

**Title:** Long Legs and Short Arms: Development and the Evolvability of Human Limbs  
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## Supplementary Information

### *Correlation Magnitude, Structure and the Relationship to Population Variance*

Initial resampling of our data suggested that in highly integrated datasets estimated correlations vary with the sampled population variance. We hypothesized that this is because if two traits are highly correlated then increasing the sampled variance will improve the estimated correlation, whereas if the correlation is low then increasing the sampled variance will not improve correlation estimates. This artifact between correlations and variance has important ramifications for the comparison of integration, because it implies that there is a significant risk of both Type I and Type II errors when statistically comparing mean estimates of integration between populations. For example, if one group has a higher estimated variance than a second, significant differences in integration between them could be due to either: (i) a real difference in integration, or (ii) an artifact of differences in sample variance. Only the former is meaningful for studies of integration while the latter indicates that conclusions from comparative studies of integration are likely to be flawed without correction.

To better understand this relationship, we conducted a simulation in which we generated known covariance structures in limb data. To generate these data, we took a factor-based approach. The value for each limb element was calculated as the sum of normally distributed deviations associated with four hypothetical variance sources added to an assumed population mean and scaled by an assumed population variance. In our simulations, we used the sample means and variances from the macaque data as the starting point. The value for each element was thus calculated as:

$$LV_E = \mu_E + \left( (W_{Org} \times N_{Org}) + (W_{Limb} \times N_{Limb}) + (W_{SH} \times N_{SH}) + (W_{LE} \times N_{LE}) \right) \times \sigma_E$$

Where:

$\mu_E$  = assumed population mean for that limb element

$\sigma_E$  = assumed population standard deviation for that limb element

$W_{Org}$  = proportion of variance determined by organism-wide variation in size

$W_{Limb}$  = proportion of variance determined by limb-specific variation in size

$W_{SH}$  = proportion of variance determined by serially homologous element-specific variation in size

$W_{LE}$  = proportion of variance determined by limb element-specific variation in size

$N$  = a normally distributed random number with a variance of one and mean of zero

In this simulation, there is no resampling from a larger sample. Instead, each individual within each sample is unique and generated *de novo* using the method described above.

We used this basic scheme to conduct two different simulations. In the first, we generated 380 samples of 50 individuals for ten different hypothetical covariation structures (total N = 190,000) that varied in the strength of each of the four factors. Out of the ten hypothetical covariation structures, six generated the effect of significant correlation of VE with population variance (here we use the trace of the covariance matrix, but similar results obtain with other measures such as the average CV%). These results are shown in **Supplementary Figure 1**. Covariation structures that did not exhibit the effect either had a single covariation determinant or very large element-specific variance. The former is unrealistic and the latter produces essentially random correlation matrices, which is also not characteristic of biological data. Within the six remaining covariation structures that generated the effect, the correlation for a log-linear regression between VE and sample variance ranged from 0.47 to 0.82, while the slope and intercept also varied. This result led us to hypothesize that the magnitude of the observed effect is dependent on covariation structure.

To further explore how covariation structure determines the nature of this sampling artifact, we examined all possible combinations of covariation structures possible within our scheme, varying the proportional contribution of each covariance factor in increments of 0.2. For each of the 58 possible combinations, we generated 50 samples of 50 individuals and calculated the VE (from the correlation matrix) and the sample variance. We next obtained the correlation between VE and the trace for each run of 50 samples per covariance structure. Analysis of these correlations showed that the strength of the artifact depends both on the average VE for that covariation structure and on the number of covariance generating factors (**Supplementary Figure 2**). Significantly, the most realistic biological model of covariance involves four factors and also exhibits the strongest effect.

This simulation demonstrates that there is a positive correlation between VE and the sample variance and that this relationship depends on covariation structure. In other words, the sampling error of VE and the sampling error of the population variance are correlated under conditions that are similar to those encountered in real biological datasets (**Supplementary Figure 3**). The implication of this finding for the comparative analysis of integration is that when the covariance structures of the samples being compared are broadly similar, this relationship can be taken into account in order to make appropriate comparisons. This is the approach taken in our study. Pairwise matrix correlations are significant between all taxa, with the exception of *Saimiri*, although this species is not significantly different than either *Homo* or *Macaca* (**Supplementary Table 2**).

## Supplementary Figure Legends:

**Supplementary Figure 1:** The relationship between the variance of the eigenvalues (VE) and the sample variance (trace of the variance-covariance matrix) for six hypothetical covariance structures as determined by simulation. For each covariance structure, 380 random populations ( $N = 50$ ) were generated, and the VE plotted against population variance. For each simulated covariance structure VE exhibited a significant log-linear relationship with sample variance although the correlation, slope, and intercept varied on the structure.

**Supplementary Figure 2:** Summary results for the simulation demonstrating the dependence of the VE variance artifact on the number of factors generating covariance structure. Each data point represents the mean VE and the Fisher's-z transformed correlation (population variance versus VE) for a simulation run ( $N = 50$ ) with a given covariance structure (range = one to four factors). This simulation demonstrates that the strength of the artifact depends on the VE as well as the number of covariance generating factors. The most realistic model of four factors exhibits the strongest relationship.

**Supplementary Figure 3:** A comparison of resampled distributions (1,000 replicates with  $r_m > 0.95$ ) of four alternative partitions of the *Homo* dataset: (i) the raw data (green), (ii) the raw data mean-centered for ethnicity and sex differences (purple), (iii) the centered data pruned of individuals outside the 95% confidence limit (orange), and (iv) the residuals of the raw data regressed on trunk length (blue). Each partition has statistically indistinguishable covariance structure (inset:  $r_m$  adjusted for repeatability below diagonal, p-values above, matrix repeatability along the diagonal) yet differ in the population variance sampled. Log-linear regression estimates for a VE at a common population variance (4%) yields consistent values (range = 1.79 - 2.15, mean = 1.94) using both within partition regressions (colored circles) and an estimate using a regression from all of the data (i.e., "Total", regression shown as dashed line). In order to be consistent across species datasets where information on body size is not available, we report VE estimates from the centered data. This analysis shows that while the population variance affects the magnitude of correlation estimates under real sampling conditions, this relationship is predictable and therefore correctable when comparing population integration among populations or species. This relationship also holds for both estimates of individual and average correlations.

**Supplementary Figure 4:** Distribution of resampled VE estimates and regressions for  $CV = 0 - 10$  in each species. At comparable population variance estimates, humans are less integrated relative to quadrupedal monkeys and similar to apes. Each species dataset was resampled with replacement and a new VE and average CV was calculated (10,000 replicates). Matrix correlation of the resampled and original dataset was  $r_m > 0.95$  in all species, indicating correlation structure was not significantly different from identity. Regressions represent the best-fit estimate for each group. (*Homo sapiens*:  $VE = \ln(CV) \cdot 3.025 - 2.195$ ,  $r^2 = 0.665$ ; *Pan troglodytes*:  $VE = \ln(CV) \cdot 3.141 -$

2.789,  $r^2 = 0.671$ ; *Gorilla gorilla*:  $VE = \ln(CV) \cdot 2.756 - 1.856$ ,  $r^2 = 0.564$ ; *Hylobates lar*:  $VE = \ln(CV) \cdot 3.296 - 2.766$ ,  $r^2 = 0.441$ ; *Macaca mulatta*:  $VE = \ln(CV) \cdot 2.867 - 0.898$ ,  $r^2 = 0.772$ ; *Trachypithecus cristatus*:  $VE = \ln(CV) \cdot 2.931 - 0.497$ ,  $r^2 = 0.736$ ; *Saimiri sciureus*:  $VE = \ln(CV) \cdot 3.071 - 1.552$ ,  $r^2 = 0.714$ ; *Aotus trivirgatus*:  $VE = \ln(CV) \cdot 3.333 - 1.369$ ,  $r^2 = 0.533$ ).

**Supplementary Table 1:** Descriptive statistics of each sample.

Species	Sample Size			Population Variance (Average trait coefficient of variation [CV])						
	Female	Male	Total	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal	Mean
<i>Homo sapiens</i>	62	71	133	5.27	6.10	5.65	5.86	6.31	6.21	5.90
<i>Pan troglodytes</i>	26	21	46	4.64	5.63	6.60	4.33	5.37	6.75	5.56
<i>Gorilla gorilla</i>	20	42	62	4.06	4.41	5.21	4.41	4.97	5.36	4.74
<i>Hylobates lar</i>	31	32	63	3.55	3.76	4.79	3.75	4.36	4.32	4.09
<i>Macaca mulatta</i>	93	83	176	3.78	4.26	4.96	4.27	4.35	4.35	4.33
<i>Trachypithecus cristatus</i>	42	17	59	3.04	3.15	4.58	3.24	3.06	4.10	3.53
<i>Saimiri sciureus</i>	60	42	102	4.51	4.06	5.88	5.02	5.13	5.36	4.99
<i>Aotus trivirgatus</i>	21	53	74	3.38	3.35	2.88	3.78	4.07	3.54	3.50

**Supplementary Table 2:** Matrix correlations (below diagonal [values scaled by repeatability]), matrix repeatability (diagonal [autocorrelation of 10,000 replicates] <sup>1</sup>, and significance value of the matrix correlation (above diagonal [Mantel's test, 10,000 replicates]) for pairwise comparisons of all species.

Species	<i>Homo</i>	<i>Pan</i>	<i>Gorilla</i>	<i>Hylobates</i>	<i>Macaca</i>	<i>Trachypithecus</i>	<i>Saimiri</i>	<i>Aotus</i>
<i>Homo</i>	0.945	0.011	0.008	0.013	0.003	0.005	0.015	0.018
<i>Pan</i>	0.908	0.907	0.021	0.010	0.025	0.008	0.128	0.010
<i>Gorilla</i>	0.841	0.768	0.948	0.000	0.029	0.039	0.195	0.008
<i>Hylobates</i>	0.891	0.905	0.999	0.950	0.017	0.035	0.150	0.005
<i>Macaca</i>	0.872	0.798	0.699	0.810	0.970	0.000	0.045	0.011
<i>Trachypithecus</i>	0.902	0.882	0.637	0.774	0.972	0.934	0.075	0.024
<i>Saimiri</i>	0.618	0.324	0.306	0.341	0.507	0.577	0.949	0.196
<i>Aotus</i>	0.747	0.773	0.751	0.835	0.775	0.706	0.336	0.968

**Supplementary Table 3:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Homo sapiens*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.188	0.260	0.368	0.088	-0.201
Radius	0.709	1	0.111	0.005	0.444	0.160
Metacarpal	0.540	0.543	1	0.109	-0.179	0.658
Femur	0.800	0.694	0.484	1	0.464	-0.179
Tibia	0.804	0.792	0.527	0.845	1	0.331
Metatarsal	0.480	0.586	0.726	0.412	0.578	1

**Supplementary Table 4:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Pan troglodytes*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.005	0.101	0.446	0.227	-0.107
Radius	0.593	1	0.303	0.111	0.316	0.177
Metacarpal	0.327	0.608	1	0.233	-0.375	0.638

Femur	0.805	0.686	0.399	1	0.551	0.054
Tibia	0.712	0.677	0.225	0.824	1	0.095
Metatarsal	0.272	0.539	0.772	0.387	0.232	1

**Supplementary Table 5:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Gorilla gorilla*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.463	0.230	0.367	0.236	-0.430
Radius	0.812	1	0.335	0.108	0.424	-0.111
Metacarpal	0.479	0.651	1	0.009	-0.306	0.803
Femur	0.717	0.733	0.544	1	0.230	0.110
Tibia	0.710	0.811	0.613	0.733	1	0.445
Metatarsal	0.161	0.383	0.778	0.246	0.467	1

**Supplementary Table 6:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Hylobates lar*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.427	-0.272	0.567	0.085	0.047
Radius	0.730	1	0.474	0.016	0.380	-0.212
Metacarpal	0.307	0.625	1	0.128	0.039	0.732
Femur	0.794	0.709	0.440	1	0.254	-0.018
Tibia	0.700	0.783	0.527	0.722	1	0.077
Metatarsal	0.128	0.362	0.782	0.278	0.352	1

**Supplementary Table 7:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Macaca mulatta*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.132	0.084	0.505	0.210	-0.102
Radius	0.797	1	0.095	0.137	0.502	0.032
Metacarpal	0.614	0.715	1	-0.081	-0.143	0.826
Femur	0.857	0.828	0.653	1	0.259	0.137
Tibia	0.829	0.904	0.724	0.871	1	0.323
Metatarsal	0.659	0.774	0.911	0.725	0.810	1

**Supplementary Table 8:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Trachypithecus cristatus*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.242	-0.055	0.344	0.041	0.215
Radius	0.859	1	0.355	0.094	0.381	-0.182
Metacarpal	0.755	0.811	1	0.006	-0.138	0.734
Femur	0.890	0.881	0.762	1	0.550	0.028
Tibia	0.872	0.902	0.777	0.929	1	0.253
Metatarsal	0.818	0.807	0.920	0.817	0.837	1

**Supplementary Table 9:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Saimiri sciureus*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.344	0.368	0.603	-0.062	-0.055
Radius	0.699	1	-0.221	-0.161	0.442	-0.033
Metacarpal	0.733	0.448	1	0.078	-0.124	0.615
Femur	0.915	0.673	0.700	1	0.595	-0.240
Tibia	0.846	0.753	0.707	0.900	1	0.557
Metatarsal	0.704	0.550	0.817	0.695	0.810	1

**Supplementary Table 10:** Estimated correlation (below diagonal) and partial correlation (above diagonal) matrix for *Aotus trivirgatus*.

	Humerus	Radius	Metacarpal	Femur	Tibia	Metatarsal
Humerus	1	0.056	-0.123	0.553	-0.032	-0.140
Radius	0.800	1	-0.193	0.096	0.568	0.366
Metacarpal	0.648	0.766	1	0.094	0.326	0.491
Femur	0.878	0.914	0.797	1	0.512	0.233
Tibia	0.833	0.935	0.810	0.951	1	-0.272
Metatarsal	0.609	0.783	0.800	0.783	0.734	1

**Supplementary Table 11:** Relative arm/leg lengths for ceboid, cercopithecoïd and hominoids used in **Figures 1C/D** and **3A** (2).

Group	Species Common Name	Arm/Trunk	Leg/Trunk	Arm/Leg
Ceboidae	Bald-headed tamarin	111.7	110.0	101.5
	True marmoset	98.4	94.8	103.8
	Marmoset	100.2	99.7	100.5
	Squirrel Monkey	95.6	92.2	103.7
	Capuchin	119.3	115.5	103.3
	Saki	118.5	115.2	102.9
	Uakari	134.7	119.8	112.4
	Owl Monkey	103.3	100.5	102.8
	Howler Monkey	146.2	117.0	125.0
	Woolly Monkey	156.1	126.7	123.2
Cercopithecoïdae	Spider Monkey	184.4	135.0	136.6
	Baboon	134.4	117.0	114.9
	Celebes Macaque	145.5	129.5	112.4
	Barbary Macaque	111.8	100.0	111.8
	Rhesus Macaque	114.0	100.8	113.1
	Managabey	127.7	120.5	106.0
	Vervet Monkey	100.7	96.5	104.4
	Red guenon	107.7	101.8	105.9
	Langur	108.0	97.8	110.4
	Proboscis Monkey	139.5	113.5	122.9
Homi-noïdea	Black Colobus	103.8	96.9	107.1
	Gibbon	251.0	152.7	164.4
	Siamang	234.1	131.4	178.2
	Orangutan	199.6	118.2	168.8
	Chimpanzee	173.5	128.3	135.2
	Gorilla	153.7	112.4	136.7
Human	149.1	167.2	89.2	

**Supplementary Table 12:** Intermembral index (IMI) for gibbon, macaque, guenon and tamarin radiations used in **Figure 3B**. All data from (3-7).

Group	Species	IMI
Apes	<i>Hylobates agilis</i>	130.9
	<i>Hylobates klossii</i>	124.0
	<i>Hylobates lar</i>	131.4
	<i>Hylobates moloch</i>	128.3
	<i>Hylobates muelleri</i>	130.2
	<i>Hylobates pileatus</i>	122.0
	<i>Hylobates (Bunopithecus) hoolock</i>	128.3
	<i>Hylobates (Nomascus) concolor</i>	142.2
	<i>Symphalangus syndactylus</i>	145.0
	<i>Pongo pygmaeus pygmaeus</i>	139.0
	<i>Pongo pygmaeus abelli</i>	139.0
	<i>Pan troglodytes schweinfurthi</i>	103.0
	<i>Pan troglodytes troglodytes</i>	106.0
	<i>Pan troglodytes verus</i>	106.0
	<i>Pan paniscus</i>	102.0
	<i>Gorilla gorilla gorilla</i>	116.0
	<i>Gorilla gorilla beringei</i>	116.0
	Old World Monkeys (Quadrupeds)	<i>Semnopithecus entellus</i>
<i>Kasi johnii</i>		80.0
<i>Trachypithecus obscura</i>		83.0
<i>Presbytis melalophos</i>		78.9
<i>Presbytis comata</i>		76.0
<i>Presbytis rubicunda</i>		76.0
<i>Presbytis frontata</i>		76.0
<i>Presbytis hosei</i>		75.0
<i>Nasalis larvatus</i>		94.0
<i>Pygathrix nemaesus</i>		94.0
<i>Mandrillus sphinx</i>		95.0
<i>Papio hamadryas</i>		95.0
<i>Papio anubis</i>		97.0
<i>Papio cynocephalus</i>		96.0
<i>Papio ursinus</i>		96.0
<i>Theropithecus gelada</i>		100.0
<i>Macaca slienus</i>		92.0
<i>Macaca nemestrina</i>		98.0
<i>Macaca tonkeana</i>		95.0
<i>Macaca ochreata</i>		100.0
<i>Macaca brunnecens</i>		99.0
<i>Macaca hecki</i>		93.0
<i>Macaca nigra</i>		84.0
<i>Macaca assamensis</i>		96.0
<i>Macaca thibetana</i>		95.0
<i>Macaca arctoides</i>		98.0
<i>Macaca fascicularis</i>		93.0
<i>Macaca mulatta</i>		93.0
<i>Cercocebus agilis</i>		84.0
<i>Cercocebus torquatus</i>		83.0
<i>Cercocebus galeritus</i>		84.0
<i>Lophocebus albigena</i>		78.0
<i>Cercopithecus mitis</i>		82.0
<i>Cercopithecus nictitans</i>	82.0	
<i>Cercopithecus ascanius</i>	79.0	



	<i>Cercopithecus cephus</i>	81.0
	<i>Cercopithecus mona</i>	86.0
	<i>Cercopithecus diana</i>	79.0
	<i>Cercopithecus preussi</i>	82.0
	<i>Cercopithecus lhoesti</i>	80.0
	<i>Cercopithecus neglectus</i>	82.0
	<i>Colobus guereza</i>	79.0
	<i>Colobus polykomos</i>	78.0
	<i>Ptilocolobus badius</i>	87.0
	<i>Procolobus verus</i>	80.0
New World Monkeys (Quadruped)	<i>Pithecia pithecia</i>	75.0
	<i>Pithecia monachus</i>	77.0
	<i>Chiropotes satanas</i>	83.0
	<i>Cacajao calvus</i>	83.0
	<i>Callicebus moloch</i>	74.0
	<i>Callicebus cupreus</i>	77.0
	<i>Callicebus donacophilus</i>	75.0
	<i>Callicebus torquatus</i>	79.0
	<i>Callicebus personatus</i>	73.0
	<i>Aotus sp.</i>	74.0
	<i>Cebus apella</i>	81.0
	<i>Cebus albifrons</i>	81.0
	<i>Cebus capucinus</i>	81.0
	<i>Cebus olivaceus</i>	83.0
	<i>Saimiri sciureus</i>	80.0
	<i>Samiri oerstedii</i>	80.0
	<i>Saguinus nigricollis</i>	78.0
	<i>Saguinus fuscicollis</i>	79.0
	<i>Saguinus tripartitus</i>	80.0
	<i>Saguinus mystax</i>	74.0
	<i>Saguinus labiatus</i>	73.0
	<i>Saguinus imperator</i>	75.0
	<i>Saguinus midas</i>	77.0
	<i>Saguinus oedipus</i>	74.0
	<i>Saguinus geoffroyi</i>	76.0
	<i>Saguinus leucopus</i>	74.0
	<i>Leontopithecus rosalia</i>	89.0
	<i>Callithrix argentata</i>	76.0
<i>Callithrix jacchus</i>	76.0	
<i>Callithrix aurita</i>	74.0	
<i>Callithrix penicillata</i>	76.0	
<i>Cebuella pygmaea</i>	83.0	

**Supplementary Table 13:** Intermembral index (IMI) for gibbon, macaque, guenon and tamarin radiations used in **Figure 3C**.

Radiation (Estimated Divergence Time) <sup>A</sup>	Species <sup>B</sup>	Intermembral Index (IMI)	Published Data Source
Gibbons <sup>C</sup> (6-7Ma)	<i>Hylobates agilis</i>	130.9	(4)
	<i>Hylobates klossii</i>	124.0	This dataset
	<i>Hylobates lar</i>	131.4	This dataset
	<i>Hylobates moloch</i>	128.3	(4)
	<i>Hylobates muelleri</i>	130.2	(4)
	<i>Hylobates pileatus</i>	122.0	This dataset

	<i>Hylobates (Bunopithecus) hoolock</i>	128.3	(4)
	<i>Hylobates (Nomascus) concolor</i>	142.2	This dataset
	<i>Symphalangus syndactylus</i>	144.5	(4)
Macaques (7.6 ±1.3Ma)	<i>Macaca silenus</i>	92.0	(3)
	<i>Macaca nemestrina</i>	98.0	(3)
	<i>Macaca tonkeana</i>	95.0	(3)
	<i>Macaca ochreata</i>	100.0	(3)
	<i>Macaca brunneceus</i>	99.0	(3)
	<i>Macaca hecki</i>	93.0	(3)
	<i>Macaca nigra</i>	92.0	(5)
	<i>Macaca maura</i>	92.0	(5)
	<i>Macaca assamensis</i>	96.0	(3)
	<i>Macaca radiata</i>	91.0	(6)
	<i>Macaca thibetana</i>	95.0	(3)
	<i>Macaca arctoides</i>	98.0	(3)
	<i>Macaca fascicularis</i>	93.0	(3)
	<i>Macaca mulatta</i>	93.0	(3)
<i>Macaca fuscata</i>	93.0	(7)	
Guenons (8.1 ±1.0Ma)	<i>Allenopithecus nigroviridis</i>	83.0	(3)
	<i>Cercopithecus ascanius</i>	79.0	(3)
	<i>Cercopithecus cephus</i>	81.0	(3)
	<i>Cercopithecus diana</i>	79.0	(3)
	<i>Cercopithecus lhoesti</i>	80.0	(3)
	<i>Cercopithecus mitis</i>	82.0	(3)
	<i>Cercopithecus mona</i>	86.0	(3)
	<i>Cercopithecus neglectus</i>	82.0	(3)
	<i>Cercopithecus nictitans</i>	82.0	(3)
	<i>Cercopithecus preussi</i>	82.0	(3)
	<i>Chlorocebus aethiops</i>	83.0	(3)
<i>Miopithecus talapoin</i>	83.0	(3)	
Tamarins (11-16Ma)	<i>Saguinus nigricollis</i>	78.0	(3)
	<i>Saguinus fuscicollis</i>	79.0	(3)
	<i>Saguinus tripartitus</i>	80.0	(3)
	<i>Saguinus mystax</i>	74.0	(3)
	<i>Saguinus labiatus</i>	73.0	(3)
	<i>Saguinus imperator</i>	75.0	(3)
	<i>Saguinus midas</i>	77.0	(3)
	<i>Saguinus oedipus</i>	74.0	(3)
	<i>Saguinus geoffroyi</i>	76.0	(3)
<i>Saguinus leucopus</i>	74.0	(3)	

<sup>A</sup> The gibbon radiation is comparable in age to the *Pan-Homo* split <sup>8</sup>, estimated at ~6-7Ma <sup>9</sup>. Divergence estimates based on paleontological and molecular data indicate that macaque <sup>9,10</sup>, and guenon <sup>10</sup> radiations are of approximately similar time depth. Tamarins diverged from other callitrichines in the Late to Middle Miocene <sup>19</sup>.

<sup>B</sup> Systematists place either all gibbon species into a single genus (*Hylobates*) <sup>4</sup>, distinguish multiple subgenera within *Hylobates* (shown in parentheses) <sup>8</sup>, or recognize the siamang as a separate genus (*Symphalangus*) based on size <sup>5</sup>. More recently, molecular systematists have recognized as many as four gibbon genera based on behavioral, geographic, karyotypic and molecular data <sup>12</sup>. These generic distinctions are listed in the table parenthetically.

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Figure S4

