

Supporting Statistical Results

Thermoregulatory requirements shape mating opportunities of male proboscis bats

Luke R. Wilde, Linus Günther, Frieder Mayer, Mirjam Knörnschild, Martina Nagy

ANOVAs on one principal component extracted from daily minimum, maximum and mean roost site temperatures

Results of one-way ANOVAs (River Station and Casa Grande) and two-way ANOVAs (Cabina 5R/L) testing the effect of roost site (site) and, if applicable, season (dry/mating season and wet/non-mating season) on one principal component (PC1) extracted from daily minimum, mean, and maximum temperature.

Roost/Social group	Factor	df	Sum of Squares	Mean Squares	F-value	p-value	α -level
River Station 2016 n=31 days	Site	3	18.30	6.10	6.99	<0.001	0.008
Casa Grande 2016 n=16 days	Site	1	0.36	0.36	0.35	0.555	0.050
Cabina 5 Left 2015 + 2016 n=10 +12 days	Site	3	3.88	1.29	2.50	0.065	0.025
	Season	1	28.81	28.81	55.82	<0.001	0.010
Cabina 5 Right 2015 + 2016 n=10 +12 days	Site	3	30.31	10.10	16.75	<0.001	0.013
	Season	1	18.69	18.69	30.99	<0.001	0.017

Results of post hoc comparisons using Tukey-HSD test to compare temperature parameters between individual roosting sites.

Roost	Daily temperature parameter	Sites compared	Difference	Lower bound	Upper bound	Adjusted p-value
River Station 2016	PC1	RS3-RS1	-1.01	-1.63	-0.39	< 0.001
		RS3-RS2	-0.77	-1.39	-0.15	0.008
		RS4-RS3	0.81	0.19	1.43	0.005
Cabina 5 Right 2015 + 2016	PC1	CR1-CR3	0.80	0.18	1.41	0.005
		CR1-CR4	0.87	0.26	1.48	0.002
		CR2-CR3	1.34	0.73	1.96	< 0.001
		CR2-CR4	1.42	0.80	2.03	< 0.001

R output for GLMM 1 (Fig 2a):

Temperature data set: iButton data from October 2015 (CL, CR) and June-July 2016 (CL, CR, CG, RS)

Site use data set: October 2015 (CL, CR), June-July 2016 (CL, CR, CG, RS)

Dependent variable: proportion of bats in alternate roost sites:

y1<-cbind(BatsNonPref1,BatsPref1)

Fixed effects:

AverageTemp1: daily mean temperature

Season1: Mating period (MP) = dry season = 2015, non-mating period (NMP) = wet season = 2016

Roost1: CL, CR, CG, RS

Random Effect:

Observation level random effect: RanDate1<-1:length(Date1)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation)

['glmerMod']

Family: binomial (logit)

Formula: y1 ~ AverageTemp1 + Season1 + Roost1 + (1 | RanDate1)

AIC	BIC	logLik	deviance	df.resid
265.5	282.1	125.7	251.5	73

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.64352	-0.16904	-0.02087	0.12407	0.65900

Random effects:

Groups	Name	Variance	Std.Dev.
RanDate1	(Intercept)	17.47	4.179

Number of obs: 80, groups: RanDate1, 80

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-28.0314	9.6135	-2.916	0.003547 **
AverageTemp1	0.8881	0.2930	3.031	0.002434 **
Season1NMP	6.1796	1.8256	-3.385	0.000712 ***
Roost1C5R	4.5972	1.5631	2.941	0.003270 **
Roost1CG	4.5207	2.3951	1.887	0.059097 .
Roost1RS	5.3711	1.7876	3.005	0.002658 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	AvrgT1	Ss1NMP	Rs1C5R	Rst1CG
AverageTnp1	-0.990				
Season1NMP	-0.343	0.273			
Roost1C5R	-0.286	0.222	-0.219		

Roost1CG	-0.199	0.170	-0.214	0.430	
Roost1RS	-0.211	0.176	-0.414	0.628	0.447

Check for overdispersion (needs package blmecco) Should be around 1; values over 1.4 suggest serious overdispersion

```
dispersion_glmmer(m10)
[1] 0.7597003
```

Multiple Comparisons of Means: Tukey Contrasts

Fit: glmmer(formula = y1 ~ AverageTemp1 + Season1 + Roost1 + (1 | RanDate1),
family = binomial)

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)
C5R - C5L == 0	4.59722	1.56306	2.941	0.0169 *
CG - C5L == 0	4.52073	2.39513	1.887	0.2261
RS - C5L == 0	5.37112	1.78757	3.005	0.0135 *
CG - C5R == 0	-0.07649	2.22770	-0.034	1.0000
RS - C5R == 0	0.77390	1.45913	0.530	0.9500
RS - CG == 0	0.85039	2.25926	0.376	0.9812

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

R output for GLMM 2 (Fig. 2b):

Site use data set: April - December 2013 and April – November 2014 (CL and CR)

Temperature data set: maximum air temperature at La Selva during April - December 2013 and April – November 2014

Dependent variable: proportion of bats in alternate roost sites:

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y<-cbind(BatsNonPref,BatsPref)
```

Fixed effects:

Tmax: daily maximum air temperature at La Selva

Season: Mating period (MP), non-mating period (NMP)

Group: CL, CR

Random effects:

Year (2013, 2014)

Observation level random effect: RanDate<-1:length(Date)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation)

['glmerMod']

Family: binomial (logit)

Formula: y ~ Tmax + Season + Group + (1 | Year) + (1 | RanDate)

AIC	BIC	logLik	deviance	df.resid
1026.4	1049.5	-507.2	1014.4	342

Scaled residuals:

Min	1Q	Median	3Q	Max
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-0.44823 -0.08602 -0.00262 0.07412 0.65190

Random effects:

Groups	Name	Variance	Std.Dev.
RanDate	(Intercept)	56.83	7.539
Year	(Intercept)	0.00	0.000

Number of obs: 348, groups: RanDate, 348; Year, 2

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-102.7103	10.9350	-9.393	< 2e-16 ***
Tmax	3.0738	0.3316	9.269	< 2e-16 ***
SeasonNMP	-3.1845	1.0928	-2.914	0.00357 **
GroupCR	4.8536	1.0193	4.762	1.92e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Tmax	SsnNMP
Tmax	-0.998		
SeasonNMP	0.055	-0.077	
GroupCR	-0.226	0.180	-0.111

Check for overdispersion (needs package blmecc) Should be around 1; values over 1.4 suggest serious overdispersion

> dispersion_glmer(m6)

[1] 0.6441327

R output for GLMM 3:

Data set: Paternity data and information of territorial males from Cabina 5 (CL and CR) 2011, 2013-2014

Dependent variable: number of pups sired per cohort

Fixed effect:

Status: non-territorial (NonTerr), territorial in primary roost site (Pref), territorial in alternate roost site (NonPref)

Centered forearm size: I(FA – 37.6); To improve GLMM convergence forearm size was centered by its mean by subtracting mean forearm size (i.e. 37.6 mm) from each forearm value.

Random Effects:

Cohort: 2011_1, 2013_1, 2013_2, 2014_1, 2014_2

ID: individual males

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation)

['glmerMod']

Family: poisson (log)

Formula: Offspring ~ Status + I (FA – 37.6) + (1 | Cohort) + (1 | ID)

AIC	BIC	logLik	deviance	df.resid
146.9	160.3	-67.5	134.9	63

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.3307	-0.5317	-0.4466	0.3796	3.0228

Random effects:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.00000	0.000
Cohort	(Intercept)	0.08882	0.298

Number of obs: 69, groups: ID, 29; Cohort, 5

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.1164	0.2799	-0.416	0.67753
StatusNonTerr	-1.1670	0.3868	-3.017	0.00256 **
StatusPref	1.0894	0.3798	2.868	0.00413 **
I(FA - 37.6)	-0.2812	0.1775	-1.584	0.11322

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	SttsNT	SttsPr
StatusNnTrr	-0.549		
StatusPref	-0.646	0.478	
I(FA-37.6)	0.276	-0.212	-0.564

Check for overdispersion (needs package blmecco) Should be around 1; values over 1.4 suggest serious overdispersion

dispersion_glmmer(mod1)

[1] 0.9489375

Multiple Comparisons of Means: Tukey Contrasts

Fit: glmer(formula = Offspring ~ Status + I(FA - 37.6) + (1 | Cohort) + (1 | ID),
family = poisson)

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)
NonTerr - NonPref == 0	-1.1670	0.3868	-3.017	0.00719 **
Pref - NonPref == 0	1.0894	0.3798	2.868	0.01148 *
Pref - NonTerr == 0	2.2564	0.3918	5.759	< 0.001 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)