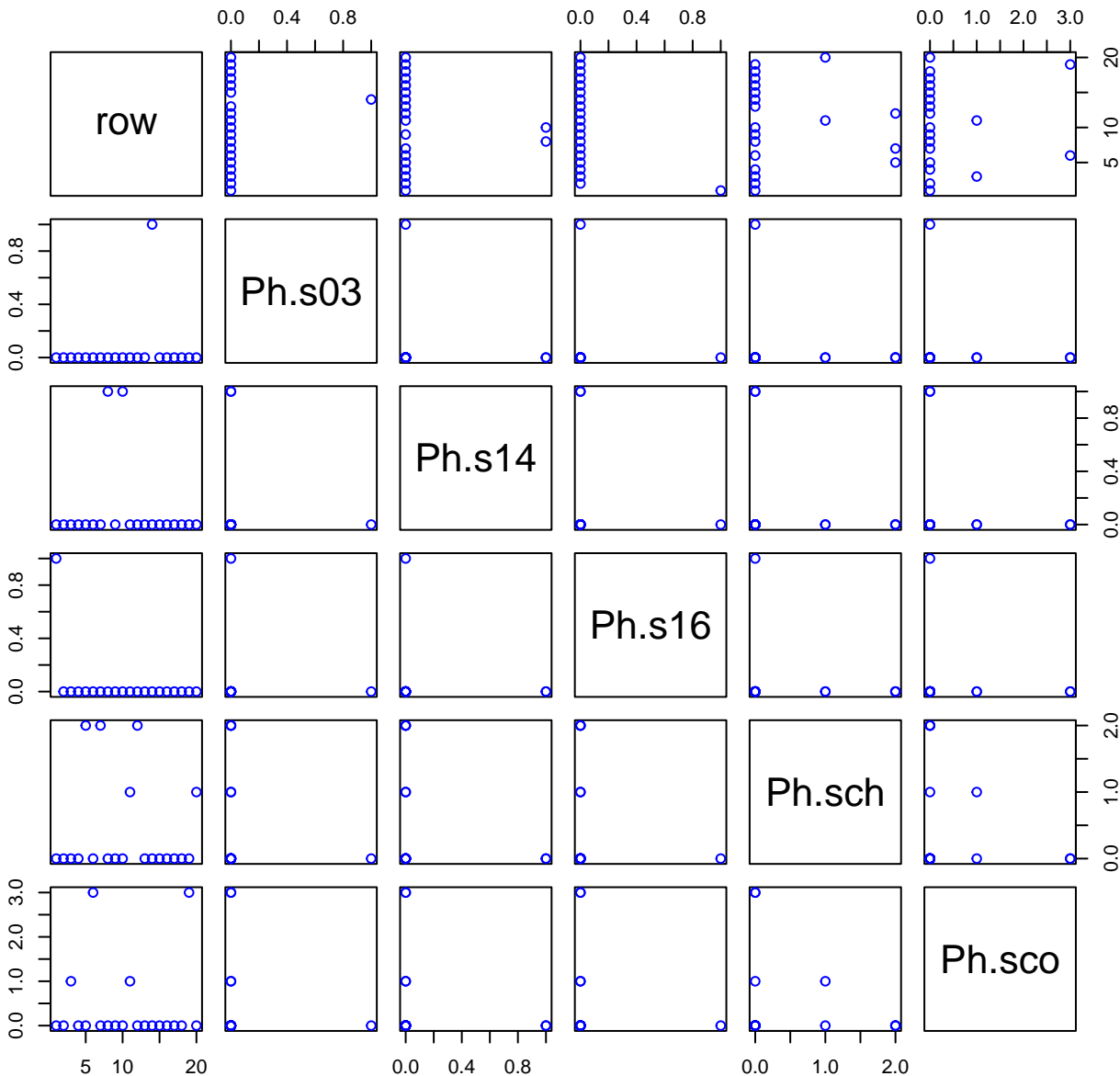


# HF351-01 Plot 12

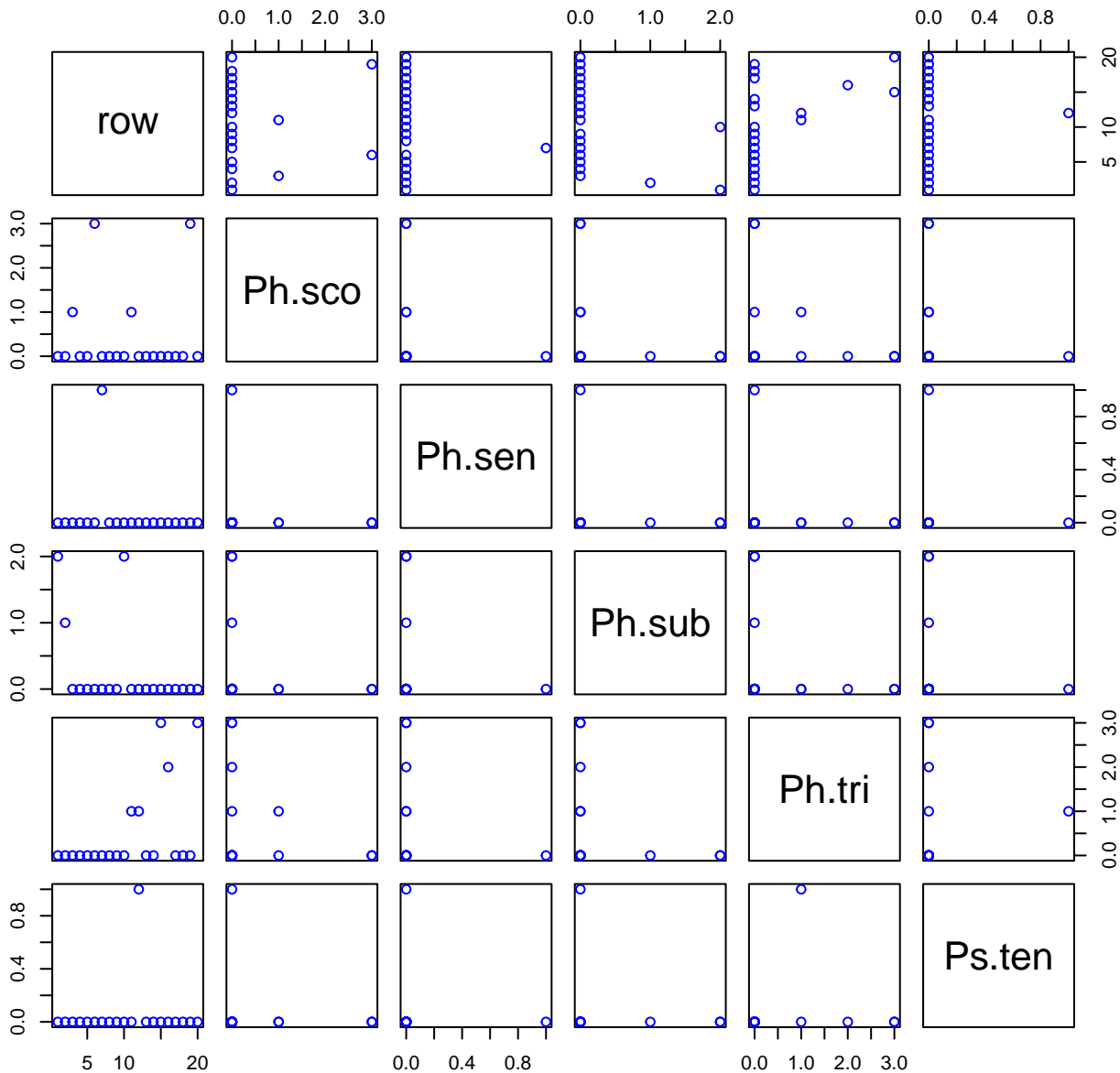




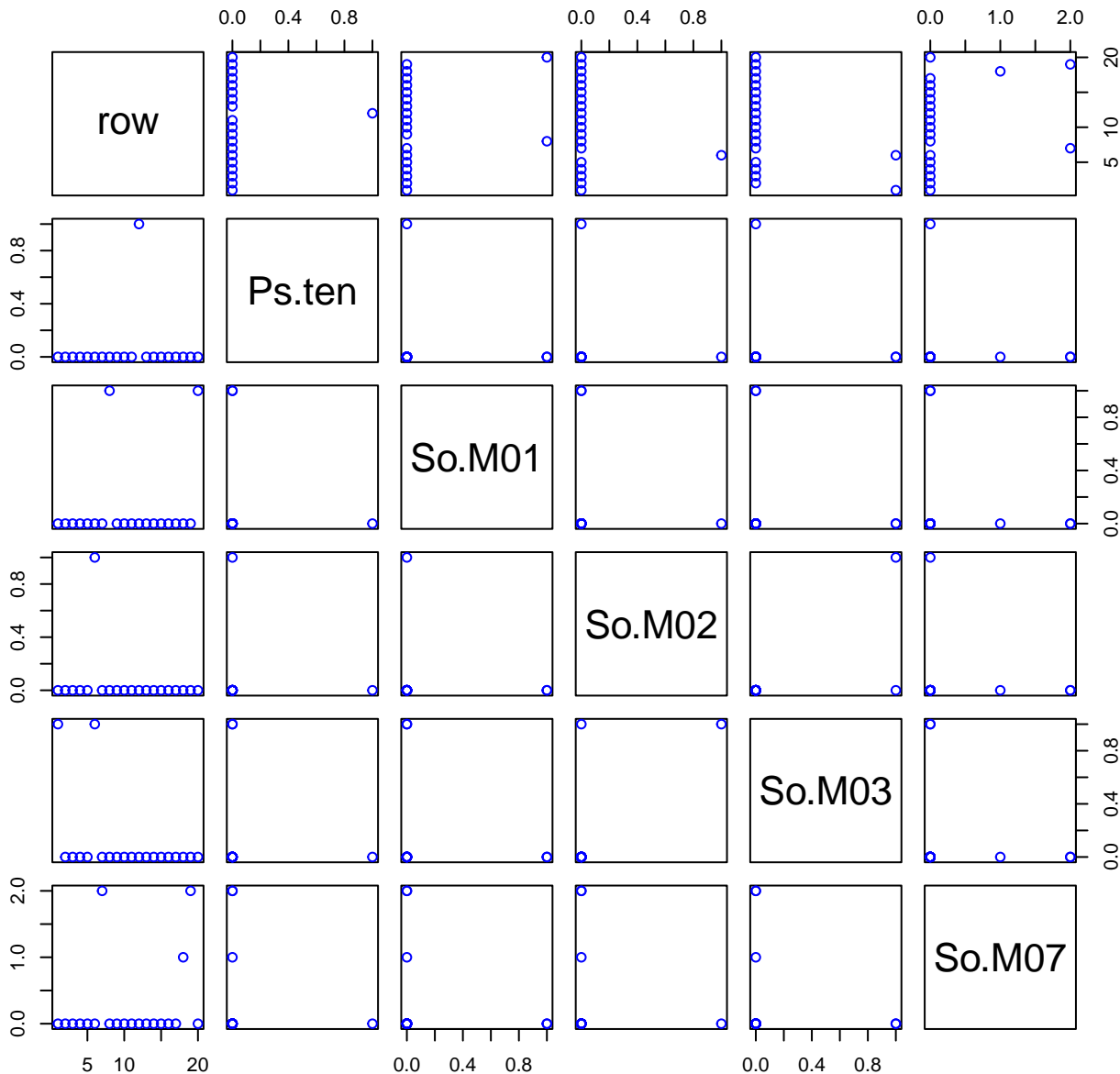
# HF351-01 Plot 14



# HF351-01 Plot 15



# HF351-01 Plot 16



# HF351-01 Plot 17

