phylogenetic examples

Christof Neumann

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Contents

This document contains the code to replicate the two analyses of macaque hierarchy steepness (one analysis in the main text, one in the appendix) from *Extending Bayesian Elo-rating to quantify the steepness of dominance hierarchies* (https://doi.org/10.1101/2022.01.28.478016). It was built using `EloSteepness` (version 0.4.0) and `EloSteepness.data` (version 0.9.4).

```
library(EloSteepness)
library(EloSteepness.data)
library(rstan)
library(cmdstanr)
library(ape)
library(xtable) # just for table generation in this document
```

1 Comparative example from the main text

```
# path to raw model code
mod1 <- system.file("extdata/phylogenetic_examples/comparative_steepness_model_1.stan",
                    package = "EloSteepness.data")
file.exists(mod1)
#> [1] TRUE
```

```
# load tree, matrices and key table
data("Primates301_nex")
data("phylo_matrices")
data("phylo_key")

# prune tree to available species
species <- unique(phylo_key$species_fixed)
tree <- keep.tip(Primates301_nex, species)
# plot(tree)
length(tree$tip.label) == length(species) # sanity check
#> [1] TRUE

# sort matrices and key so they have the same order
```

```
interaction_matrices <- phylo_matrices[sort(names(phylo_matrices))]
key <- phylo_key[order(phylo_key$datasetname), ]
all(names(interaction_matrices) == key$datasetname) # sanity check
#> [1] TRUE

# summary data for each group
specdata <- data.frame(datasetname = key$datasetname,
                       spec = gsub(" ", "_", key$species_fixed),
                       groupsize = NA,
                       n_interactions = NA,
                       dyads = NA,
                       prunks = NA)

for (m in seq_len(nrow(specdata))) {
  mat <- interaction_matrices[[specdata$datasetname[m]]]
  specdata$groupsize[m] <- ncol(mat)
  specdata$n_interactions[m] <- sum(mat)
  specdata$dyads[m] <- ncol(mat) * (ncol(mat) - 1) / 2
  specdata$prunks[m] <- EloRating::prunk(mat)[1]
}
```

For the sake of this vignette we reduce the number of species and also the number of interactions in the networks. We do this just because it speeds up the sampling from the model. With the full data set, this would take several hours (about four on my fairly old laptop). With the reduced data set this takes less time to run (but still takes a few minutes).

```
# ignore these lines if you want to run the full data set
specdata <- specdata[specdata$groupsize < 7, ]
interaction_matrices <- interaction_matrices[specdata$datasetname]
tree <- keep.tip(tree, specdata$spec)
interaction_matrices <- lapply(interaction_matrices, function(x) ceiling(x / 5))
```

```
# prepare the data set as list for sending it to Stan
xdata <- list()
xdata$n_datasets <- length(interaction_matrices)
xdata$n_ids_per_dataset <- as.integer(unlist(lapply(interaction_matrices, ncol)))
xdata$n_total_ids <- sum(xdata$n_ids_per_dataset)
xdata$n_interactions_per_dataset <- as.integer(unlist(lapply(interaction_matrices, sum)))
xdata$n_total_interactions <- sum(xdata$n_interactions_per_dataset)
xdata$interaction_index <- as.integer(seq_len(xdata$n_total_interactions))
xdata$individual_index <- as.integer(seq_len(xdata$n_total_ids))


# generate sequences
set.seed(1)
s <- lapply(interaction_matrices, randomized_sequence_from_matrix)
# global winner and loser indices
xdata$winner <- do.call("rbind", lapply(s, function(x)x$winnermat))
xdata$loser <- do.call("rbind", lapply(s, function(x)x$losermat))

xdata$index_dataset_interactions_start <- cumsum(xdata$n_interactions_per_dataset) -
                                          xdata$n_interactions_per_dataset + 1
xdata$index_individuals_start <- cumsum(xdata$n_ids_per_dataset) -
                                 xdata$n_ids_per_dataset + 1
```
```

```r
xdata$y <- rep(1, xdata$n_total_interactions)

# phylogeny-related
n_spec <- length(tree$tip.label)
tree_mat <- vcv.phylo(tree, corr = TRUE)
species_index <- integer(nrow(specdata))
for (i in seq_len(nrow(specdata))) {
  species_index[i] <- which(colnames(tree_mat) == specdata$spec[i])
}

# for phylogeny part of the model
xdata$N_phyl <- n_spec # N_1
xdata$N_coeff_phyl <- 1 # number of parameters: 1 = SD for phyl 'intercepts'
xdata$spec_index <- species_index
xdata$chol_mat <- t(chol(tree_mat)) # Cholesky factor of phylogenetic correlation matrix
xdata$phyl_predictor <- rep(1, nrow(specdata)) # group-level predictor values

# for repeated measures part of the model
xdata$N_repeated <- n_spec # the same as for the phylogeny part
# number of parameters: 1 = SD for repeated measurements (species intercepts)
xdata$N_coeff_repeated <- 1
xdata$index_rep_measures <- species_index # the same as for the phyl part
# group-level predictor values, the same as for the phyl part
xdata$rep_measures_predictor <- rep(1, nrow(specdata))

# compile stan model
xmod1 <- cmdstan_model(stan_file = mod1, compile = TRUE)

# sampling
res1 <- xmod1$sample(data = xdata,
                     refresh = 100,
                     parallel_chains = 2,
                     iter_warmup = 1500,
                     iter_sampling = 2500,
                     seed = 1,
                     adapt_delta = 0.9)

stanfit <- rstan::read_stan_csv(res1$output_files())
xsummary <- summary(stanfit)$summary
round(summary(stanfit, pars = c("sd_repeated_measures", "sd_phyl"))$summary, 2)
#>                          mean se_mean   sd 2.5%  25%  50%  75% 97.5%   n_eff
#> sd_repeated_measures[1] 0.19    0.00 0.16 0.01 0.07 0.15 0.26  0.57 1213.93
#> sd_phyl[1]              0.21    0.01 0.19 0.01 0.08 0.17 0.29  0.68 1003.37
#>                         Rhat
#> sd_repeated_measures[1]    1
#> sd_phyl[1]                 1

# optional saving of results
# save(xmod1, xsummary, res1, stanfit, xdata, specdata, tree, file = "comp_analysis_1.RData")

par(mfrow = c(1, 2), family = "serif")
par(family = "serif", mgp = c(1.8, 0.7, 0), las = 1, mar = c(2, 1, 1, 1))

plot.phylo(tree, cex = 0.8, show.tip.label = FALSE, x.lim = c(0, 19))
```

```r
tips <- tree$tip.label
for (i in seq_along(tips)) {
  x <- sum(specdata$spec == tips[i])
  y <- gsub("_", " ", tips[i])
  tiplabels(text = bquote(italic(.(y))~.(paste0(" (", x, ")"))),
            tip = i, bg = NULL, adj = 0, frame = "none", offset = 0.3, cex = 0.8)
}

par(mar = c(3, 2.5, 1.5, 1))

# posteriors
x <- as.numeric(extract(stanfit, pars = c("sd_phyl"))$sd_phyl)
y <- as.numeric(extract(stanfit, pars = c("sd_repeated_measures"))$sd_repeated_measures)

# priors
pr_phyl <- as.numeric(extract(stanfit, pars = c("prior_sd_phyl"))$prior_sd_phyl)
pr_rep <- as.numeric(extract(stanfit, pars = c("prior_sd_repeated_measures"))$prior_sd_repeated_measures
# and their densities
pr_phyl <- density(pr_phyl[pr_phyl < 10], adjust = 1) # truncated for smoother display
pr_rep <- density(pr_rep[pr_rep < 10], adjust = 1)


p1 <- density(x, adjust = 1)
p2 <- density(y, adjust = 1)
yr <- c(0, max(p1$y, p2$y) * 1.05)
xr <- c(0, max(p1$x, p2$x) * 1.05)
xr[2] <- 2
plot(0, 0, type = "n", xlim = xr, ylim = yr, xaxs = "i", yaxs = "i", las = 1,
     axes = FALSE, xlab = "SD", ylab = "density")
axis(1)

polygon(c(p1$x, rev(p1$x)), c(rep(0, length(p1$y)), rev(p1$y)),
        border = NA, col = adjustcolor("#3B99B1", 0.5))
polygon(c(p2$x, rev(p2$x)), c(rep(0, length(p2$y)), rev(p2$y)),
        border = NA, col = adjustcolor("#EACB2B", 0.5))
polygon(c(pr_phyl$x, rev(pr_phyl$x)), c(rep(0, length(pr_phyl$y)), rev(pr_phyl$y)),
        border = NA, col = adjustcolor("grey", 0.4))
polygon(c(pr_rep$x, rev(pr_rep$x)), c(rep(0, length(pr_rep$y)), rev(pr_rep$y)),
        border = NA, col = adjustcolor("grey", 0.4))

points(p1$x, p1$y, type = "l", lwd = 0.5)
points(p2$x, p2$y, type = "l", lwd = 0.5)
points(pr_phyl$x, pr_phyl$y, type = "l", lwd = 0.5)
points(pr_rep$x, pr_rep$y, type = "l", lwd = 0.5)
box(bty = "l")

legend("topright", ncol = 1, col = c("#3B99B1", "#EACB2B", "grey"),
       legend = c("phylogenetic", "repeated measurements", "priors"),
       pch = 15, bty = "n")
```
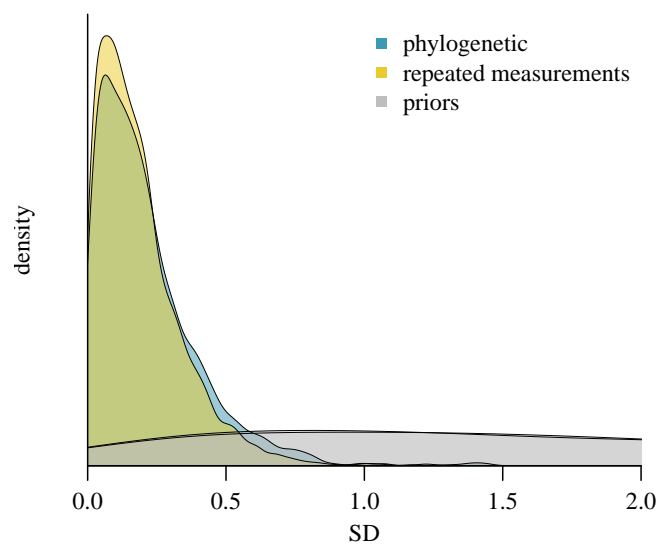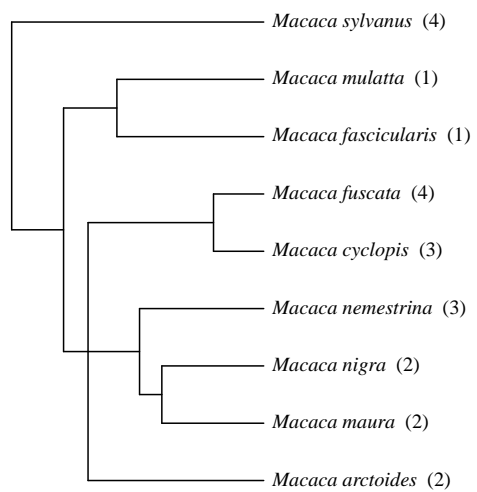
2 Reanalysis of Balasubramaniam et al data set

```r
# path to raw model code
mod2 <- system.file("extdata/phylogenetic_examples/comparative_steepness_model_2.stan",
                    package = "EloSteepness.data")
file.exists(mod2)
#> [1] TRUE
```

```r
# tree data
data("Primates301_nex")

# data from Balasubramaniam et al 2012 (table 2)
sp <- c("Macaca_assamensis", "Macaca_fascicularis", "Macaca_fascicularis",
        "Macaca_fuscata", "Macaca_fuscata", "Macaca_mulatta", "Macaca_mulatta",
        "Macaca_nigra", "Macaca_radiata", "Macaca_sylvanus", "Macaca_thibetana",
        "Macaca_thibetana", "Macaca_tonkeana", "Macaca_tonkeana")
st <- c(0.65, 0.94, 0.79, 0.56, 0.92, 0.65, 0.78,
        0.49, 0.60, 0.45, 0.87, 0.80, 0.22, 0.20)
specdata <- data.frame(spec = sp,
                       steepness = st)

# prune tree to 9 macaque species
species <- unique(specdata$spec)
tree <- keep.tip(Primates301_nex, species)
# plot(tree)
length(tree$tip.label) == length(species) # sanity check
#> [1] TRUE


# prepare data set to be handed over to stan
xdata <- list()
xdata$N <- nrow(specdata)
xdata$the_steepness <- specdata$steepness


# phylogeny-related
tree_mat <- vcv.phylo(tree, corr = TRUE) # covariance matrix
n_spec <- length(tree$tip.label)
# index for species
species_index <- integer(nrow(specdata))
for (i in seq_len(nrow(specdata))) {
  species_index[i] <- which(colnames(tree_mat) == specdata$spec[i])
}

# for phylogeny part
xdata$N_phyl <- n_spec # number of levels
xdata$N_coeff_phyl <- 1 # number of pars: SD for phyl 'intercepts'
xdata$spec_index <- species_index
xdata$chol_mat <- t(chol(tree_mat)) # cholesky factor of phylogenetic correlation matrix
xdata$phyl_predictor <- rep(1, nrow(specdata)) # group-level predictor values

# for repeated measures part
xdata$N_repeated <- n_spec # the same as for the phyl part (number of levels)
# number of pars: SD for repeated measurements (species intercepts)
```

```r
xdata$N_coeff_repeated <- 1
xdata$index_rep_measures <- species_index # the same as for the phyl part
# group-level predictor values, the same as for the phyl part
xdata$rep_measures_predictor <- rep(1, nrow(specdata))

# compile stan model
xmod2 <- cmdstan_model(stan_file = mod2, compile = TRUE)

# sampling
res2 <- xmod2$sample(data = xdata,
                     refresh = 0,
                     parallel_chains = 2,
                     seed = 123,
                     adapt_delta = 0.9)

# convert back to rstan (for easier handling of output)
stanfit2 <- read_stan_csv(res2$output_files())
xsummary2 <- summary(stanfit2)$summary
round(summary(stanfit2,
      pars = c("sd_phyl", "sd_repeated_measures", "phi", "Intercept"))$summary, 2)
#>                            mean se_mean    sd   2.5%   25%   50%    75%  97.5%  n_eff
#> sd_phyl[1]                 0.80    0.02  0.51   0.05  0.41  0.75   1.11   1.90  421.67
#> sd_repeated_measures[1]    0.68    0.02  0.45   0.04  0.33  0.61   0.94   1.69  646.94
#> phi                       10.90    0.20  5.62   3.03  6.78  9.79  13.91  24.59  804.95
#> Intercept                  0.58    0.02  0.56  -0.61  0.27  0.57   0.89   1.72  971.02
#>                            Rhat
#> sd_phyl[1]                 1.01
#> sd_repeated_measures[1]    1.00
#> phi                        1.00
#> Intercept                  1.00

# optional saving of results
# save(xmod2, xsummary2, res2, stanfit2, xdata, specdata, tree, file = "comp_analysis_2.RData")

# plot in the manuscript
sd_phyl <- sprintf("%.2f", xsummary2["sd_phyl[1]", 1])
sd_rep <- sprintf("%.2f", xsummary2["sd_repeated_measures[1]", 1])

par(mfrow = c(1, 2), family = "serif")
par(family = "serif", mgp = c(1.8, 0.7, 0), las = 1, mar = c(2, 1, 1, 1))

# plot tree with number of groups
ape::plot.phylo(tree, cex = 0.8, show.tip.label = FALSE, x.lim = c(0, 19))
tips <- tree$tip.label
for (i in seq_along(tips)) {
  x <- sum(specdata$spec == tips[i])
  y <- gsub("_", " ", tips[i])
  ape::tiplabels(text = bquote(italic(.(y))~.(paste0(" (", x, ")"))),
                 tip = i, bg = NULL, adj = 0,
                 frame = "none", offset = 0.3, cex = 0.8)
}
par(mar = c(3, 2.5, 1.5, 1))

# extract posterior samples for SDs and corresponding priors
```

```r
est_phyl <- as.numeric(extract(stanfit2, pars = c("sd_phyl"))$sd_phyl)
est_rep <- as.numeric(extract(stanfit2, pars = c("sd_repeated_measures"))$sd_repeated_measures)

pr_phyl <- as.numeric(extract(stanfit2, pars = c("prior_sd_phyl"))$prior_sd_phyl)
pr_rep <- as.numeric(extract(stanfit2, pars = c("prior_sd_repeated_measures"))$prior_sd_repeated_measure

# and densities of posteriors
est_phyl <- density(est_phyl, adjust = 1)
est_rep <- density(est_rep, adjust = 1)

# and for priors
pr_phyl <- density(pr_phyl[pr_phyl < 10], adjust = 1) # truncated for smoother display
pr_rep <- density(pr_rep[pr_rep < 10], adjust = 1)


# data ranges for plot
yr <- c(0, max(est_phyl$y, est_rep$y) * 1.05)
xr <- c(0, max(est_phyl$x, est_rep$x) * 1.05)


plot(0, 0, type = "n", xlim = xr, ylim = yr, xaxs = "i", yaxs = "i",
     las = 1, axes = FALSE, xlab = "SD", ylab = "density")
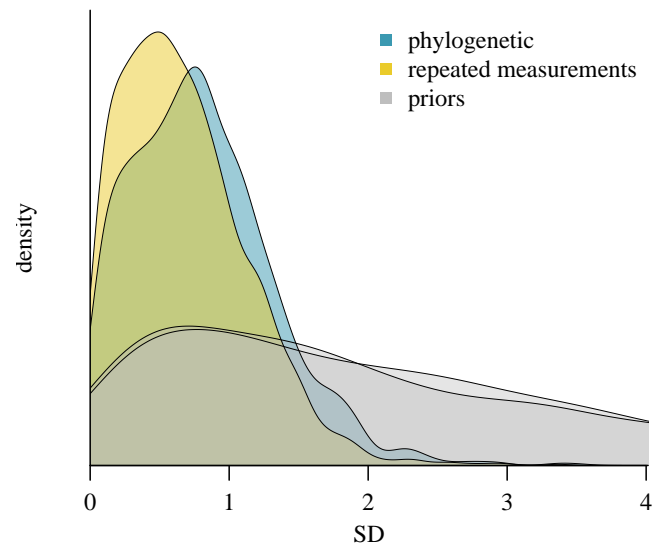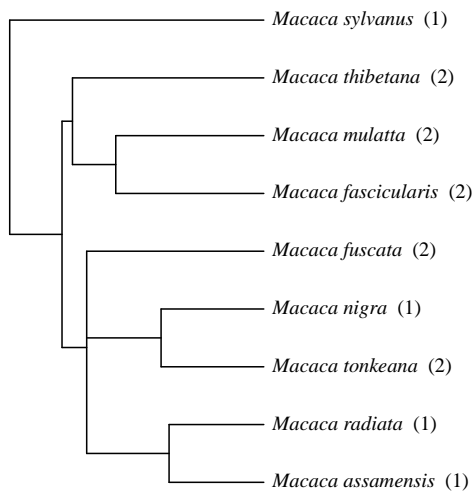axis(1)

polygon(c(est_phyl$x, rev(est_phyl$x)), c(rep(0, length(est_phyl$y)), rev(est_phyl$y)),
        border = NA, col = adjustcolor("#3B99B1", 0.5))
polygon(c(est_rep$x, rev(est_rep$x)), c(rep(0, length(est_rep$y)), rev(est_rep$y)),
        border = NA, col = adjustcolor("#EACB2B", 0.5))
polygon(c(pr_phyl$x, rev(pr_phyl$x)), c(rep(0, length(pr_phyl$y)), rev(pr_phyl$y)),
        border = NA, col = adjustcolor("grey", 0.4))
polygon(c(pr_rep$x, rev(pr_rep$x)), c(rep(0, length(pr_rep$y)), rev(pr_rep$y)),
        border = NA, col = adjustcolor("grey", 0.4))

points(est_phyl$x, est_phyl$y, type = "l", lwd = 0.5)
points(est_rep$x, est_rep$y, type = "l", lwd = 0.5)
points(pr_phyl$x, pr_phyl$y, type = "l", lwd = 0.5)
points(pr_rep$x, pr_rep$y, type = "l", lwd = 0.5)

box(bty = "l")

legend("topright", ncol = 1, col = c("#3B99B1", "#EACB2B", "grey"),
       legend = c("phylogenetic", "repeated measurements", "priors"),
       pch = 15, bty = "n")
```

Macaca sylvanus (1)

Macaca thibetana (2)

Macaca mulatta (2)

Macaca fascicularis (2)

Macaca fuscata (2)

Macaca nigra (1)

Macaca tonkeana (2)

Macaca radiata (1)

Macaca assamensis (1)

density

SD

- phylogenetic
- repeated measurements
- priors

3 Data summary

Table 1 provides data summaries and references for the analyses run above.

Table 1: Macaque dominance interaction networks

data set	species	common name	group size	interactions	sparseness	reference
anderson2016b_dom_1	*Macaca fuscata*	Japanese macaque	6	80	0.20	Anderson et al. (2016); Anderson (2016)
anderson2016b_dom_2	*Macaca fuscata*	Japanese macaque	5	28	0.30	Anderson et al. (2016); Anderson (2016)
balasubramaniam2014_dom_1	*Macaca tonkeana*	Tonkean macaque	9	174	0.14	Balasubramaniam (2014); Demaria & Thierry (2001)
balasubramaniam2014_dom_2	*Macaca nigra*	crested macaque	6	516	0.00	Balasubramaniam (2014)
bartlett1971_dom_1	*Macaca mulatta*	rhesus macaque	9	37	0.31	Bartlett & Meier (1971)
bartlett1971_dom_2	*Macaca mulatta*	rhesus macaque	9	90	0.06	Bartlett & Meier (1971)
berman2004_dom_1	*Macaca thibetana*	Tibetan macaque	13	263	0.09	Berman et al. (2004)
berman2004_dom_2	*Macaca thibetana*	Tibetan macaque	13	379	0.20	Berman et al. (2004)
berman2004_dom_3	*Macaca thibetana*	Tibetan macaque	10	428	0.02	Berman et al. (2004)
birky2002_dom_01	*Macaca cyclopis*	Formosan macaque	6	109	0.00	Birky (2002)
birky2002_dom_02	*Macaca cyclopis*	Formosan macaque	6	61	0.07	Birky (2002)
birky2002_dom_12	*Macaca cyclopis*	Formosan macaque	6	66	0.07	Birky (2002)
chacko2014_dom_1	*Macaca radiata*	bonnet macaque	11	354	0.04	Chacko (2014)
chapais1985_dom_1	*Macaca fuscata*	Japanese macaque	10	97	0.40	Chapais (1985)
cooper1999_dom_1	*Macaca assamensis*	Assamese macaque	22	1077	0.16	Cooper (1999)
deng1987_dom_1	*Macaca thibetana*	Tibetan macaque	15	383	0.26	Deng & Zhao (1987)
dewaal1977_dom_1	*Macaca fascicularis*	longtailed macaque	6	102	0.20	de Waal (1977)
dewaal1977_dom_2	*Macaca fascicularis*	longtailed macaque	11	542	0.09	de Waal (1977)
dewaal1985_dom_1	*Macaca mulatta*	rhesus macaque	20	856	0.10	de Waal & Luttrell (1985)
duboscq2013_dom_1	*Macaca nigra*	crested macaque	15	561	0.04	Duboscq et al. (2013)
duboscq2013_dom_2	*Macaca nigra*	crested macaque	15	210	0.23	Duboscq et al. (2013)
duboscq2013_dom_3	*Macaca nigra*	crested macaque	15	407	0.10	Duboscq et al. (2013)
duboscq2013_dom_4	*Macaca nigra*	crested macaque	21	283	0.36	Duboscq et al. (2013)
duboscq2013_dom_5	*Macaca nigra*	crested macaque	21	732	0.11	Duboscq et al. (2013)
duboscq2013_dom_6	*Macaca nigra*	crested macaque	21	711	0.12	Duboscq et al. (2013)
fa1986_dom_1	*Macaca sylvanus*	Barbary macaque	6	70	0.00	Fa (1986)
fa1986_dom_2	*Macaca sylvanus*	Barbary macaque	6	43	0.20	Fa (1986)
fa1986_dom_3	*Macaca sylvanus*	Barbary macaque	6	51	0.07	Fa (1986)
fa1986_dom_4	*Macaca sylvanus*	Barbary macaque	6	38	0.13	Fa (1986)
funkhouser2018a_dom_5	*Macaca thibetana*	Tibetan macaque	13	53	0.63	Funkhouser et al. (2018)
funkhouser2018a_dom_6	*Macaca thibetana*	Tibetan macaque	13	69	0.49	Funkhouser et al. (2018)
furuichi1983_dom_1	*Macaca fuscata*	Japanese macaque	7	15	0.48	Furuichi (1983)
furuichi1983_dom_2	*Macaca fuscata*	Japanese macaque	7	21	0.38	Furuichi (1983)
giacoma1992_dom_1	*Macaca nemestrina*	pigtailed macaque	6	1105	0.00	Giacoma & Messeri (1992)
giacoma1992_dom_2	*Macaca nemestrina*	pigtailed macaque	6	287	0.00	Giacoma & Messeri (1992)
giacoma1992_dom_3	*Macaca nemestrina*	pigtailed macaque	6	419	0.00	Giacoma & Messeri (1992)
gumert2000_dom_1	*Macaca fascicularis*	longtailed macaque	10	16	0.73	Gumert (2000)
gumert2000_dom_3	*Macaca fascicularis*	longtailed macaque	10	35	0.73	Gumert (2000)
hanya2008_dom_1	*Macaca fuscata*	Japanese macaque	9	96	0.08	Hanya et al. (2008)
hanya2008_dom_2	*Macaca fuscata*	Japanese macaque	7	22	0.38	Hanya et al. (2008)
hill1995_dom_1	*Macaca fuscata*	Japanese macaque	7	291	0.00	Hill & Okayasu (1995)
kaburu2012_dom_1	*Macaca sylvanus*	Barbary macaque	7	584	0.00	Kaburu et al. (2012)
matsumura1998_dom_1	*Macaca maura*	moor macaque	10	112	0.29	Matsumura (1998)
micheletta2011_dom_1	*Macaca nigra*	crested macaque	6	277	0.07	Micheletta (pers. comm.)
missakian1972_dom_1	*Macaca mulatta*	rhesus macaque	22	5159	0.00	Missakian (1972)
murray1984_dom_1	*Macaca arctoides*	stumptailed macaque	20	1176	0.06	Murray (1984)
oi1988_dom_1	*Macaca fuscata*	Japanese macaque	16	45	0.69	Oi (1988)
oi1988_dom_2	*Macaca fuscata*	Japanese macaque	5	3	0.70	Oi (1988)
oi1988_dom_3	*Macaca fuscata*	Japanese macaque	10	85	0.27	Oi (1988)
oi1990_dom_1	*Macaca nemestrina*	pigtailed macaque	15	359	0.17	Oi (1990)
petit1992_dom_1	*Macaca maura*	moor macaque	5	70	0.30	Petit & Thierry (1992)
petit1992_dom_2	*Macaca maura*	moor macaque	5	231	0.00	Petit & Thierry (1992)
raney1981_dom_1	*Macaca radiata*	bonnet macaque	24	276	0.54	Raney et al. (1981)
rhine1972_dom_1	*Macaca arctoides*	stumptailed macaque	4	154	0.00	Rhine (1972); Rhine (1972)a
rhine1972_dom_3	*Macaca arctoides*	stumptailed macaque	4	204	0.00	Rhine (1972); Rhine (1972)a
rizaldi2010_dom_2	*Macaca fuscata*	Japanese macaque	5	81	0.00	Rizaldi & Watanabe (2010)

Continued on next page

Table 1: Macaque dominance interaction networks

data set	species	common name	group size	interactions	sparseness	reference
sade1972_dom_1	*Macaca mulatta*	rhesus macaque	9	136	0.00	Sade (1972)
scanlon1984_dom_1	*Macaca mulatta*	rhesus macaque	9	116	0.08	Scanlon (1984)
silk1981_dom_1	*Macaca radiata*	bonnet macaque	29	1413	0.25	Silk et al. (1981)
sterck1997_dom_01	*Macaca fascicularis*	longtailed macaque	9	15	0.69	Sterck & Steenbeek (1997)
sterck1997_dom_02	*Macaca fascicularis*	longtailed macaque	9	36	0.42	Sterck & Steenbeek (1997)
su2003_dom_1	*Macaca cyclopis*	Formosan macaque	8	245	0.04	Su (2003)
su2003_dom_2	*Macaca cyclopis*	Taiwanese macaque	8	42	0.25	Su (2003)
tully1975_dom_1	*Macaca radiata*	bonnet macaque	8	247	0.00	Tully (1975)
tully1975_dom_2	*Macaca nemestrina*	pigtailed macaque	8	100	0.11	Tully (1975)
zhang2014b_dom_1	*Macaca thibetana*	Tibetan macaque	9	288	0.00	Zhang et al. (2014)
zumpe1986_dom_1	*Macaca mulatta*	rhesus macaque	4	55	0.00	Zumpe & Michael (1986)

References

Anderson, E. J. (2016). *The behaviour and welfare of zoo-housed Japanese macaques (*Macaca fuscata*)* [MSc thesis]. Concordia University.

Anderson, E. J., Weladji, R. B., & Paré, P. (2016). Changes in the dominance hierarchy of captive female Japanese macaques as a consequence of merging two previously established groups: Consequences of merging macaque groups. *Zoo Biology*, *35*, 505–512. https://doi.org/10.1002/zoo.21322

Balasubramaniam, K. N. (2014). *Variation in dominance relationships in macaques from phylogenetic and socioecological perspectives* [PhD thesis]. University at Buffalo, State University of New York.

Bartlett, D. P., & Meier, G. W. (1971). Dominance status and certain operants in a communal colony of rhesus macaques. *Primates*, *12*, 209–219. https://doi.org/10.1007/BF01730411

Berman, C. M., Ionica, C. S., & Li, J. (2004). Dominance style among *Macaca thibetana* on Mt. Huangshan, China. *International Journal of Primatology*, *25*, 1283–1312. https://doi.org/10.1023/B:IJOP.0000043963.77801.c3

Birky, W. A. (2002). *Mating patterns and social structure in a wild group of Formosan macaques (*Macaca cyclopis*)* [PhD thesis]. Rutgers University.

Chacko, S. R. (2014). *Why do females live in groups? Dominance, grooming, and experimental testing of the effects of food distribution on the behavior of commensal bonnet macaque (*Macaca radiata*) females* [PhD thesis]. University of California.

Chapais, B. (1985). An experimental analysis of a mother-daughter rank reversal in Japanese macaques (*Macaca fuscata*). *Primates*, *26*, 407–423. https://doi.org/10.1007/BF02382456

Cooper, M. A. (1999). *Social tolerance in Assamese macaques (*Macaca assamensis*)* [PhD thesis]. University of Georgia.

de Waal, F. B. M. (1977). The organization of agonistic relations within two captive groups of Java-monkeys (*Macaca fascicularis*). *Zeitschrift Für Tierpsychologie*, *44*, 225–282. https://doi.org/10.1111/j.1439-0310.1977.tb00995.x

de Waal, F. B. M., & Luttrell, L. M. (1985). The formal hierarchy of rhesus macaques: An investigation of the bared-teeth display. *American Journal of Primatology*, *9*, 73–85. https://doi.org/10.1002/ajp.1350090202

Demaria, C., & Thierry, B. (2001). A comparative study of reconciliation in rhesus and Tonkean macaques. *Behaviour*, *138*, 397–410. https://doi.org/10.1163/15685390152032514

Deng, Z., & Zhao, Q. (1987). Social structure in a wild group of *Macaca thibetana* at Mount Emei, China. *Folia Primatologica*, *49*, 1–10. https://doi.org/10.1159/000156304

Duboscq, J., Micheletta, J., Agil, M., Hodges, J. K., Thierry, B., & Engelhardt, A. (2013). Social tolerance in wild female crested macaques (*Macaca nigra*) in Tangkoko-Batuangus Nature Reserve, Sulawesi, Indonesia. *American Journal of Primatology*, *75*, 361–375. https://doi.org/10.1002/ajp.22114

Fa, J. E. (1986). *Use of time and resources by provisioned troops of monkeys.* Karger.

Funkhouser, J. A., Mayhew, J. A., Sheeran, L. K., Mulcahy, J. B., & Li, J.-H. (2018). Comparative investigations of social context-dependent dominance in captive chimpanzees (*Pan troglodytes*) and wild Tibetan macaques (*Macaca thibetana*). *Scientific Reports*, *8*, 13909. https://doi.org/10.1038/s41598-018-32243-2

Furuichi, T. (1983). Interindividual distance and influence of dominance on feeding in a natural Japanese macaque troop. *Primates*, *24*, 445–455. https://doi.org/10.1007/BF02381678

Giacoma, C., & Messeri, P. (1992). Attributes and validity of dominance hierarchy in the female pigtail macaque. *Primates*, *33*, 181–189. https://doi.org/10.1007/BF02382748

Gumert, M. D. (2000). *Reciprocity in an wild group of long tailed macaques (*Macaca fascicularis*) at Tanjung Puting National Park, Kalimantan Tengah, Indonesia: An analysis of social currency exchange* [MSc thesis]. Bucknell University.

Hanya, G., Matsubara, M., Hayaishi, S., Zamma, K., Yoshihiro, S., Kanaoka, M. M., Sugaya, S., Kiyono, M., Nagai, M., Tsuriya, Y., Hayakawa, S., Suzuki, M., Yokota, T., Kondo, D., & Takahata, Y. (2008). Food conditions, competitive regime, and female social relationships in Japanese macaques: Within-population variation on yakushima. *Primates*, *49*, 116–125. https://doi.org/10.1007/s10329-007-0073-y

Hill, D. A., & Okayasu, N. (1995). Absence of "youngest ascendancy" in the dominance relations of sisters in wild Japanese macaques (*Macaca fuscata yakaui*). *Behaviour*, *132*, 367–379. https://doi.org/10.1163/156853995X00612

Kaburu, S. S. K., MacLarnon, A., Majolo, B., Qarro, M., & Semple, S. (2012). Dominance rank and

self-scratching among wild female Barbary macaques (*Macaca sylvanus*). *African Zoology*, *47*, 74–79. https://doi.org/10.3377/004.047.0111

Matsumura, S. (1998). Relaxed dominance relations among female moor macaques (*Macaca maurus*) in their natural habitat, south Sulawesi, Indonesia. *Folia Primatologica*, *69*, 346–356. https://doi.org/10.1159/000021650

Missakian, E. A. (1972). Genealogical and cross-genealogical dominance relations in a group of free-ranging rhesus monkeys (*Macaca mulatta*) on Cayo Santiago. *Primates*, *13*, 169–180. https://doi.org/10.1007/BF01840878

Murray, R. D. (1984). *Mating patterns among kin and nonkin in a captive group of stumptail macaques* [PhD thesis]. Ohio State University.

Oi, T. (1988). Sociological study on the troop fission of wild Japanese monkeys (*Macaca fuscata yakui*) on Yakushima Island. *Primates*, *29*, 1–19. https://doi.org/10.1007/BF02380846

Oi, T. (1990). Patterns of dominance and affiliation in wild pig-tailed macaques (*Macaca nemestrina nemestrina*) in west Sumatra. *International Journal of Primatology*, *11*, 339–356. https://doi.org/10.1007/BF02193005

Petit, O., & Thierry, B. (1992). Affiliative function of the silent bared-teeth display in moor macaques (*Macaca maurus*): Further evidence for the particular status of Sulawesi macaques. *International Journal of Primatology*, *13*, 97–105. https://doi.org/10.1007/BF02547729

Raney, D. F., Abernethy, V., & Rodman, P. S. (1981). Dominance and the social behavior of adult female bonnet macaques (*Macaca radiata*). *Primates*, *22*, 368–378. https://doi.org/10.1007/BF02381577

Rhine, R. J. (1972). Changes in the social structure of two groups of stumptail macaques (*Macaca arctoides*). *Primates*, *13*, 181–194. https://doi.org/10.1007/BF01840879

Rhine, R. J., & Kronenwetter, C. (1972). Interaction patterns of two newly formed groups of stumptail macaques (*Macaca arctoides*). *Primates*, *13*, 19–33. https://doi.org/10.1007/BF01757933

Rizaldi, & Watanabe, K. (2010). Early development of peer dominance relationships in a captive group of Japanese macaques *Macaca fuscata*. *Current Zoology*, *56*, 190–197.

Sade, D. S. (1972). Sociometrics of *Macaca mulatta* I. Linkages and cliques in grooming matrices. *Folia Primatologica*, *18*, 196–223. https://doi.org/10.1159/000155480

Scanlon, K. (1984). *Play and development of social skills in infant rhesus macaques* [PhD thesis, Open University]. https://doi.org/10.21954/ou.ro.0000de55

Silk, J. B., Samuels, A., & Rodman, P. S. (1981). Hierarchical organization of female *Macaca radiata* in captivity. *Primates*, *22*, 84–95. https://doi.org/10.1007/BF02382559

Sterck, E. H. M., & Steenbeek, R. (1997). Female dominance relationships and food competition in the sympatric Thomas langur and long-tailed macaque. *Behaviour*, *134*, 749–774. https://doi.org/10.1163/156853997X00052

Su, H.-H. (2003). *Within-group female-female feeding competition and inter-matriline feeding competition in Taiwanese macaques (*Macaca cyclopis*) at Fushan Experimental Forest, Taiwan* [PhD thesis]. Rutgers University.

Tully, M. S. (1975). *Social relations among adult females in two species of macaque* [PhD thesis]. University of Colorado.

Zhang, Q.-X., Li, J.-H., Xia, D.-P., Zhu, Y., Wang, X., & Zhang, D. (2014). Influence of dominance rank and affiliation relationships on self-directed behavior in female Tibetan macaques (*Macaca thibetana*). *Zoological Research*, *35*, 214–221. https://doi.org/10.11813/j.issn.0254-5853.2014.3.214

Zumpe, D., & Michael, R. P. (1986). Dominance index: A simple measure of relative dominance status in primates. *American Journal of Primatology*, *10*, 291–300. https://doi.org/10.1002/ajp.1350100402