

Individual Condition vs Nest Size with instar sex and instar number as a factor

Ruth Sharpe

12 September, 2016

AIC Values of all possible models with instar always included

note: InstarNumber is a factor

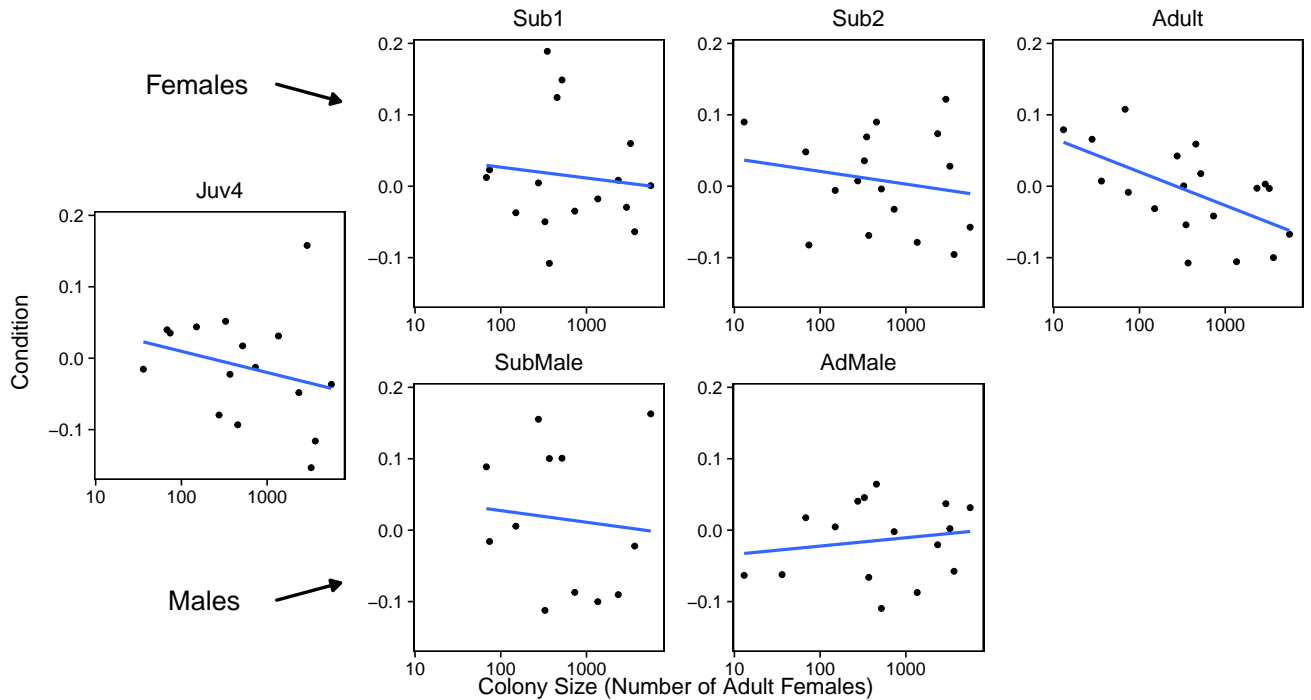
AIC_Diff	AIC	model	num.predictors
0	-2086	condResiduals ~ logCtFm + logCtFm + logCtFm:InstarNumber + (1 NestID)	7
2	-2084	condResiduals ~ logCtFm + logCtFm + logCtFm:InstarNumber + InstarSex:logCtFm + (1 NestID)	8
3.15	-2083	condResiduals ~ logCtFm + logCtFm + logCtFm:InstarNumber + InstarSex:InstarNumber + (1 NestID)	9
3.29	-2083	condResiduals ~ logCtFm + logCtFm + logCtFm:InstarNumber + InstarSex:InstarNumber + InstarSex:logCtFm + (1 NestID)	10
4.17	-2082	condResiduals ~ logCtFm + logCtFm + (1 NestID)	4
5.67	-2080	condResiduals ~ logCtFm + logCtFm + InstarSex:InstarNumber + InstarSex:logCtFm + (1 NestID)	10
5.78	-2080	condResiduals ~ logCtFm + logCtFm + InstarSex:logCtFm + (1 NestID)	5
6.04	-2080	condResiduals ~ logCtFm + logCtFm + InstarSex:InstarNumber + (1 NestID)	9

Graph with lowest AIC model superimposed

Model:

`condResiduals ~ logCtFm + InstarNumber + InstarSex + logCtFm:InstarNumber + (1 | NestID)`

Note: If line on graph is blue R could not plot the lmer, plotting a simple lm instead



Statistics using model with lowest AIC

Full Model: `condResiduals ~ logCtFm + InstarNumber + InstarSex + logCtFm:InstarNumber + (1 | NestID)`

Anova of full model alone

	Sum Sq	Mean Sq	NumDF	DenDF	F.value	Pr(>F)
logCtFm	0.038	0.038	1	22.406	3.542	0.073
InstarNumber	0.099	0.033	3	1,250.800	3.093	0.026
InstarSex	0.0001	0.0001	1	1,250.752	0.007	0.931
logCtFm:InstarNumber	0.130	0.043	3	1,257.371	4.045	0.007

Testing Individual Variables by performing an Anova of full vs reduced model)

Testing Interaction Term nest size * instar against full model. - p < 0.01 SIGNIFICANT **

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	8	-2,081.356	-2,040.201	1,048.678	-2,097.356			
object	11	-2,087.432	-2,030.844	1,054.716	-2,109.432	12.076	3	0.007

Reduced Model: `condResiduals = logCtFm + InstarNumber + InstarSex + (1 | NestID)`

Testing Instar Number against full model. - p < 0.01 SIGNIFICANT **

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	5	-2,080.018	-2,054.296	1,045.009	-2,090.018			
object	11	-2,087.432	-2,030.844	1,054.716	-2,109.432	19.414	6	0.004

Reduced Model: condResiduals = logCtFm + InstarSex + (1 | NestID)

Testing Instar Sex against full model. - NOT significant

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	10	-2,089.425	-2,037.980	1,054.712	-2,109.425			
object	11	-2,087.432	-2,030.844	1,054.716	-2,109.432	0.007	1	0.931

Reduced Model: condResiduals = logCtFm + InstarNumber + +logCtFm:InstarNumber + (1 | NestID)

Testing Nest Size against full model. - p < 0.01 SIGNIFICANT **

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	7	-2,078.512	-2,042.501	1,046.256	-2,092.512			
object	11	-2,087.432	-2,030.844	1,054.716	-2,109.432	16.920	4	0.002

Reduced Model: condResiduals = InstarNumber + InstarSex + (1 | NestID)

Testing Individual Instars

As the interaction is significant testing instar individually

note: pops up saying 'refitting model(s) with ML (instead of REML)' but if make anova refit = FALSE results don't make sense

Adult

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	3	-764.8555	-753.1558	385.4278	-770.8555	NA	NA	NA
object	4	-770.4985	-754.8989	389.2492	-778.4985	7.642948	1	0.0056995

Sub2

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	3	-346.0882	-335.5359	176.0441	-352.0882	NA	NA	NA
object	4	-344.5367	-330.4669	176.2683	-352.5367	0.4484218	1	0.5030854

Sub1

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	3	-415.8428	-404.9064	210.9214	-421.8428	NA	NA	NA
object	4	-413.9760	-399.3942	210.9880	-421.9760	0.133194	1	0.7151432

Juv4

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
..1	3	-338.6935	-328.3403	172.3467	-344.6935	NA	NA	NA
object	4	-337.8281	-324.0239	172.9140 ₃	-345.8281	1.134603	1	0.2867956