

ERRATUM 3 APRIL 2025; SEE BELOW



## Supplementary Materials for

### Whale song shows language-like statistical structure

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#### The PDF file includes:

Materials and Methods  
Figs. S1 to S18  
Tables S1 to S3  
References

#### Other Supplementary Material for this manuscript includes the following:

MDAR Reproducibility Checklist  
Code S1  
Data S1 to S3

Erratum (3 April 2025): After publication of the Research Article “Whale song shows language-like statistical structure” (7 February 2025, p. 649), the authors spotted a minor error in the code used for calculating R<sup>2</sup> for the analysis of the brevity law. A corrected analysis, using Poisson regression, gives the same results, demonstrating that the detected subsequences show a strong relation between frequency and length, as predicted by Zipf’s law of brevity. The error in the code only affected the analysis of Zipf’s law of brevity and not the main analyses of Zipf’s law of frequency, for which the R<sup>2</sup> analysis was appropriately applied. The authors have replaced the Zipf’s law of brevity R<sup>2</sup> analysis with a Poisson mixed-effects regression, the state-of-the-art method recommended by Youngblood [Proc. Biol. Sci. 291, 20240250 (2024)]. This shows that the brevity law does indeed hold with P < 0.00001 for all the authors’ segmentation methods. Figure 3 and figs. S11 and S12 have been amended to reflect this, and section 6.2 of the code S1 supplementary file has been updated to include the new analysis. These corrections do not affect the conclusions of the paper in any way.

## **Materials and Method**

### Field site and song recording

Humpback whale songs were recorded in New Caledonia (South Lagoon) from 2010-2017. The New Caledonian population is a genetically distinct, small (1,732 - 2,384 males) population of humpback whales that breeds in the lagoons and seamounts surrounding New Caledonia, in the western South Pacific (56-59).

Recordings were made using boat-based hydrophones (2010–2017 HiTech) and Zoom recorder (16 bit, sampling rate of 44 kHz, WAV files), and a single passive acoustic recorder (2014–2017, SM2M + Whalesong recorder, Wildlife Acoustics with a sampling rate of 22 kHz) (55). As some singers in this study were not identified, each song recording was treated as a separate singer unless singer ID information was present. This occurred as singers were not always sighted, and/or a photo-ID (or genetic) sample was not possible (e.g., from the autonomous recorder). All recordings included in the analyses were thus taken on different days to minimize pseudoreplication. Further, recordings with less than 10 dB signal-to-noise ratio were excluded from further analysis to ensure only high-quality recordings were included. This resulted in 31 hours of song from 55 recordings (including from 27 identified singers) included in further analyses (Table S1).

This study was approved by the University of St Andrews School of Biology Ethics Committee (ref: SEC2018004). Humpback whales were sampled by the NGO Opération Cétacés (1995-2014) and IRD (2015-2019) under licenses by the Province Sud, Province Nord and the government of New Caledonia.

### Song transcription and sound element classification

Previous analyses have classified the sound elements (termed ‘units’ in humpback literature; we use the term ‘sound elements’ herein to avoid confusion with sub-sequences detected by the segmentation method described below), themes and songs of this dataset (2010-2015 (55)). Specifically, spectrograms were viewed in Raven Pro 1.6 ([www.birds.cornell.edu/raven](http://www.birds.cornell.edu/raven)) and sound elements transcribed based on a quantitative dictionary (self-organizing map, SOM) following (60). Sound elements were first qualitatively and then quantitatively grouped into phrases and themes each year to assign the song type (55). The 2016 and 2017 songs were transcribed following the above procedure (Fig. S13, S14). As a final, overarching check of the robustness of the sound element classification across the 8-year dataset, a subset of sound elements (N=1,694, Table S3; all elements from the first clear rendition of a phrase for each theme) were measured for 11 acoustic parameters (following previous humpback classification analyses (29, 31, 61)) from the highest quality recording each year and all identified singers in the dataset. A random forest analysis was run in R (v. 4.2.1) using the *randomForest* package (62) (*mtry* = 3, 10,000 trees) which resulted in an out-of-bag error rate of 19.19% indicating a very good level of agreement in classification of sound element types across the dataset.

### Data preparation for applying the segmentation method

Each recording was represented as a sequence of sound elements, without any higher-level classification. We removed the coding for phrases, themes, and song cycles since we wanted to see what would be detected solely on the basis of the transitional probabilities between sound

elements. We only used recordings that had at least one complete song cycle, defined as a sequence of themes without repetition of a theme. Since songs differ across years, we applied the segmentation method separately to each year. Note, however, that one singer in 2016 sang the ‘old’ 2015 song; this song was therefore included in the 2015 analysis. We created one file containing all the recordings from a given ‘year’ (without marking theme or song cycle boundaries, but retaining boundaries between recordings taken at different times). See Table S1 for information about the songs.

#### Statistical information

All statistical analyses on the whale song were performed using Python. Details on song element classification (Random Forest) are provided above. The human infant-inspired segmentation pipelines and all subsequent analyses were performed in Python and R. A Pearson product moment correlation from the *scipy.stats* library was used to calculate  $R^2$ . Shuffling and rotating of the data and the analyses of these datasets were performed using custom-written code, available in the Supplementary Materials. The Poisson mixed effects regression was carried out in R (see code in Supplementary Materials for details).

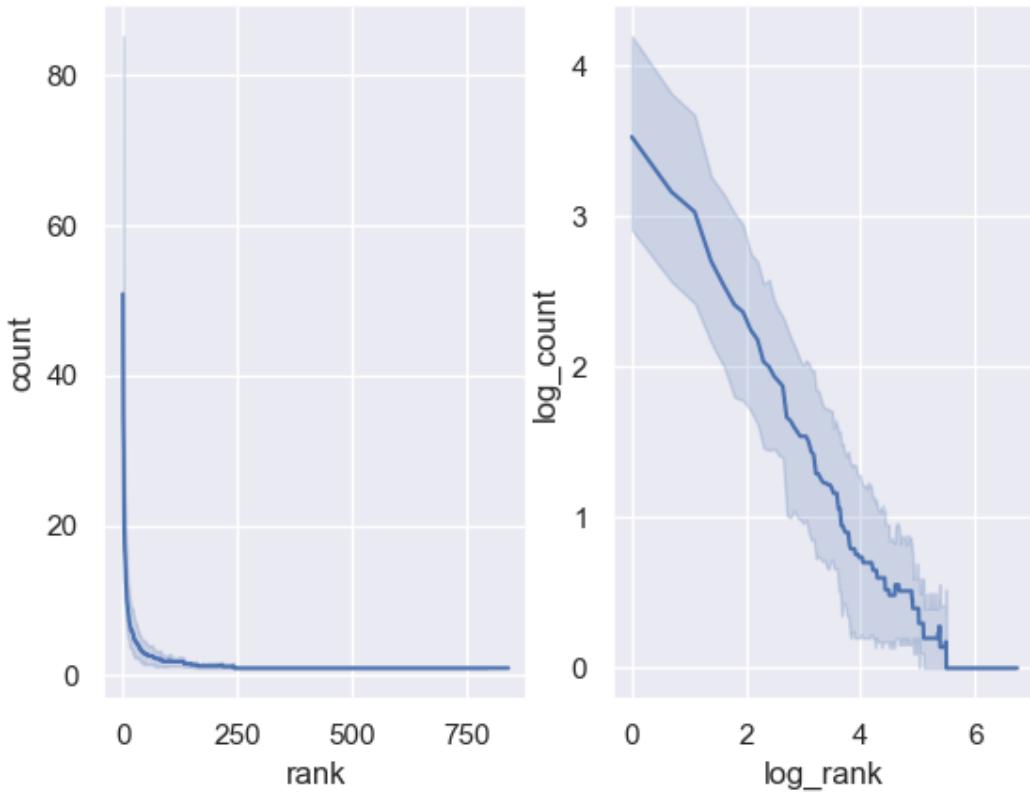
#### Data Availability

Data that support the findings of this study are available in the Supplementary Materials. Data used in the analysis is available for the purposes of reproducing or extending the Zipfian analysis.

#### Code availability

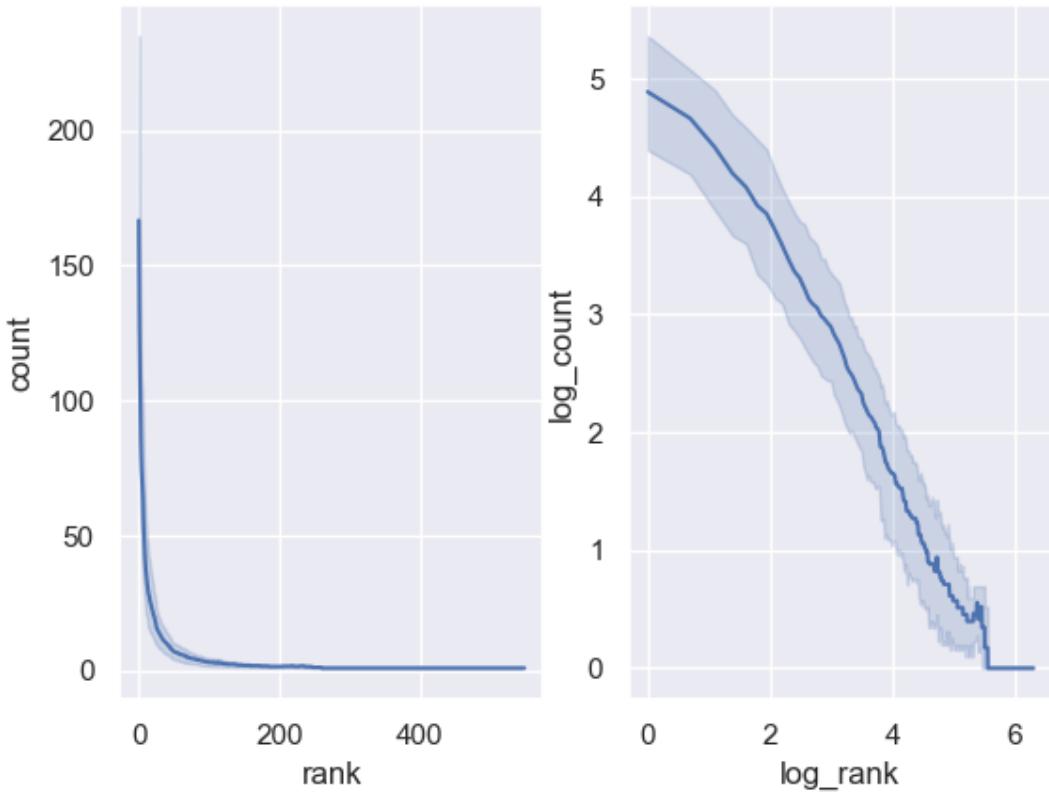
Python code for recreating all the analyses and graphs in this paper is included in the Supplementary Materials.

Erratum (3 April 2025):



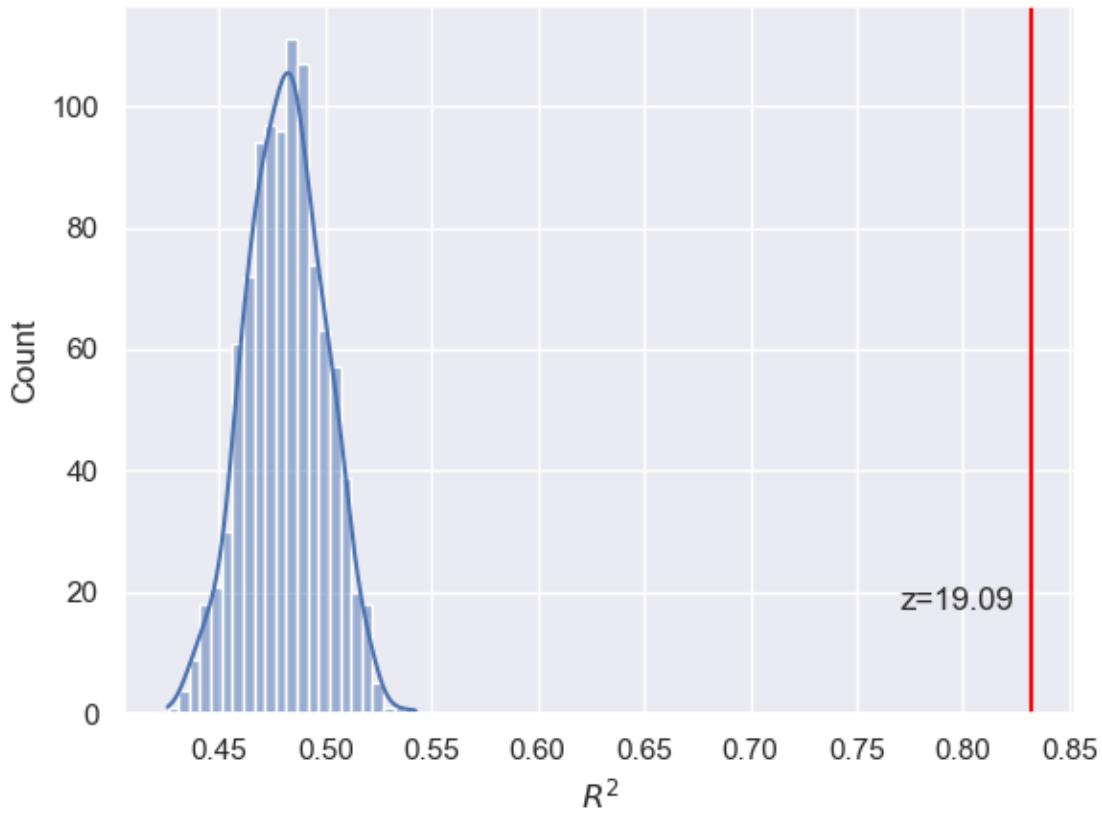
**Fig. S1. Sub-sequences detected by our segmentation method based on a cutting threshold of 0.25 also follow a Zipfian frequency distribution:** we cut whenever the ratio between two consecutive transitional probabilities was lower than 0.25 (compare with Fig. 2A in main paper, which has a cutting ratio of 0.5, and Fig. S2, which has a cutting ratio of 0.75). The left-hand plot shows the frequency of each detected sub-sequence ordered by rank frequency. The right-hand plot shows the same data but with a log scale for both axes. We calculated the frequency of the sub-sequences independently for each year in the dataset, and then aggregated the frequency by rank over the different years (we show the mean and 95% bootstrapped confidence intervals around the mean for each frequency rank over the eight years in the dataset). The straight line we see here on the log-log plot is similar to the one with other thresholds, indicating that our result is robust to different levels of sensitivity for cutting the data. In other words, we find a Zipfian distribution at multiple levels in the data, irrespective of whether we detect lots of smaller units, or fewer larger ones.

Erratum (9 April 2023)



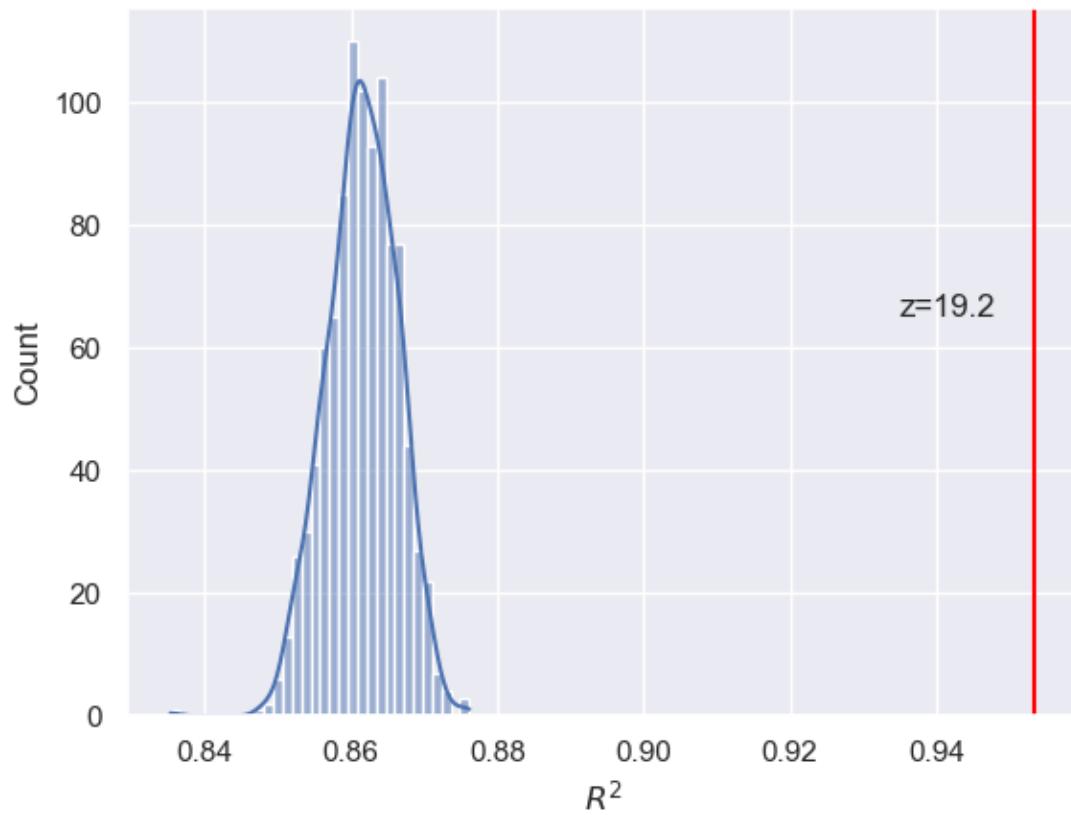
**Fig. S2. Sub-sequences detected by our segmentation method based on a cutting threshold of 0.75 also follow a Zipfian frequency distribution:** we cut whenever the ratio between two consecutive transitional probabilities was lower than 0.75 (compare with Fig. 2A in main paper, which has a cutting ratio of 0.5, and Fig. S1, which has a cutting ratio of 0.25). The left-hand plot shows the frequency of each sub-sequence ordered by rank frequency. The right-hand plot shows the same data but with a log scale for both axes. We calculated the frequency of the sub-sequences independently for each year in the dataset, and then aggregated the frequency by rank over the different years (we show the mean and 95% bootstrapped confidence intervals around the mean for each frequency rank over the eight years in the dataset). The straight line we see here on the log-log plot is similar to the one with other thresholds, indicating that our result is robust to different levels of sensitivity for cutting the data. In other words, we find a Zipfian distribution at multiple levels in the data, irrespective of whether we detect lots of smaller units, or fewer larger ones.

Erratum (9 April 2023)



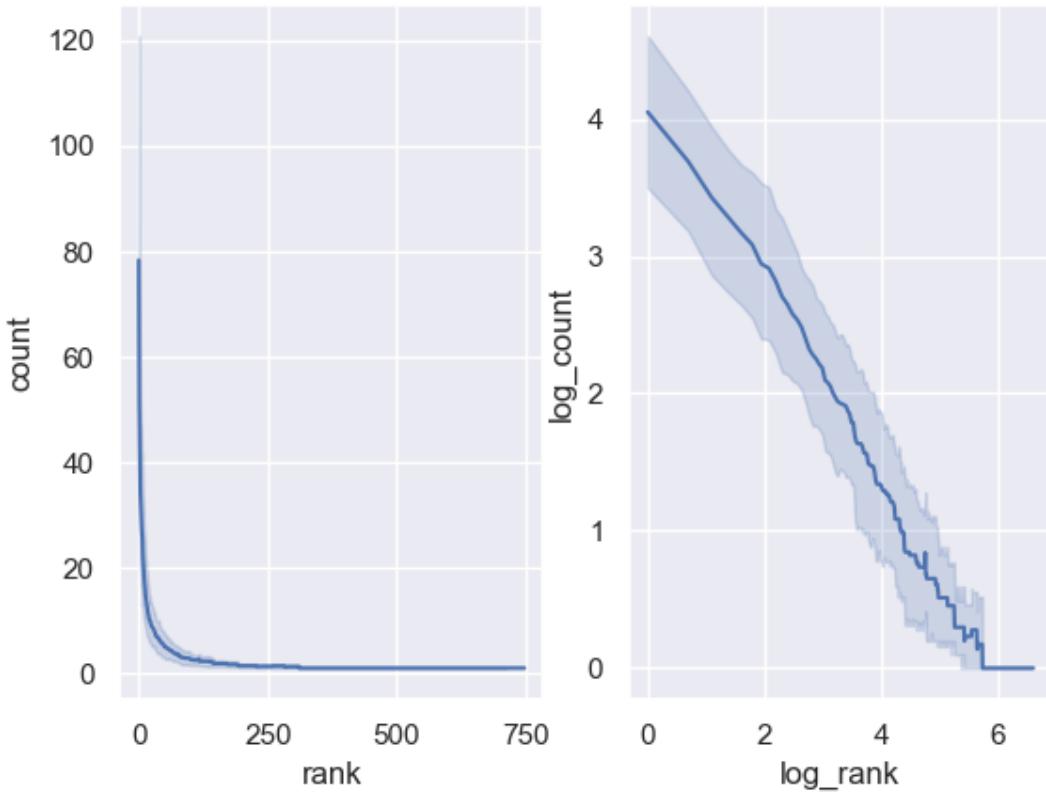
**Fig. S3. Sub-sequences detected by our segmentation method based on a 0.25 cutting ratio (compare with Fig. 2D and Fig. S4) show a better fit to a Zipfian distribution than any of the shuffled datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived by running our full analytic pipeline on 1000 randomly shuffled datasets. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the shuffled datasets.

Erratum (3 April 2025):



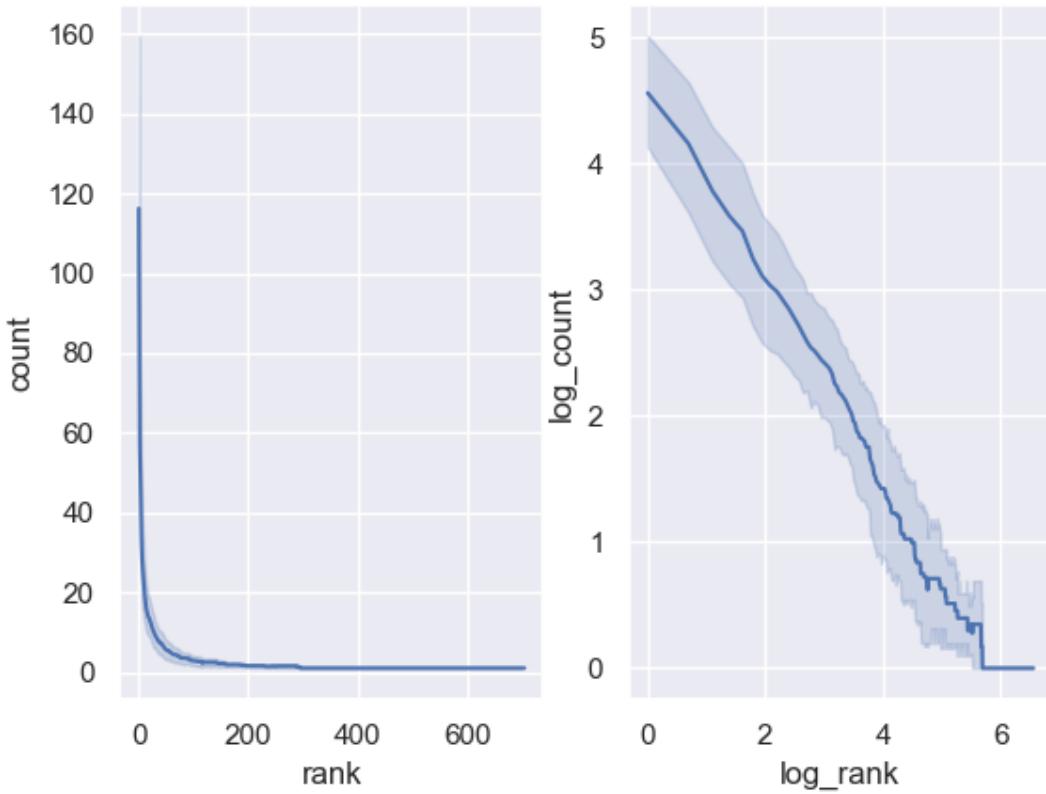
**Fig. S4. Sub-sequences detected by our segmentation method based on a 0.75 cutting ratio (compare with Fig. 2D and Fig. S3) show a better fit to a Zipfian distribution than any of the shuffled datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived by running our full analytic pipeline on 1000 randomly shuffled datasets. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the shuffled datasets.

Erratum (3 April 2025):

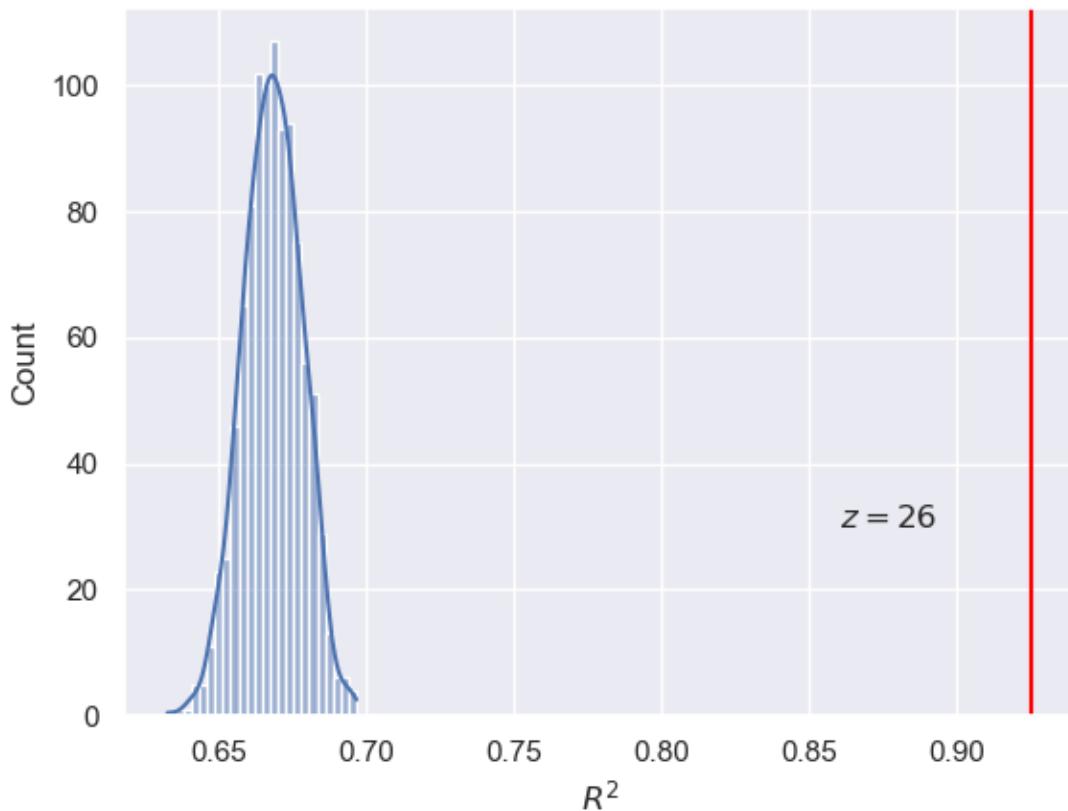


**Fig. S5. Sub-sequences detected by our segmentation method based on expanded context also follow a Zipfian frequency distribution:** we repeated the cutting method in the paper, but instead of basing transition probabilities on bigrams, we used trigrams. The left-hand plot shows the frequency of each detected sub-sequence ordered by rank frequency. The right-hand plot shows the same data but with a log scale for both axes. We calculated the frequency of the sub-sequences independently for each year in the dataset, and then aggregated the frequency by rank over the different years (we show the mean and 95% bootstrapped confidence intervals around the mean for each frequency rank over the eight years in the dataset). The straight line we see here on the log-log plot is similar to the one with the bigram-based method, indicating that our result is robust to a different method for cutting the data.

Erratum (3 April 2025):

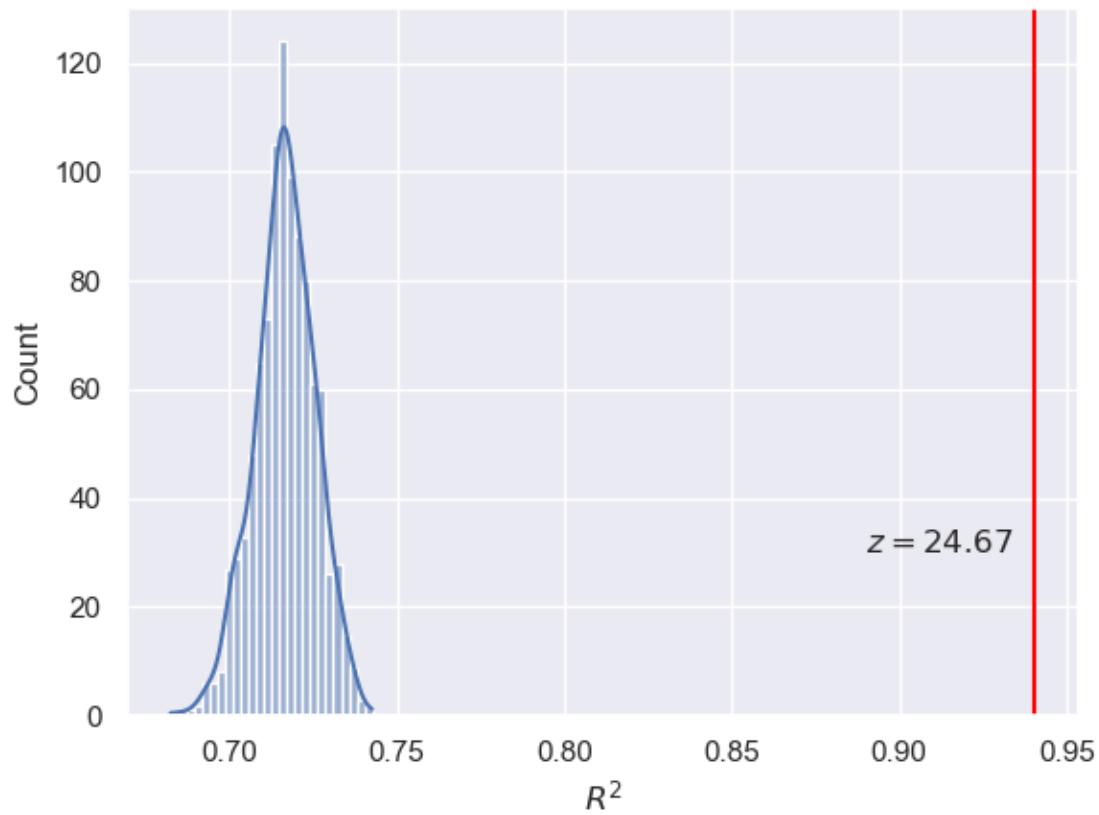


**Fig. S6. Sub-sequences detected by our segmentation method based on backwards transitional probabilities also follow a Zipfian frequency distribution:** we repeated the cutting method in the paper, but instead of using forward transitional probabilities, we used backwards transitional probabilities, estimating the probability of an element in the song coming before the element that follows. This method is particularly appropriate given that we know infants are sensitive to these probabilities. The left-hand plot shows the frequency of each detected sub-sequence ordered by rank frequency. The right-hand plot shows the same data but with a log scale for both axes. We calculated the frequency of the sub-sequences independently for each year in the dataset, and then aggregated the frequency by rank over the different years (we show the mean and 95% bootstrapped confidence intervals around the mean for each frequency rank over the eight years in the dataset). The straight line we see here on the log-log Erratum<sup>1</sup>(8 Apr 2023) the one with the method based on forward transition probabilities, indicating that our result is robust to a different method for cutting the data.



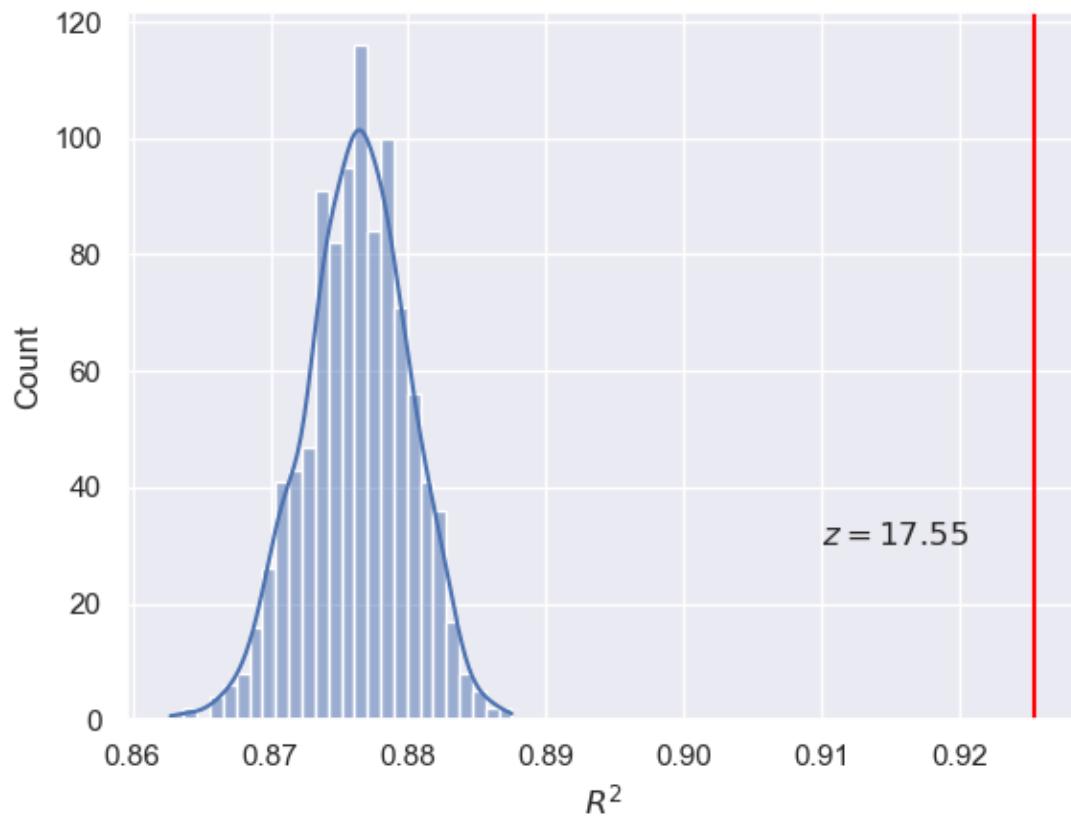
**Fig. S7. Sub-sequences detected by our segmentation method based on expanded context show a better fit to a Zipfian distribution than any of the shuffled datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived by running our full analytic pipeline on 1000 randomly shuffled datasets. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the shuffled datasets.

Erratum (3 April 2025):



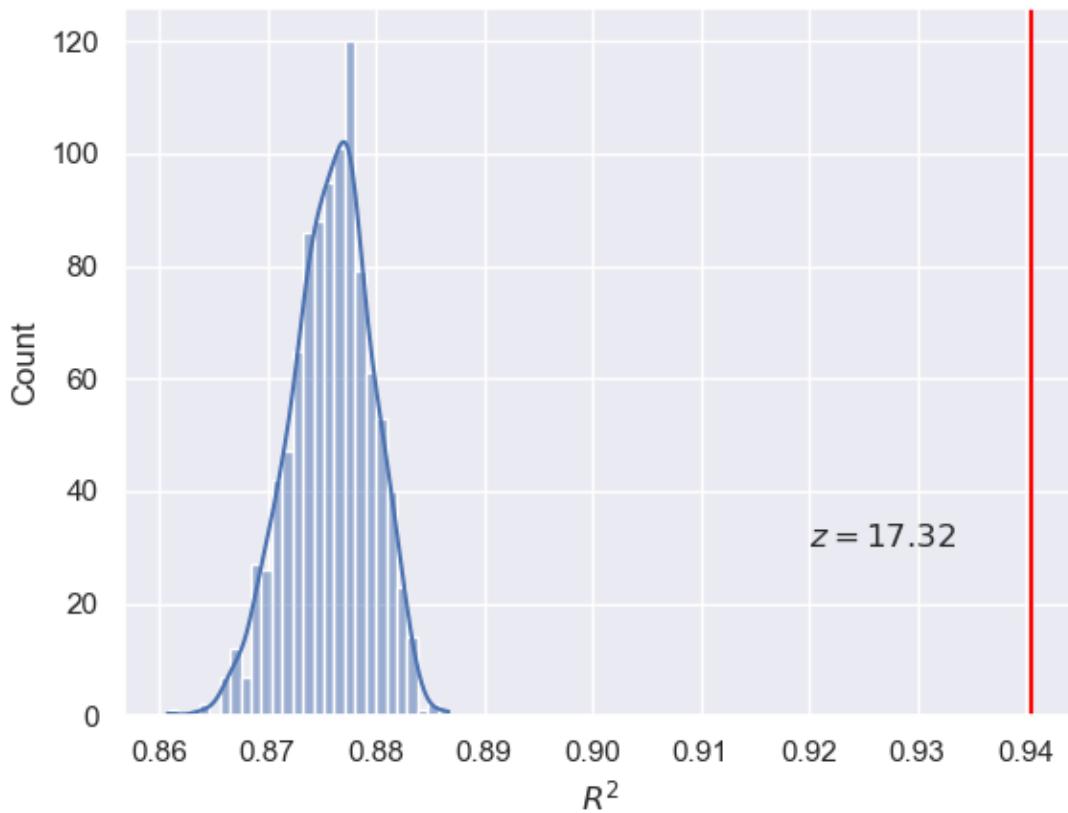
**Fig. S8. Sub-sequences detected by our segmentation method based on backwards transitional probabilities show a better fit to a Zipfian distribution than any of the shuffled datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived by running our full analytic pipeline on 1000 randomly shuffled datasets. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the shuffled datasets.

Erratum (3 April 2025):



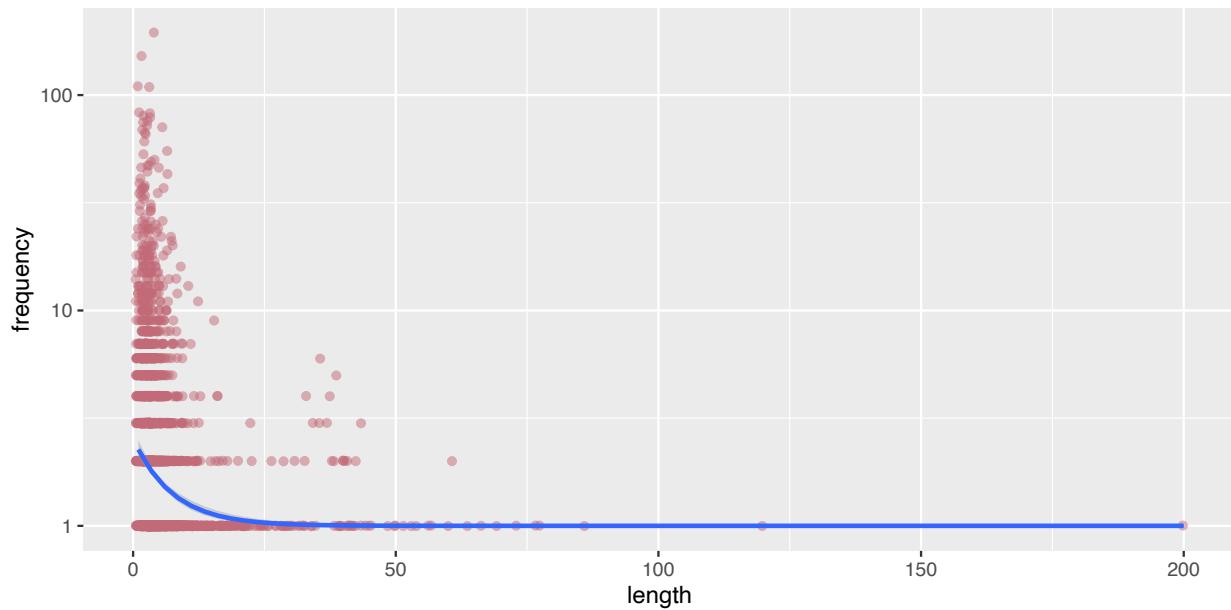
**Fig. S9. Sub-sequences detected by our segmentation method based on expanded context show a better fit to a Zipfian distribution than any of the rotated datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived from any of 1000 randomly rotated datasets after trigram-based segmentation. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the rotated datasets.

Erratum (3 April 2025):



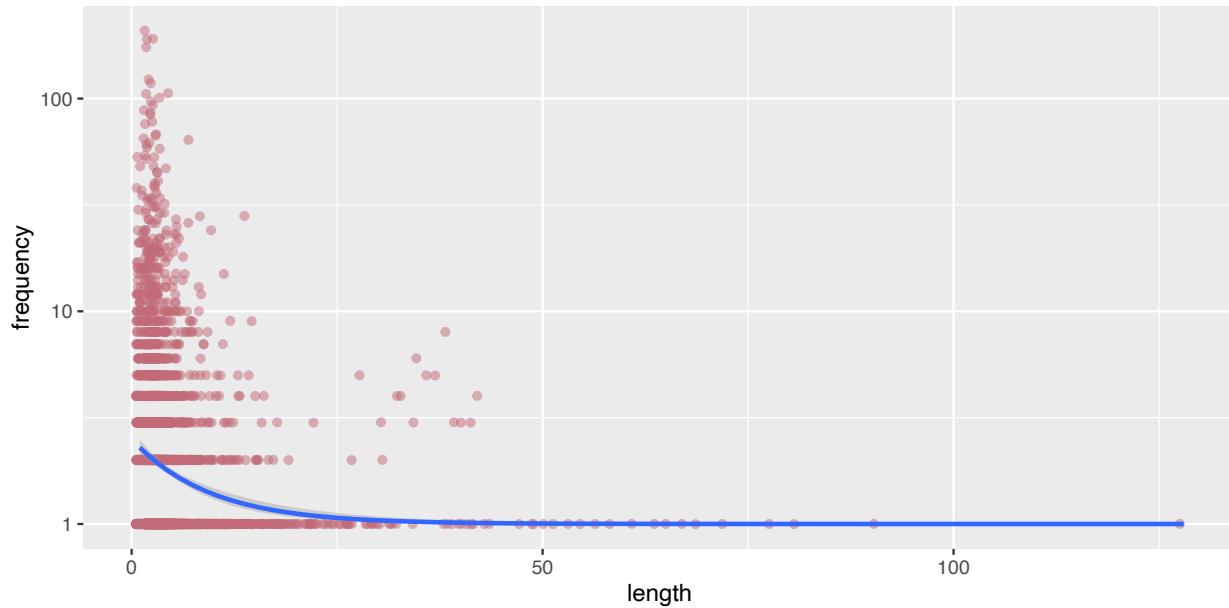
**Fig. S10. Sub-sequences detected by our segmentation method based on backwards transitional probabilities show a better fit to a Zipfian distribution than any of the rotated datasets.** The red line indicates the real data, and the blue histogram shows the distribution of  $R^2$  values derived from any of 1000 randomly rotated datasets after segmentation using backwards transitional probabilities. The z-score for the veridical data is shown, demonstrating that the real data shows a far better fit to a Zipfian distribution than any of the rotated datasets.

Erratum (3 April 2025):



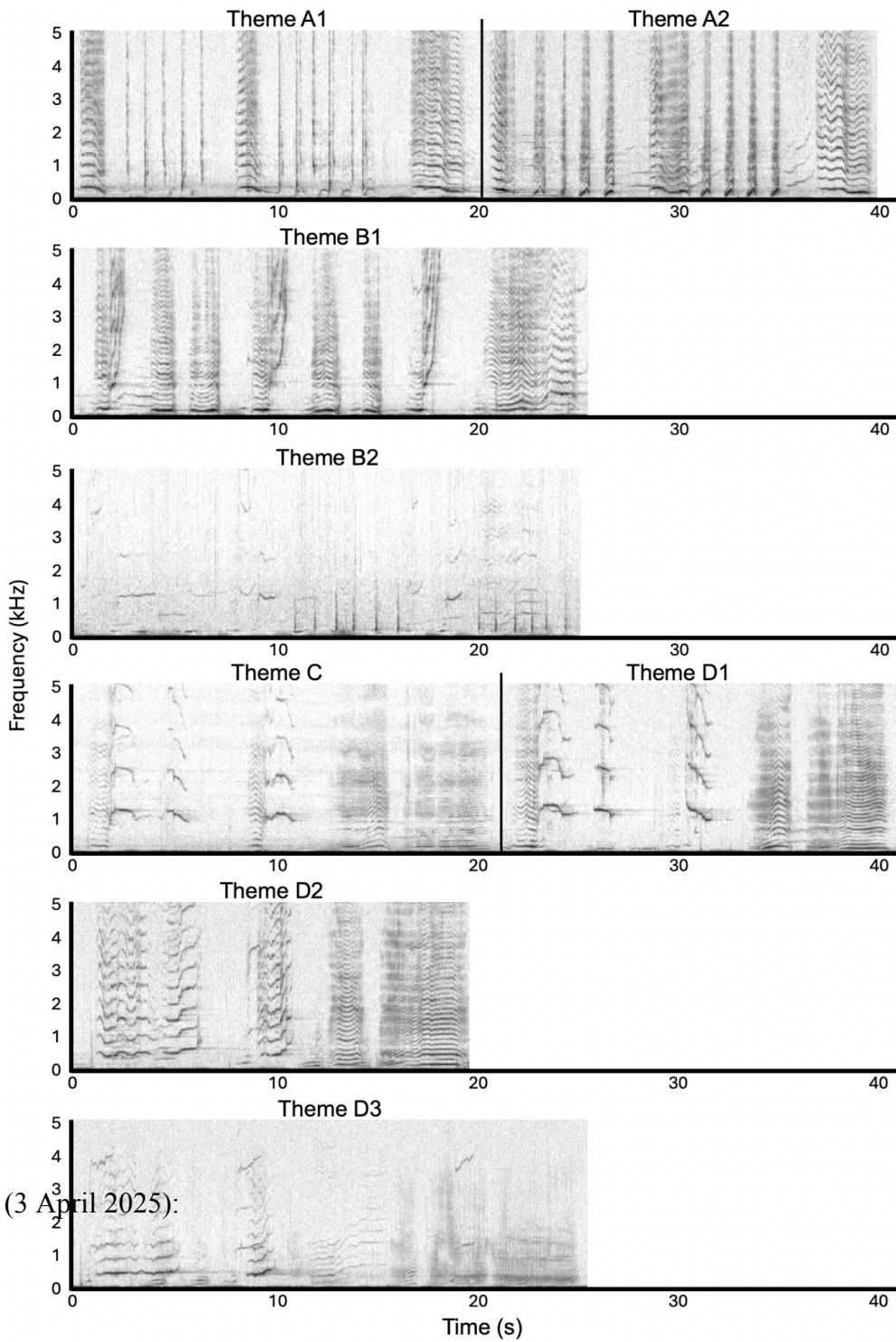
**Fig. S11. Subsequences detected by our segmentation method follow Zipf's law of brevity, also when using expanded context.** Each point is one subsequence. The figure shows the frequency distribution of all subsequences discovered by our segmentation method across the entire dataset plotted by length (number of sound elements). More frequent subsequences are shorter than less frequent ones, indicating that the detected subsequences not only follow a Zipfian distribution but also follow Zipf's second law, the law of brevity, that is typical of human language and other animal communication systems. The data show a strong relation between frequency and length, assessed using a Poisson mixed effects regression ( $P < 0.00001$ ). The Poisson regression line collapsing over all data is shown here in blue.

Erratum (3 April 2025):



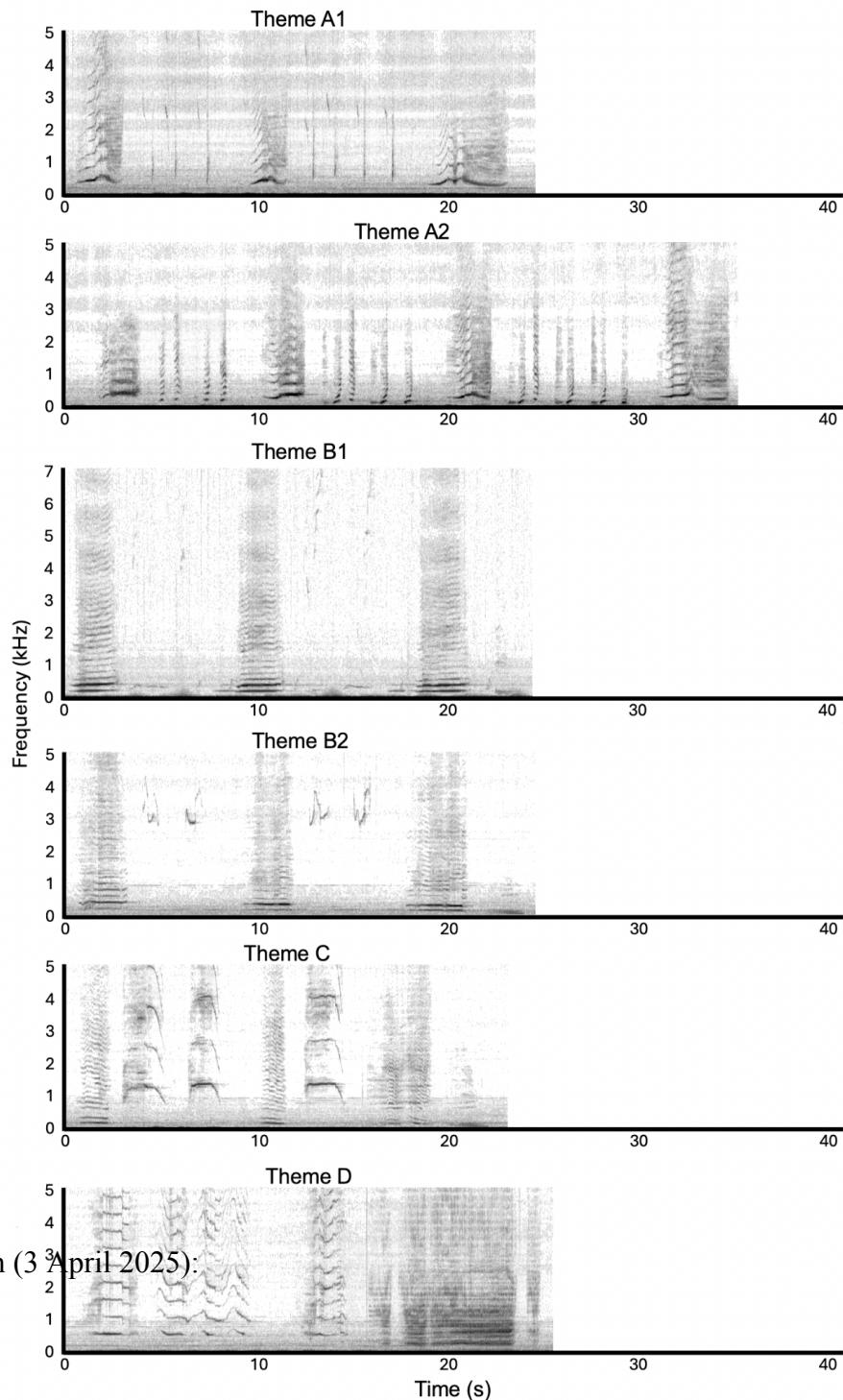
**Fig. S12. Subsequences detected by our segmentation method follow Zipf's law of brevity, also when using backwards transitional probabilities.** Each point is one subsequence. The figure shows the frequency distribution of all subsequences discovered by our segmentation method across the entire dataset plotted by length (number of sound elements). More frequent subsequences are shorter than less frequent ones, indicating that the detected subsequences not only follow a Zipfian distribution but also follow Zipf's second law, the law of brevity, that is typical of human language and other animal communication systems. The data show a strong relation between frequency and length, assessed using a Poisson mixed effects regression ( $P < 0.00001$ ). The Poisson regression line collapsing over all data is shown here in blue.

Erratum (3 April 2025):



Erratum (3 April 2025):

**Fig. S13. Spectrograms of the 2016 New Caledonia song (Themes A-D). A representative phrase for each theme is shown.** Note that some themes contain “1” and “2” phrases. These were all classified as the 2016 song. Spectrograms were produced in Raven Pro 1.6 (fast Fourier transform 2048; Hann window, 50% overlap).



**Fig. S14. Spectrograms of the 2017 New Caledonia song (Themes A-D).** A representative phrase for each theme is shown. Note that some themes contain “1” and “2” phrases. These were all classified as the 2017 song. Spectrograms were produced in Raven Pro 1.6 (fast Fourier transform 2048; Hann window, 50% overlap).

**Table S1.** Sample sizes included in the study.

Year	# Recordings	# Singers	# ID'ed singers	Hr:min:sec	# Sound elements
2010	4	4	3	00:41:28	1,053
2011	6	6	1	01:26:05	2,028
2012	6	6	3	02:25:49	3,351
2013	6	5	4	01:52:32	2,664
2014	7	7	1	04:03:29	5,765
2015	12	11	5	07:49:38	13,251
2016	7	7	5	05:48:57	8,469
2017	7	7	5	06:51:01	9,179
<b>Totals</b>	<b>55</b>	<b>53</b>	<b>27</b>	<b>30:58:59</b>	<b>45,760</b>

Erratum (3 April 2025):

**Table S2. Ten most frequent sub-sequences detected by our method based on the human statistical learning literature per year.** Sound element names can be found in Table S3. N= frequency.

Year	Sub-sequence	N	Year	Sub-sequence	N
2010	gr, gr, m	31	2014	agr(pul-s), w	167
	m, ac, ac, ac	17		agr(pul), w	110
	m	11		ac, be, ac	107
	v, ba	11		aws(s), agr(pul-s), w	80
	ac(l), m	9		gr(l), ac	77
	dm, ngr, ngr	8		ac	66
	m(pul), ngr(s), ngr(s)	8		dgr	48
	ngr(s), ngr(s), m	7		gr(s)-modhc, gr(s)-nc(s)	34
	m, ac, ac, ac, ac	7		gr(s)-nc(s), gr(s)-dc	28
	agr, agr, m	7		ti(a), w	28
2011	ba, p(l), ba	37	2015	gr(s)-dws(s), sq, sq, sq	204
	dws, m	33		gr(s)-dws(s), gr, gr(s)-dws(s), sq, sq, sq	74
	m(s), dws	28		gr(s)-dws(s)	67
	gr(s), ba	23		gr(s)-dws(s), ba, ba	62
	c, m	21		gr	61
	m	18		gw(l), gw(l), gr	49
	m(s), dws, m	17		gr(s)-dws, gr, gr(s)-dws	47
	m(s)	13		gr(s)-dws(s), gr, gr(s)-dws(s), ba, ba	47
	ngr, ngr, m	13		gr(s)-dws(s), sq, sq, sq, sq	46
	m, dws, m	12		gr(s)-dws(s), sq, sq	44
2012	w, gr, w	52	2016	dm(l), dm	129
	gr, ba	46		gr(s)	98
	gr(pul), m(pul), gr	45		hsq, w	73
	w, gr, w, gr	44		ngr(s), ngr(s), ngr(s), ngr(s)	38
	m, gr	44		dm	35
	ba, gr, ba	39		dm, ngr(s), ngr(s), ngr(s), ngr(s)	35
	ba	37		gr(s)-aws, nm, nm	35
	ahq, ba	33		gr(s)-aws, nm, nm, sn, gr(s)-aws, am(l)	31
	gw, hs(pul), hs(pul)	26		gr(s)-uws(s), ngr(s), ngr(s)	27
	ba, lb, gw, hs(pul), hs(pul)	25		ngr(s), ngr(s), ngr(s)	25
2013	lb, sn, lb, sn, hs(pul), ba, lb	68	2017	gw(low), gr	125
	aws(s), sq	52		ns, ns	120
	lb	30		dhq, w	113
	hs(pul), ba, lb	18		ds(s), gr	111
	ba, lb	17		hq, w	109
	dsq, aws(s)	15		gw, gr	100
	agr(l), sq	9		hq, sq	93
	ba	9		gr, gw(low), gr	78
	lb, gr(s), sq	9		sn, gr(s), gr(s)	75
	gr(s), hs(pul), ba, lb	9		ns, ns, gr, gw(low), gr	71

Erratum (3 April 2025):

**Table S3. Sound element names and sample size for Random Forest analysis.** Note that sound elements can be combined to make compound units (e.g., lm-as, represents a ‘long moan’ connected to (-) an ‘ascending shriek’). (l)= long, (s)= short, (pul)= pulsative, (step)=staircase change in frequency. Sample sizes (N) provided for units included in random forest analysis.

Sound code	N	Sound name	Sound code	N	Sound name
ac	30	Ascending cry	hs(pul)	15	Pulsative high shriek
ac(s)	6	Short ascending cry	hs(pul)-sq(series)	3	Pulsative high shriek-squeak series
agr	12	Ascending groan	lb	18	Long bark
agr(l)	3	Long ascending groan	lm	3	Long moan
agr(s)	22	Short ascending groan	lm(pul)	8	Long pulsative moan
ahq	8	Ascending high squeak	m	19	Moan
am	23	Ascending moan	m(pul)	2	Pulsative moan
am(l)	16	Long ascending moan	m(s)	4	Short moan
am(pul-s)	1	Short pulsative ascending moan	mgr	1	Modulated groan
am(pul)	20	Pulsative ascending moan	mgr(pul-l)	1	Long pulsative modulated groan
am(s)	36	Short ascending moan	mgr(pul)	2	Pulsative modulated groan
as	2	Ascending shriek	mm	15	Modulated moan
aws	6	Ascending whistle	mm(l)	7	Long modulated moan
aws(pe)	1	Ascending whistle-pulsative element	mm(pul)	10	Pulsative modulated moan
aws(s)	82	Short ascending whistle	modhc	4	Short modulated high cry
aws(step)	2	Stepped ascending whistle	modhs	4	Modulated high shriek
ba	66	Bark	modws	6	Modulated whistle
bd	1	Balloon deflate	modws(pe)	2	Short modulated whistle-pulsative element
be-sq(series)	2	Bellows-squeak series	modws(s)	2	Short modulated whistle
bt	1	Bird trill	nc(s)	5	Short n-shaped cry
c	7	Croak	ngr	2	N-shaped groan
dc	8	Descending cry	ngr(s)	37	Short n-shaped groan
dgr(l)	2	Long descending groan	ngr(s)-ba	4	Short n-shaped groan-bark
dhq	31	Descending high squeak	nm	12	N-shaped moan
dm	28	Descending moan	nm(pul)	22	Pulsative n-shaped moan
dm(l)	9	Long descending moan	nm(s)	6	Short n-shaped moan
dm(pul-l)	1	Long pulsative descending moan	ns	8	N-shaped shriek
dm(pul)	3	Pulsative descending moan	ns(s)	2	Short n-shaped shriek
ds(s)	2	Descending shriek	nws	5	N-shaped whistle
dsq	17	Descending squeak	nws(s)	9	Short n-shaped whistle
dws	3	Descending whistle	p	26	Purr
dws(s)	6	Short descending whistle	p(ch-l)	1	Long chainsaw purr
gr	115	Groan	p(ch)	1	Chainsaw purr
gr(l)	4	Long groan	p(l)	11	Long purr
gr(s)	68	Short groan	p(s)	3	Short purr
gr(s)-ac(s)	4	Short groan-short ascending cry	pe	11	Pulsative element
gr(s)-aws(s)	9	Short groan-short ascending whistle	sn	19	Snort
gr(s)-ba	2	Short groan-bark	sn-gr(s)	2	Snort-short groan
gr(s)-dws	6	Short groan-descending whistle	sq	228	Squeak
gr(s)-dws(s)	21	Short groan-short descending whistle	sq-dws	1	Squeak-descending whistle
gr(s)-modhc	6	Short groan-modulated high cry	sq(low)	207	Low squeak
Erratum (3 April 2025): Short groan- short n-shaped cry		ti	6	Trill	
gr(s)-uws(s)	6	Short groan-short u-shaped whistles	ti(a-l)	14	Long ascending trill
gt	2	Grunt	ti(a)	22	Ascending trill
gw	33	Growl	ti(d)	1	Short descending trill
gw(l)	27	Long growl	ti(s)	1	Short trill
gw(low)	4	Low growl	uc	2	U-shaped cry
gw(s)	1	Short growl	uws	16	U-shaped whistle
hc	5	High cry	uws(s)	14	Short u-shaped whistle
hc(s)	2	Short high cry	v	2	Violin
hq	42	High squeak	w	48	Whoop
			Total	1,694	106 Sound types

**Code S1. Whale song analysis.**

**Data S1. Sound element measurements.**

**Data S2. Song strings.**

**Data S3. Theme frequencies.**

Erratum (3 April 2025):

## References and Notes

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