Repeated measures and the GLM

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www.youtube.com/user/ProfAndyField/

www.discoveringstatistics.com

www.milton-the-cat.rocks

www.discovr.rocks

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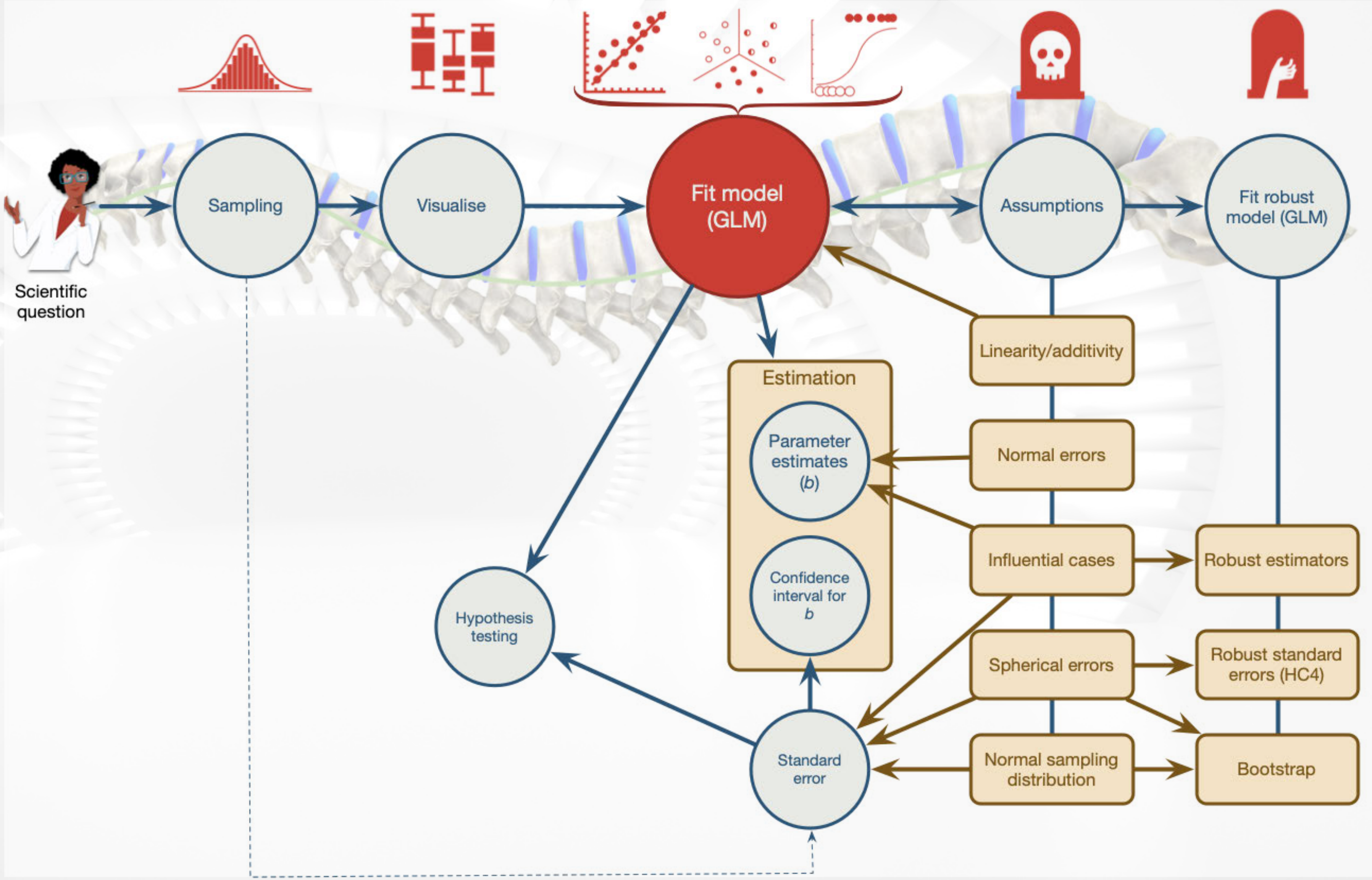

Scientific question
Sampling
Visualise
Fit model (GLM)
Assumptions
Fit robust model (GLM)
Estimation
Parameter estimates (*b*)
Confidence interval for *b*
Hypothesis testing
Standard error
Linearity/additivity
Normal errors
Influential cases
Spherical errors
Normal sampling distribution
Robust estimators
Robust standard errors (HC4)
Bootstrap

- Systematic variance: created by our manipulation
- Unsystematic variance: variance created by unknown factors

Benefits of repeated measures designs

- Sensitivity
  - Unsystematic variance is reduced
  - More sensitive to experimental effects
- Economy
  - Less participants are needed
  - But, be careful of fatigue

Can puppies sniff out aliens?

- Outcome = vocalisations during 1 min sniffing (vocalisations)
- Predictor: type of entity being sniffed (entity)
  - Alien (not in humanoid form)
  - Human (control for alien vs human)
  - Mannequin (control for humanoid form)
  - Shapeshifter (alien in humanoid form)
- dog_name indicates the name of the dog (*N* = 8)

The data

	dog_name	Alien	Human	Mannequin	Shapeshifter	Mean	Variance
	Milton	8	7	1	6	5.50	9.67
	Woofy	9	5	2	5	5.25	8.25
	Ramsey	6	2	3	8	4.75	7.58
	Mr. Snifficus III	5	3	1	9	4.50	11.67
	Willock	8	4	5	8	6.25	4.25
	The Venerable Dr. Waggy	7	5	6	7	6.25	0.92
	Lord Scenticle	10	2	7	2	5.25	15.58
	Professor Nose	12	6	8	1	6.75	20.92
Mean	—	8.12	4.25	4.12	5.75	—	—

The data in R

Table 2: Data for the sniffer dog example

	dog_name	entity	vocalisations
1	Milton	Alien	8
2	Milton	Human	7
3	Milton	Mannequin	1
4	Milton	Shapeshifter	6
5	Woofy	Alien	9
6	Woofy	Human	5
7	Woofy	Mannequin	2
8	Woofy	Shapeshifter	5
9	Ramsey	Alien	6
10	Ramsey	Human	2

Repeated measures and the linear model

To keep things simple, imagine a design where dogs sniff only aliens or humans (e.g., two conditions)

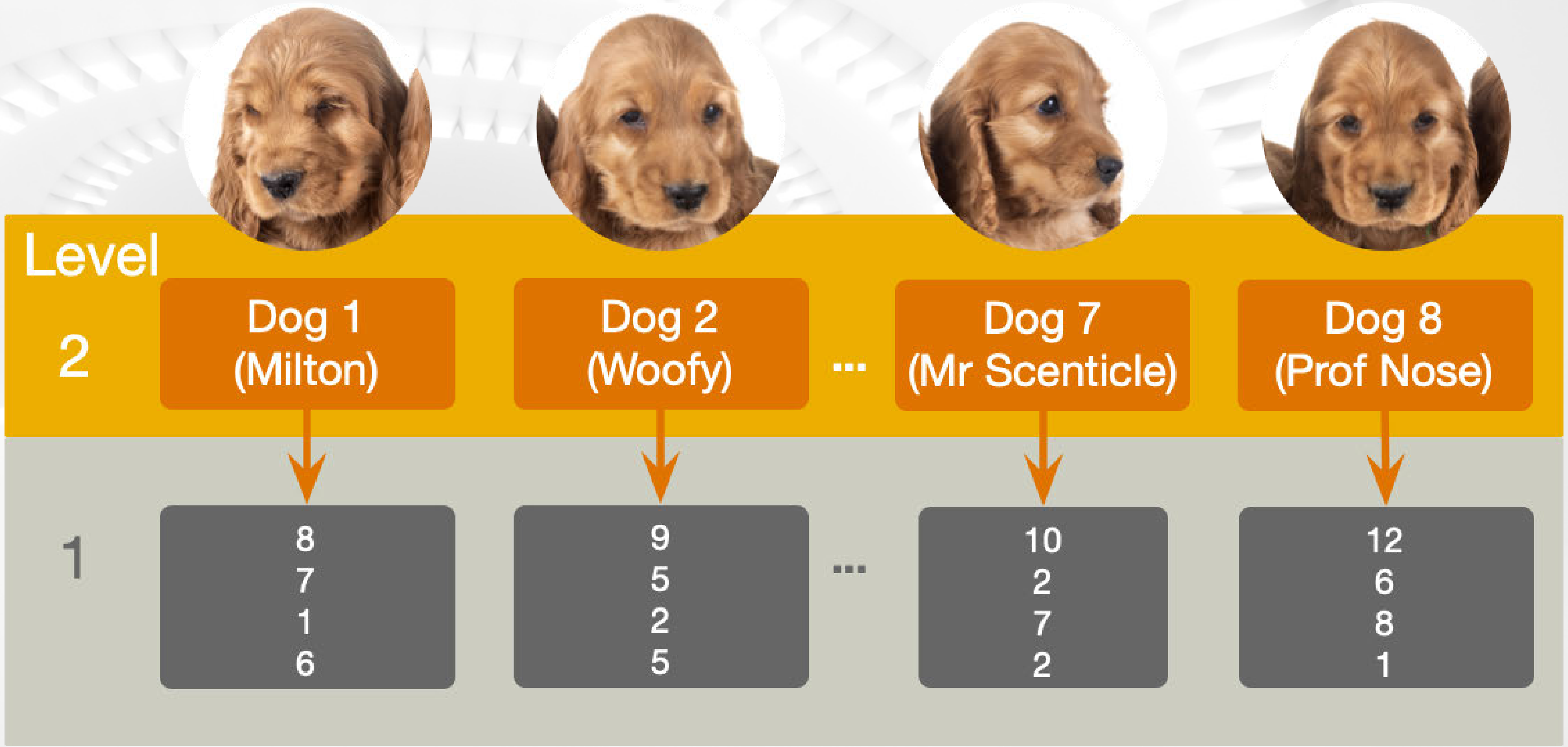
$$\widehat{\text{vocalisations}}_i = \hat{b}_0 + \hat{b}_1\text{entity}_i + e_i$$

Entity sniffed	Dummy variable (entity)
Alien	1
Human	0

Same participants in all conditions

- Scores across conditions correlate
- Violates the assumption of independent residuals (think back to the lecture on bias)

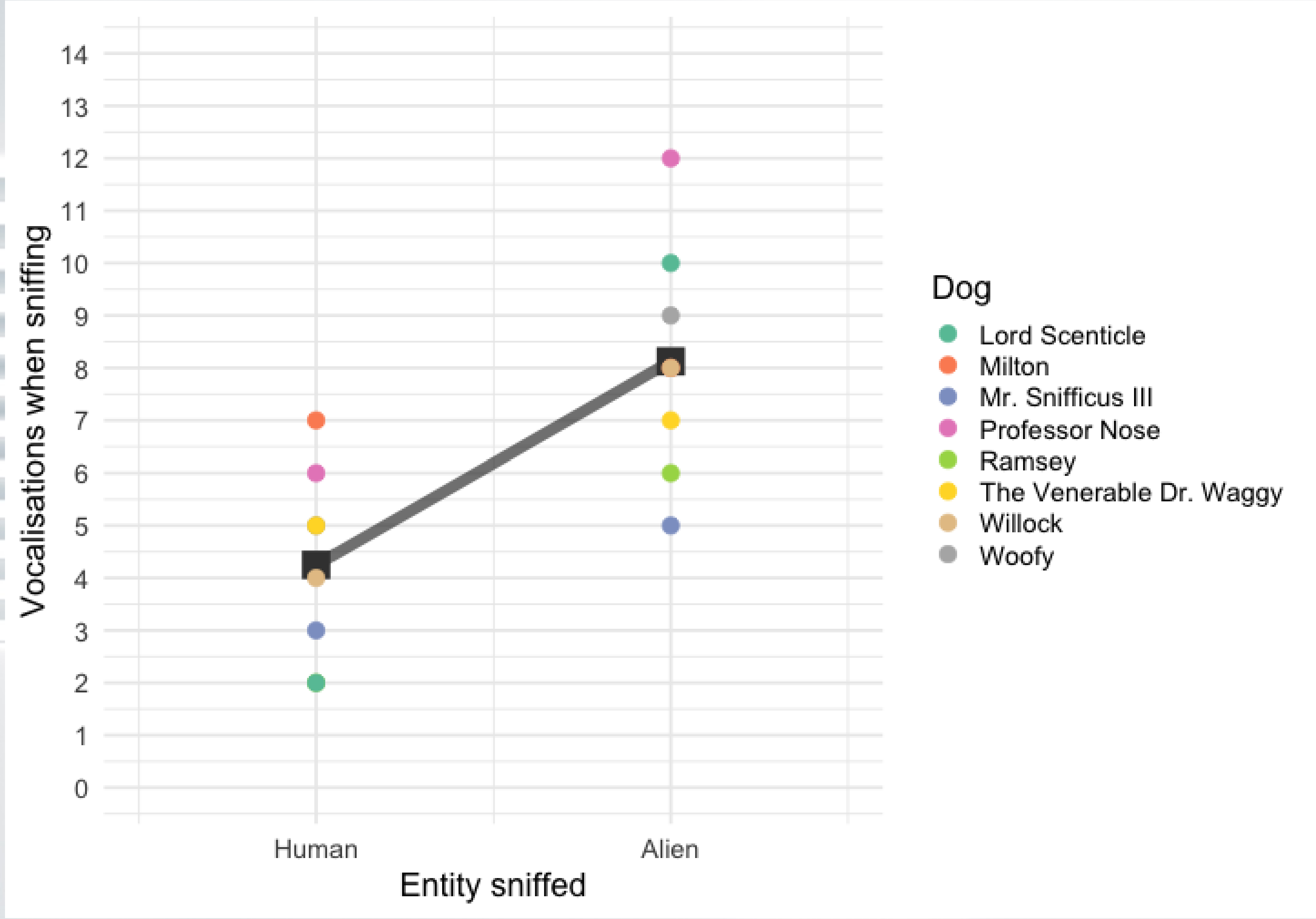
Repeated measures: hierrachical data structure



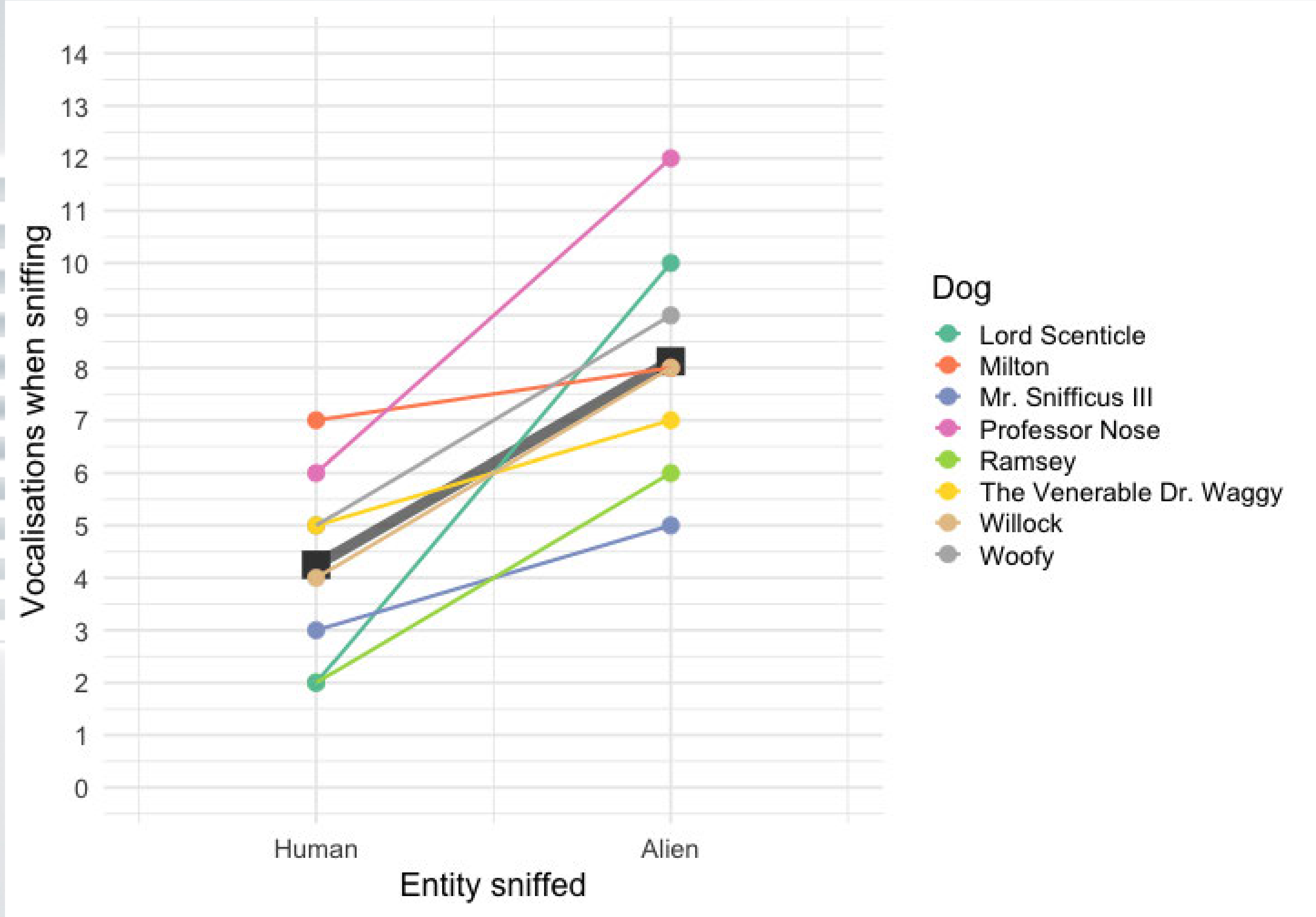
Repeated measures and the linear model

Need to adjust the model to estimate this dependency

$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{entity}_{ij} + e_{ij}$$
$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$
$$\hat{\gamma}_{1j} = \hat{\gamma}_1 + \hat{u}_{1j}$$



$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1\text{entity}_{ij} + e_{ij} + \hat{u}_{0j}$$



$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1 \text{entity}_{ij} + e_{ij} + \hat{u}_{0j} + \hat{u}_{1j}$$

Repeated measures and the linear model

Back to our actual design (with 4 conditions: Alien, Human, Mannequin, Shapeshifter)

- entity would be split into 3 dummy/contrast variables
- Let's just use default dummy coding

Entity sniffed	Dummy 1 (Alien vs. mannequin)	Dummy 2 (Shapeshifter vs. mannequin)	Dummy 3 (Human vs. mannequin)
Alien	1	0	0
Shapeshifter	0	1	0
Human	0	0	1
Mannequin	0	0	0

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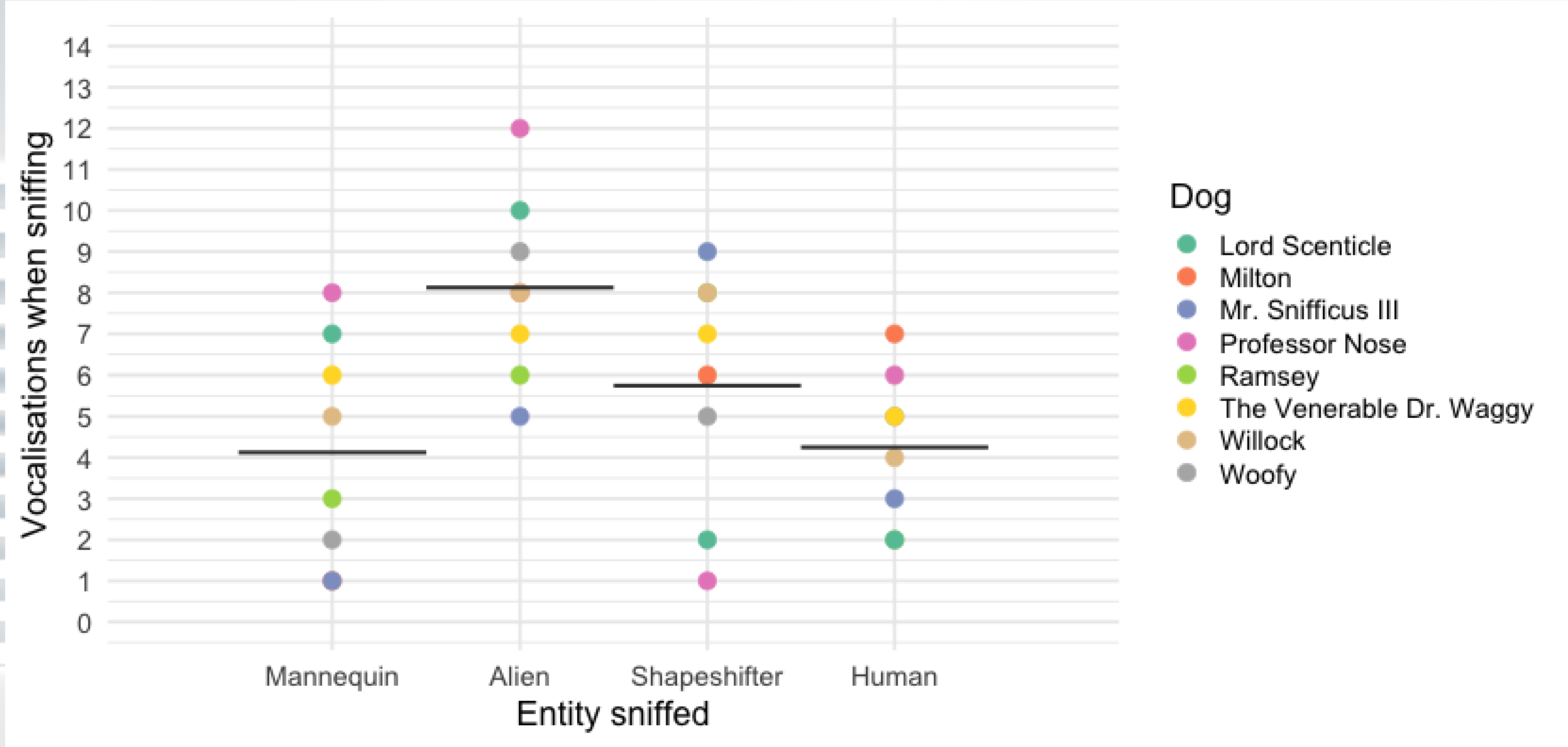
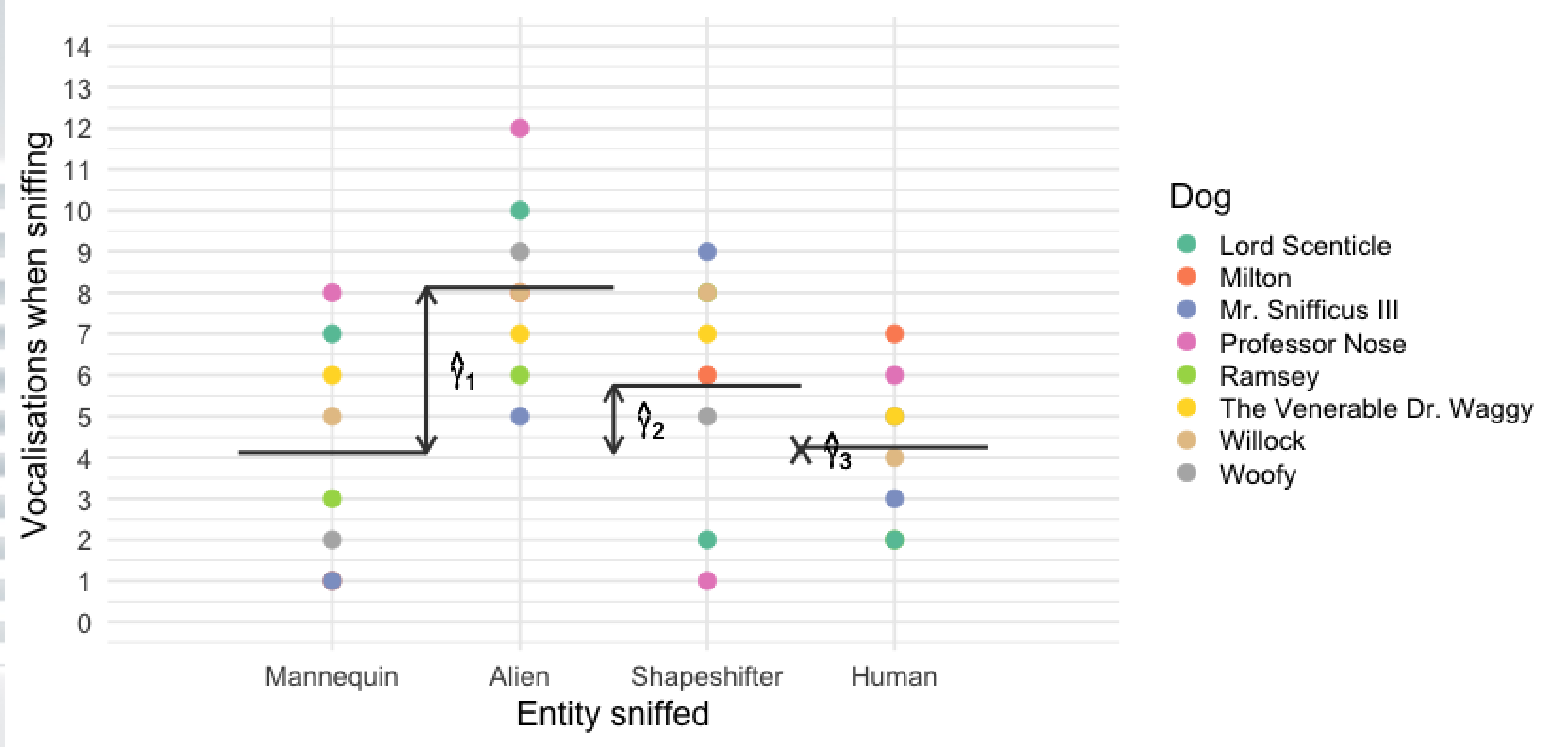
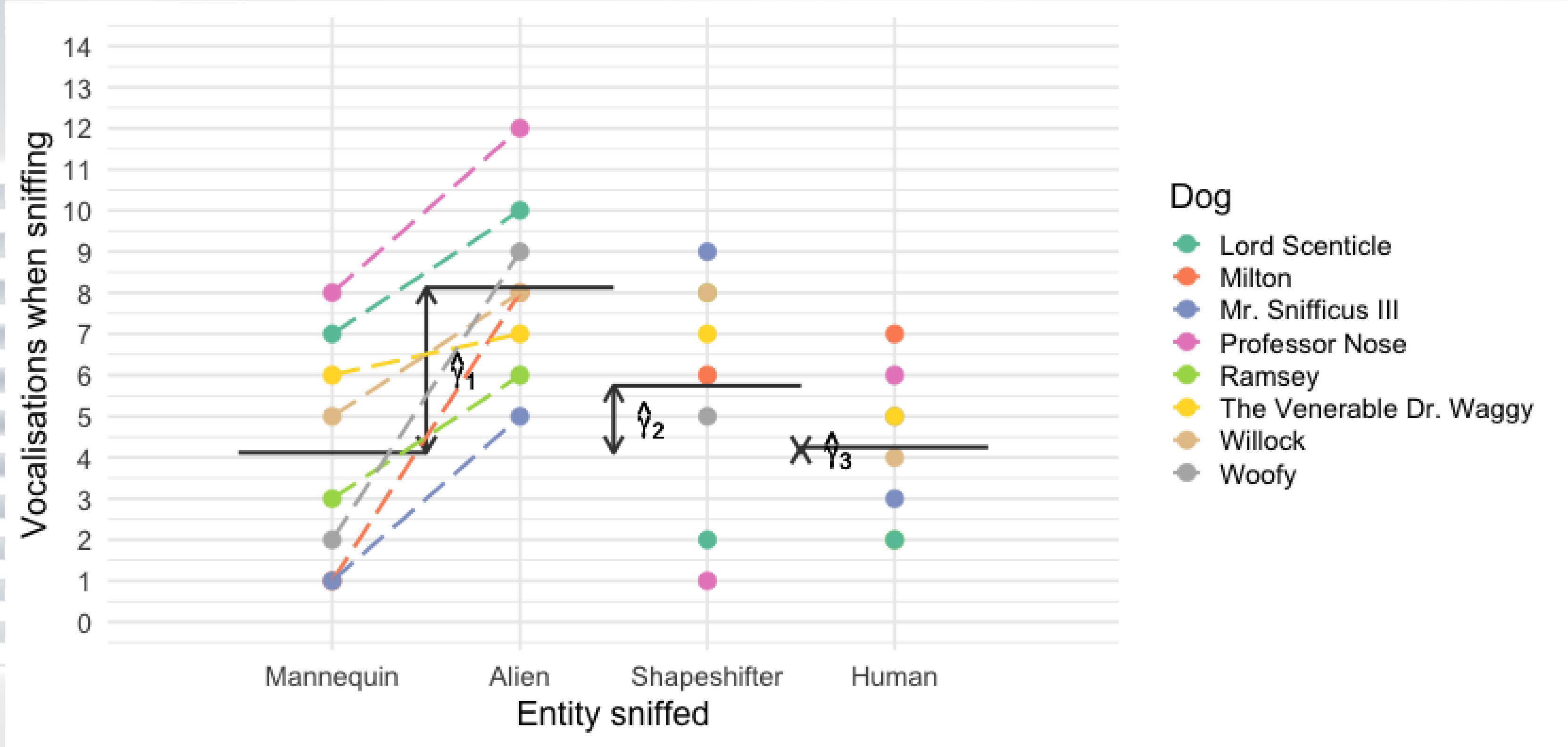


Vocalisations when sniffing
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
Mannequin
Alien
Shapeshifter
Human
Entity sniffed
Dog
Lord Scenticle
Milton
Mr. Snifficus III
Professor Nose
Ramsey
The Venerable Dr. Waggy
Willock
Woofy



$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_1 \text{alien vs. manq}_{ij} + \hat{\gamma}_2 \text{shape vs. manq}_{ij} + \hat{\gamma}_3 \text{human vs. manq}_{ij} + e_{ij}$$

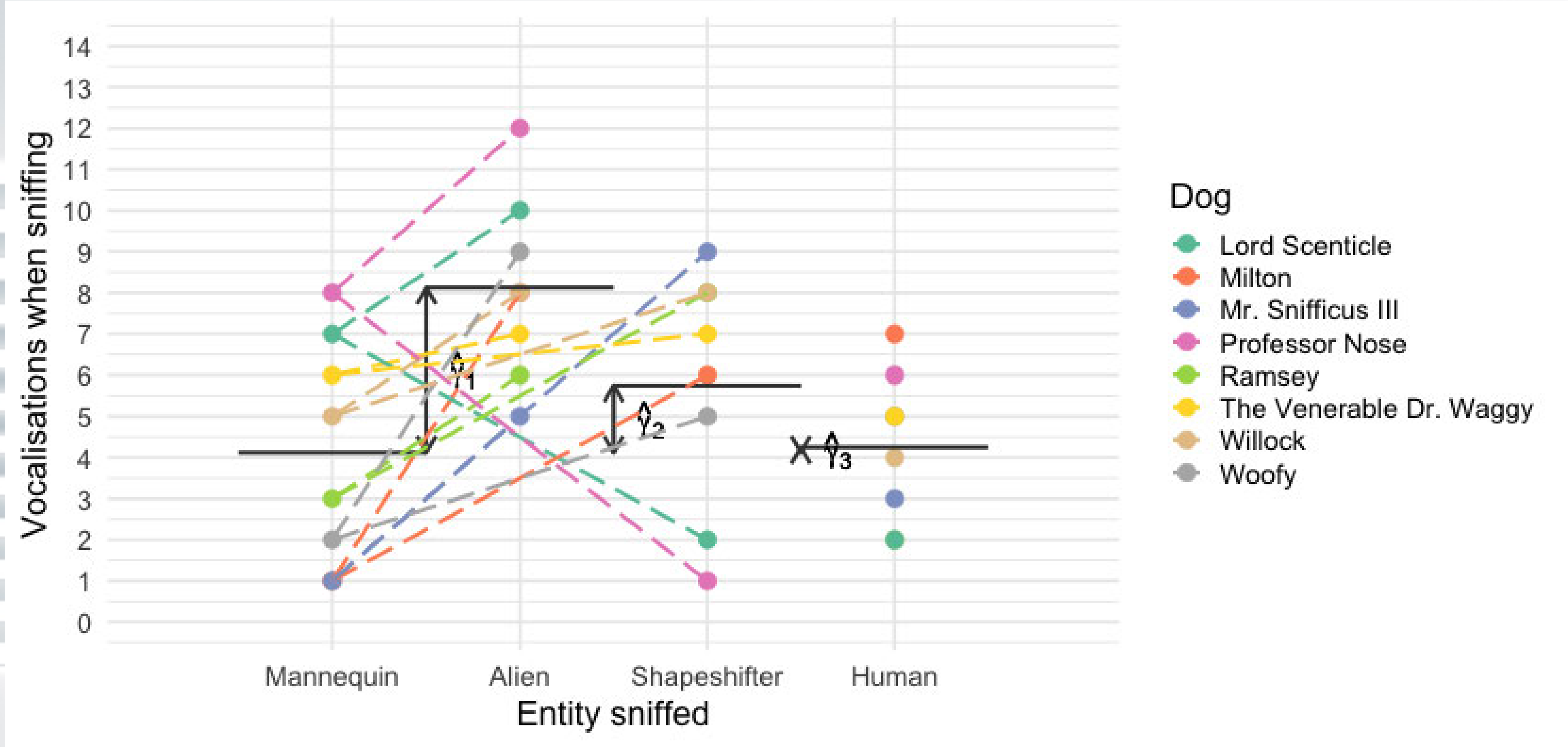
$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$



$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{alien vs. manq}_{ij} + \hat{\gamma}_{2j}\text{shape vs. manq}_{ij} + \hat{\gamma}_{3j}\text{human vs. manq}_{ij} + e_{ij}$$

$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$

$$\hat{\gamma}_{1j} = \hat{\gamma}_1 + \hat{u}_{1j}$$

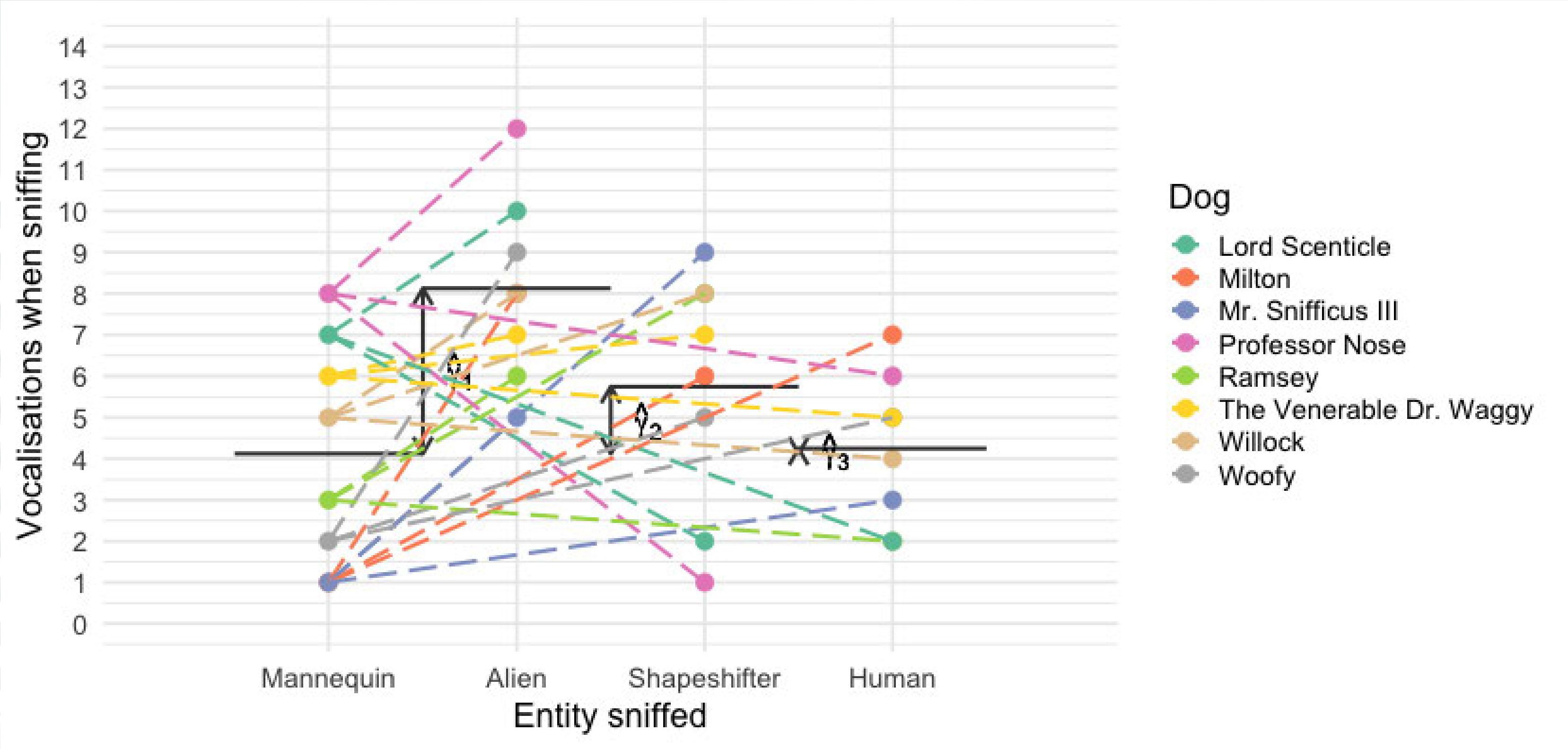


$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{alien vs. manq}_{ij} + \hat{\gamma}_{2j}\text{shape vs. manq}_{ij} + \hat{\gamma}_{3j}\text{human vs. manq}_{ij} + e_{ij}$$

$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$

$$\hat{\gamma}_{1j} = \hat{\gamma}_1 + \hat{u}_{1j}$$

$$\hat{\gamma}_{2j} = \hat{\gamma}_2 + \hat{u}_{2j}$$



$$\widehat{\text{vocalisations}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{alien vs. manq}_{ij} + \hat{\gamma}_{2j}\text{shape vs. manq}_{ij} + \hat{\gamma}_{3j}\text{human vs. manq}_{ij} + e_{ij}$$

$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$

$$\hat{\gamma}_{1j} = \hat{\gamma}_1 + \hat{u}_{1j}$$

$$\hat{\gamma}_{2j} = \hat{\gamma}_2 + \hat{u}_{2j}$$

$$\hat{\gamma}_{3j} = \hat{\gamma}_3 + \hat{u}_{3j}$$

Approaches to repeated measures designs

Historic: Repeated measures ANOVA (RM-ANOVA)

- Restricts the model in two ways
- Assumes effects are equivalent across participants (the effect in participant 1 is the same as in participant 2)
- Errors have compound symmetry/sphericity
  - CS: The correlation between scores across conditions is the same
  - Sphericity: differences between scores in pairs of conditions have the same variance
  - These restrictions may be unrealistic

Multilevel modelling (MLM) approach

- Fewer restrictions: doesn't require CS or sphericity
- MLM can include multiple hierarchical structures (e.g., observations within people, within clinics)
- MLMs can (in general) cope with missing values RM-ANOVA cannot.
- MLMs can be extended to categorical outcomes, RM-ANOVA cannot.
- Contrast coding is possible

Fitting the model

- Use `lme4::lme()` or `nlme:lme()`
  - A trickier but more flexible option
  - Manually set contrasts
  - Can get parameter estimates, diagnostic plots, and robust methods

Contrasts

If the dog training has been successful then we'd expect sniffer dogs to make more vocalisations when sniffing alien entities than non alien-entities.

- Contrast 1: {alien, shapeshifter} vs. {human, mannequin}

We have two 'chunks' in contrast 1 that would then need to be decomposed:

- Contrast 2: {alien} vs. {shapeshifter}
- Contrast 3: {human} vs. {mannequin}

Using the rules for contrast coding we'd get the codes in Table 4:

Table 4: Contrast coding for the entity variable

Group	Contrast 1	Contrast 2	Contrast 3
Alien	1/2	1/2	0
Human	-1/2	0	1/2
Mannequin	-1/2	0	-1/2
Shapeshifter	1/2	-1/2	0

Fitting the model


```
aliens_vs_non = c(1/2, -1/2, -1/2, 1/2)
alien_vs_shape = c(1/2, 0, 0, -1/2)
human_vs_manquin = c(0, 1/2, -1/2, 0)

contrasts(sniff_tib$entity) <- cbind(aliens_vs_non, alien_vs_shape, human_vs_manquin)

sniff_ri <- nlme::lme(
  vocalisations ~ 1,
  random = ~1|dog_name, #
  data = sniff_tib
  )

sniff_ent <- nlme::lme(
  vocalisations ~ entity, #
  random = ~1|dog_name,
  data = sniff_tib
  )

sniff_rs <- nlme::lme(
  vocalisations ~ entity,
  random = ~entity|dog_name, #
  data = sniff_tib)
```

The model

```
anova(sniff_ent)
```

Effect	numDF	denDF	F-value	p-value
(Intercept)	1	21	162.36	0.00
entity	3	21	4.54	0.01

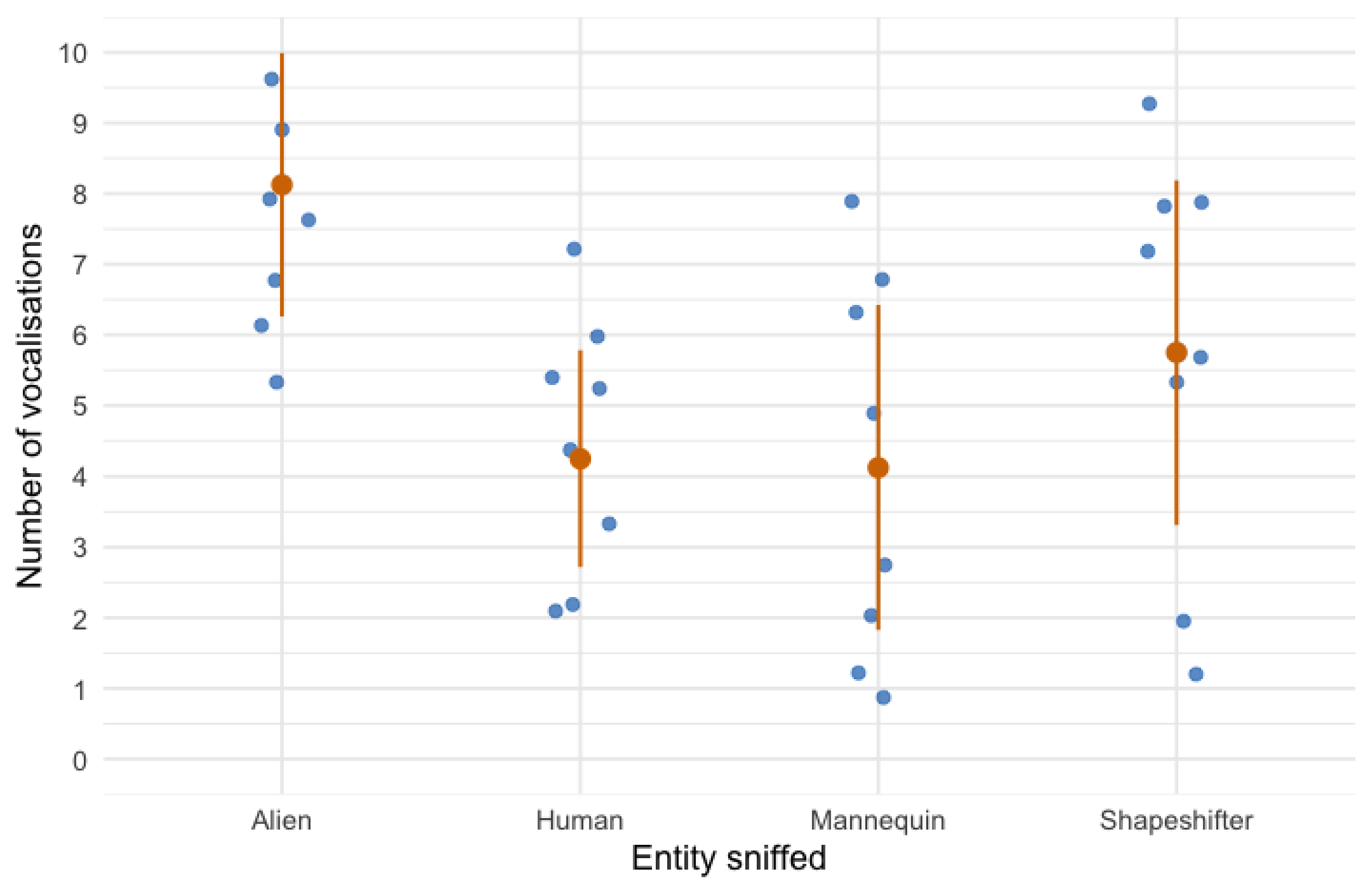
✎ The entity sniffed had a significant effect on the number of vocalisations by sniffer dogs, $F(3, 21) = 4.54$, $p = 0.01$.

Contrasts

```
broom.mixed::tidy(sniff_ent, effects = "fixed")
```

term	estimate	std.error	df	statistic	p.value
(Intercept)	5.562	0.437	21	12.742	0.000
entityaliens_vs_non	2.750	0.873	21	3.150	0.005
entityalien_vs_shape	2.375	1.235	21	1.924	0.068
entityhuman_vs_manquin	0.125	1.235	21	0.101	0.920

Interpretation




Scenting a victory … factorial repeated measures designs
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Can scents distract the sniffer dogs?

- 50 sniffer dogs
  - Participated in all conditions
  - Sniffed 9 different 'things'
- Predictor: entity
  - Human: the dog sniffs a human
  - Shapeshifter the dog sniffs an alien in humanoid form
  - Alien the dog sniffs an alien in lizard form
- Predictor: scent_mask
  - The entity had no masking scent (none)
  - The entity was smeared with human pheromones
  - The entity was smeared with fox pheromones
- Outcome:
  - Number of vocalisations during each 1 minute sniff

The model

- Let's simplify things by ignoring the fact that entity and scent_mask will be represented by two dummy variables each (and the interaction by 4!)
- We can model individual differences in all parameters

$$
\begin{aligned}
\widehat{\text{vocalisations}}_{ij} &= \hat{b}_{0j} + \hat{b}_{1j}\text{entity}_{ij} + \hat{b}_{2j}\text{scent}_{ij} + \hat{b}_{3j}(\text{entity}_{ij} \times \text{scent}_{ij}) + e_{ij} \\
\hat{b}_{0j} &= \hat{b}_0 + \hat{u}_{0j} \\
\hat{b}_{1j} &= \hat{b}_1 + \hat{u}_{1j} \\
\hat{b}_{2j} &= \hat{b}_2 + \hat{u}_{2j} \\
\hat{b}_{3j} &= \hat{b}_3 + \hat{u}_{3j}
\end{aligned}
$$

- This model will be too complex to fit
- The simplest version of the repeated measures model instead treats the effects of predictor variables as fixed, but acknowledges that dogs, overall, will vary in their vocalisations:

$$
\begin{aligned}
\widehat{\text{vocalisations}}_{ij} &= \hat{b}_{0j} + \hat{b}_{1}\text{entity}_{ij} + \hat{b}_{2}\text{scent}_{ij} + \hat{b}_{3}(\text{entity}_{ij} \times \text{scent}_{ij}) + e_{ij} \\
\hat{b}_{0j} &= \hat{b}_0 + \hat{u}_{0j}
\end{aligned}
$$

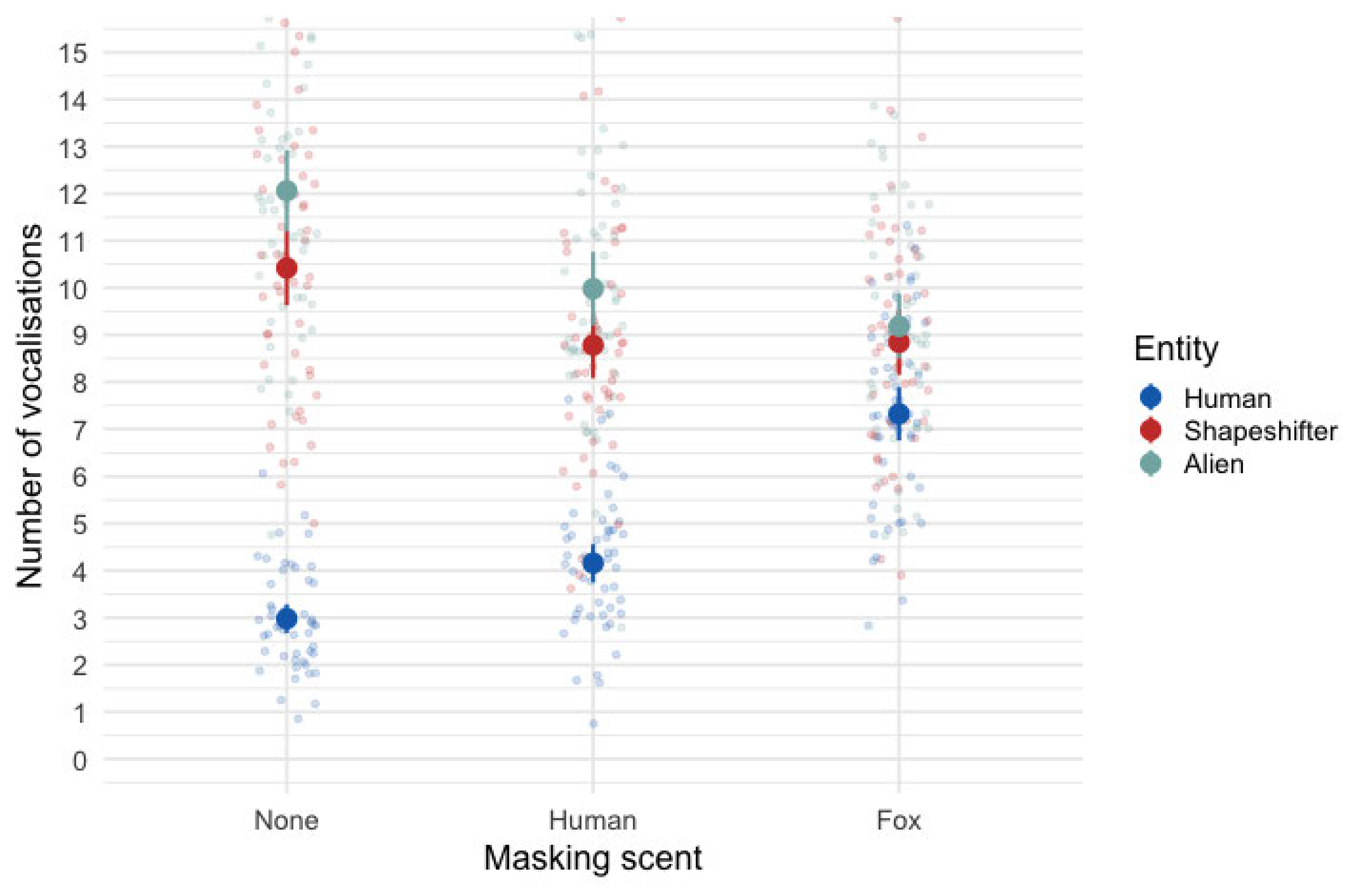
The data

Table 7: Data for the scent masking example

	dog_id	entity	scent_mask	vocalisations
1	56f9p	Alien	Fox	7
2	56f9p	Alien	Human	9
3	56f9p	Alien	None	8
4	56f9p	Shapeshifter	Fox	11
5	56f9p	Shapeshifter	Human	6
6	56f9p	Shapeshifter	None	8
7	56f9p	Human	Fox	3
8	56f9p	Human	Human	3
9	56f9p	Human	None	3
10	2m89y	Alien	Fox	8

Previous 1 2 3 4 5 … 45 Next

The data



Number of vocalisations
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
None
Human
Fox
Masking scent
Entity
Human
Shapeshifter
Alien

Contrasts

We have a natural control group for the entity (human) so a natural contrast is to use dummy coding.

- Contrast 1: {alien} vs. {human}
- Contrast 2: {shapeshifter} vs. {human}

We have a natural control group for the scent masks (no scent) so a natural contrast is to use dummy coding.

- Contrast 1: {human} vs. {none}
- Contrast 2: {fox} vs. {none}

Specifying contrasts

The level order of the variables is:

```
levels(scent_tib$entity)
```

```
## [1] "Human"        "Shapeshifter" "Alien"
```

```
levels(scent_tib$scent_mask)
```

```
## [1] "None"  "Human" "Fox"
```

We can do nothing (default dummy coding will do the above) or set up contrasts explicitly with:

```
contrasts(scent_tib$entity) <- contr.treatment(3, base = 1)
contrasts(scent_tib$scent_mask) <- contr.treatment(3, base = 1)
```

Building models


```
scent_base <- nlme::lme(
  vocalisations ~ 1, #
  random = ~1|dog_id,
  data = scent_tib
  )

scent_ent <- nlme::lme(
  vocalisations ~ entity, #
  random = ~1|dog_id,
  data = scent_tib
  )

scent_scent <- nlme::lme(
  vocalisations ~ entity + scent_mask, #
  random = ~1|dog_id,
  data = scent_tib
  )

scent_int <- nlme::lme(
  vocalisations ~ entity + scent_mask + entity:scent_mask, #
  random = ~1|dog_id,
  data = scent_tib
  )
```

```
anova(scent_base, scent_ent, scent_scent, scent_int)
```

Name	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
scent_base	1	3	2428.57	2440.89	-1211.29		NA	NA
scent_ent	2	5	2107.09	2127.60	-1048.54	1 vs 2	325.48	<.001
scent_scent	3	7	2099.80	2128.48	-1042.90	2 vs 3	11.29	.004
scent_int	4	11	1925.05	1970.03	-951.53	3 vs 4	182.74	<.001

```
anova(scent_base, scent_ent, scent_scent, scent_int)
```

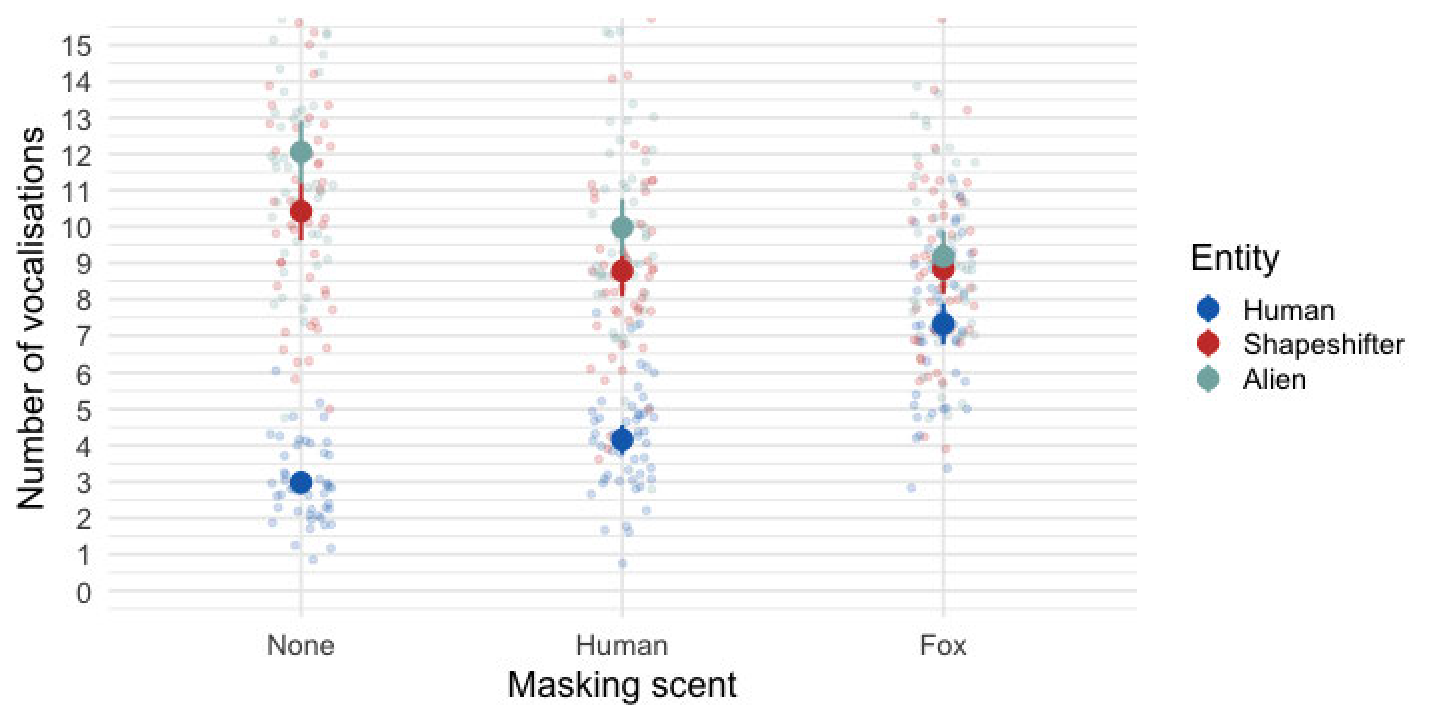
Name	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
scent_base	1	3	2428.57	2440.89	-1211.29		NA	NA
scent_ent	2	5	2107.09	2127.60	-1048.54	1 vs 2	325.48	<.001
scent_scent	3	7	2099.80	2128.48	-1042.90	2 vs 3	11.29	.004
scent_int	4	11	1925.05	1970.03	-951.53	3 vs 4	182.74	<.001

Repeat the following mantra:

"It is never sensible to interpret main effects in the presence of a significant interaction effect."

Entity × scent_mask interaction

✎ The interaction effect suggests that the effect of entity on vocalisations was significantly moderated by what scent the entity was wearing, $\chi^2(4) = 11.29$, $p < .001$.

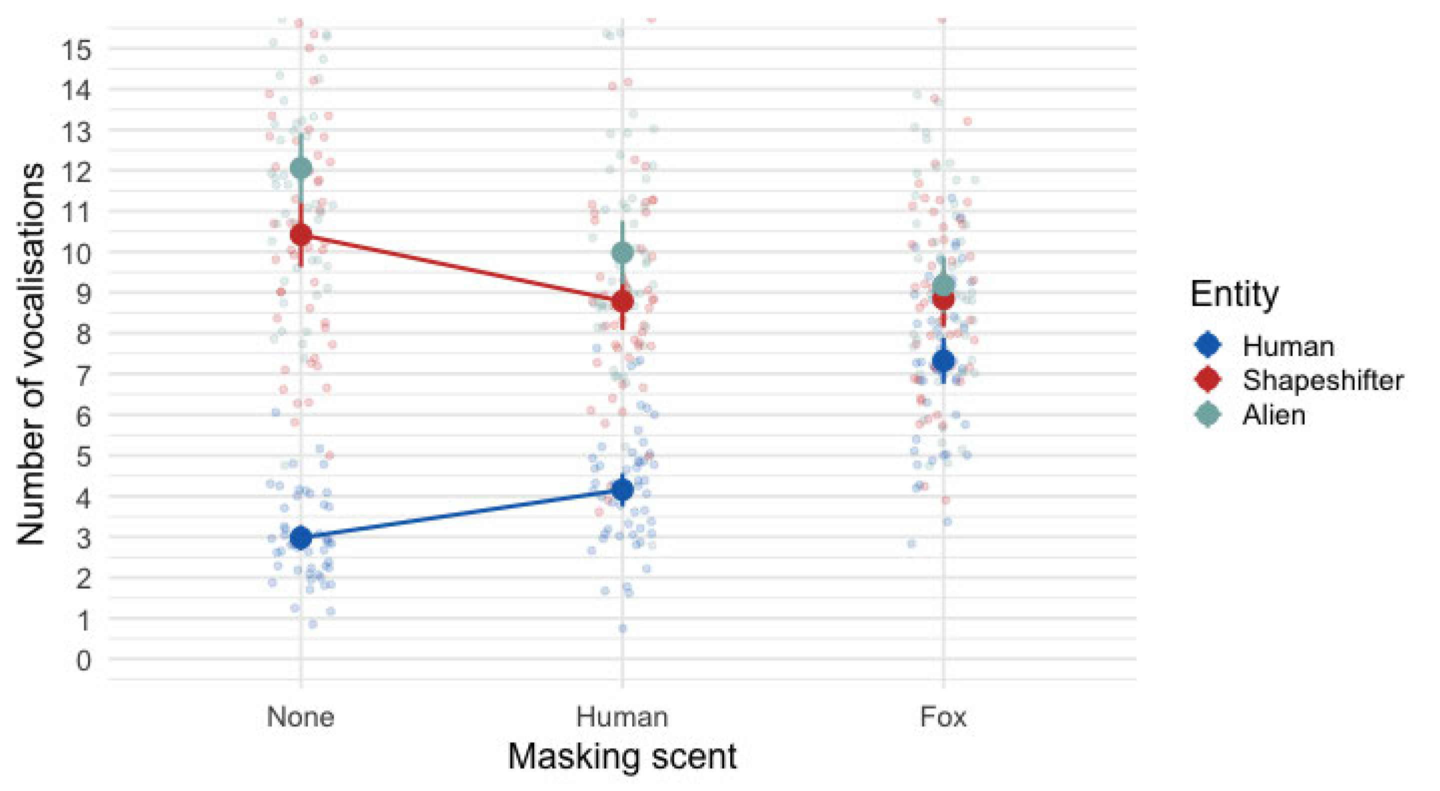


```
broom.mixed::tidy(scent_int, effects = "fixed")
```

term	estimate	std.error	df	statistic	p.value
(Intercept)	2.98	0.331	392	8.993	0.000
entityShapeshifter	7.44	0.360	392	20.641	0.000
entityAlien	9.08	0.360	392	25.191	0.000
scent_maskHuman	1.18	0.360	392	3.274	0.001
scent_maskFox	4.34	0.360	392	12.041	0.000
entityShapeshifter:scent_maskHuman	-2.82	0.510	392	-5.532	0.000
entityAlien:scent_maskHuman	-3.26	0.510	392	-6.395	0.000
entityShapeshifter:scent_maskFox	-5.92	0.510	392	-11.614	0.000
entityAlien:scent_maskFox	-7.22	0.510	392	-14.164	0.000

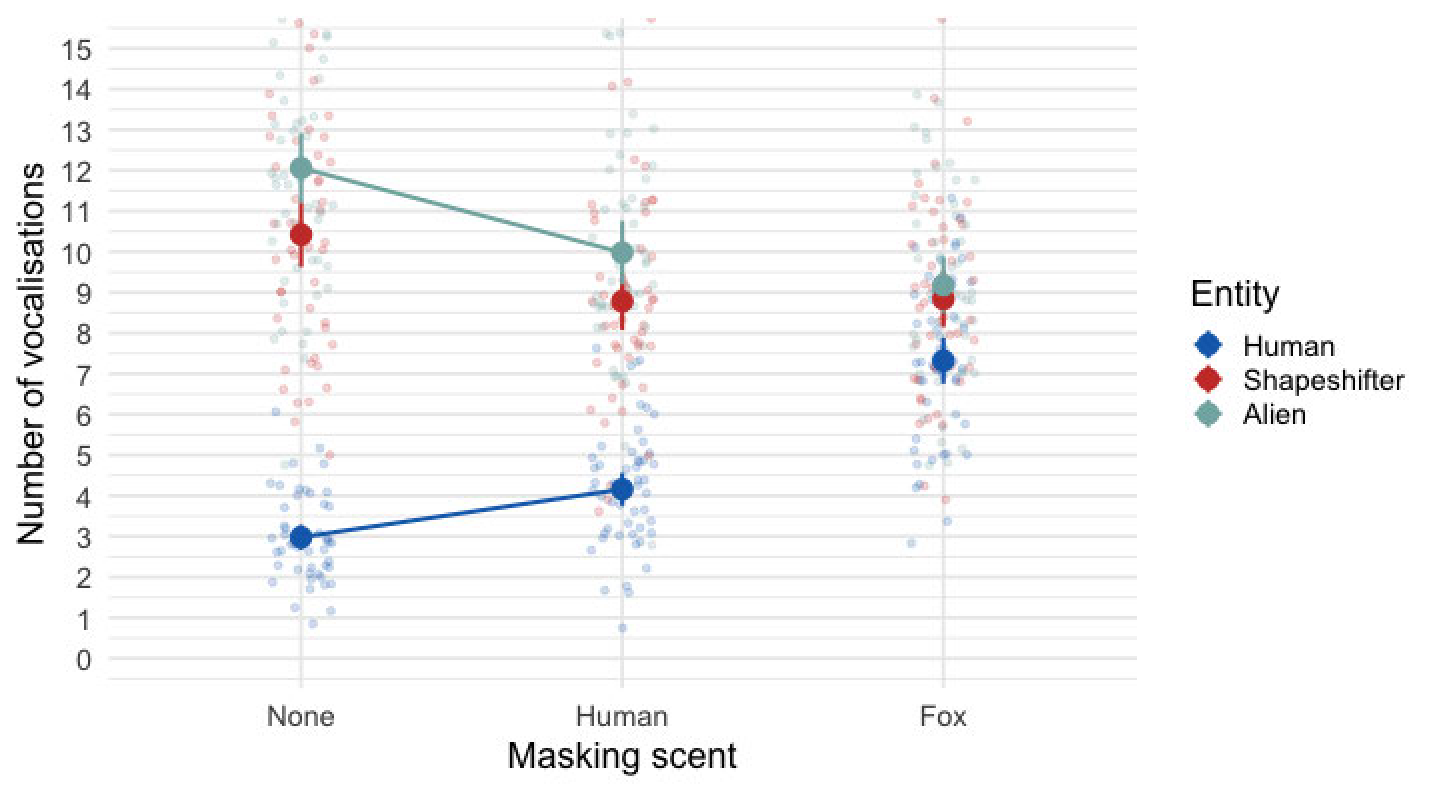
Entity × scent_mask interaction: parameter 1

term	estimate	std.error	df	statistic	p.value
entityShapeshifter:scent_maskHuman	-2.82	0.51	392	-5.53	0



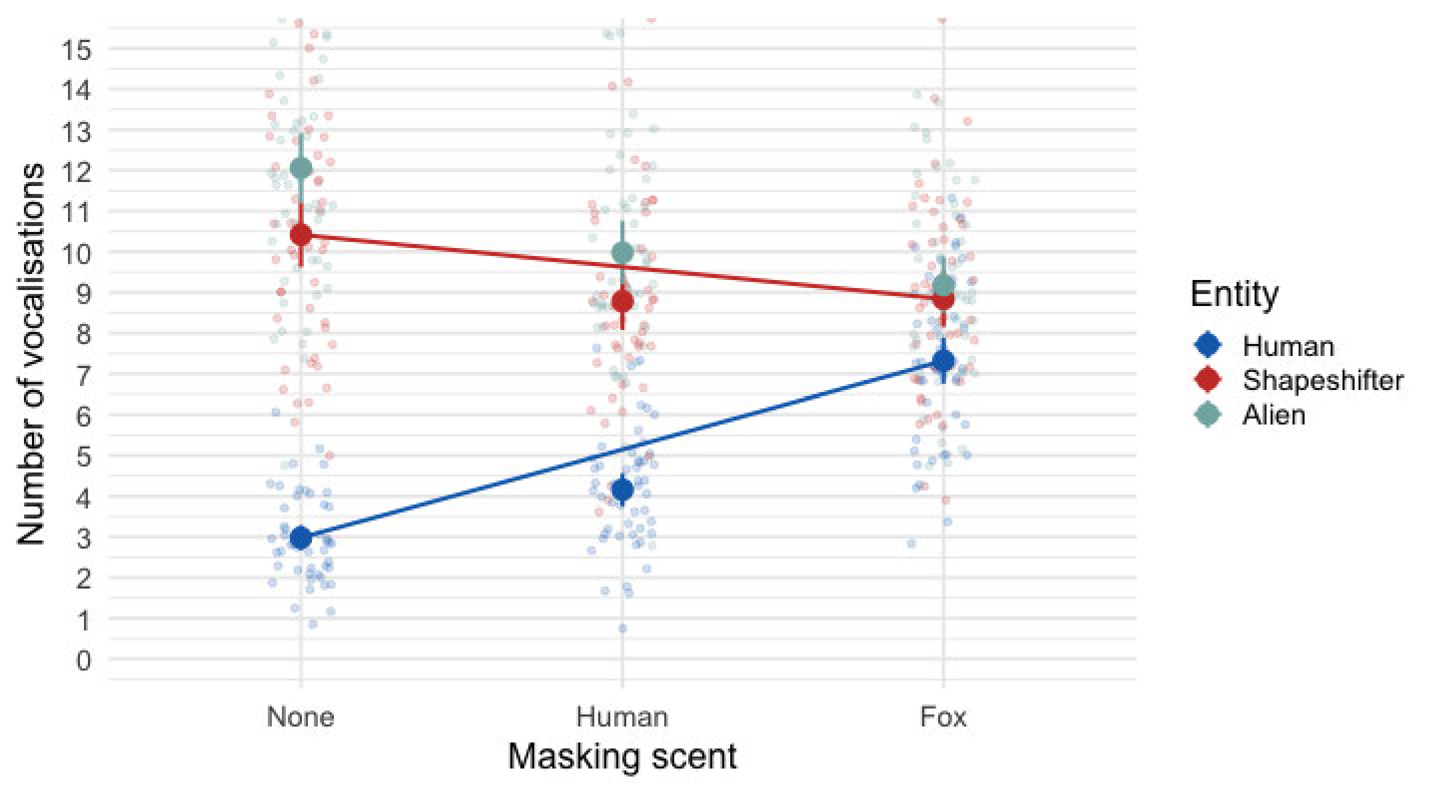
Entity × scent_mask interaction: parameter 2

term	estimate	std.error	df	statistic	p.value
entityAlien:scent_maskHuman	-3.26	0.51	392	-6.4	0



Entity × scent_mask interaction: parameter 3

term	estimate	std.error	df	statistic	p.value
entityShapeshifter:scent_maskFox	-5.92	0.51	392	-11.61	0



Entity × scent_mask interaction: parameter 4

term	estimate	std.error	df	statistic	p.value
entityAlien:scent_maskFox	-7.22	0.51	392	-14.16	0