

## Metadata for HormoneBase

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### Data Citation:

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### Data Paper:

Vitousek, M. N.\*, Johnson, M. A.\*, Donald, J. W., Francis, C. D., Fuxjager, M., Goymann, W., Hau, M., Husak, J. F., Kircher, B. K. Knapp, R., Martin, L. B., Miller, E. T., Schoenle, L. A., Uehling, J. J., and Williams, T. D. HormoneBase, a population-level database of circulating hormone concentrations across vertebrates. (submitted to *Scientific Data*, Dec 2017)

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### General Description:

The HormoneBase database contains compiled measures of steroid hormone levels (androgens and glucocorticoids) from free-living populations of vertebrates to facilitate large-scale comparative analyses.

### Taxonomic Coverage:

All relevant data from vertebrates (Kingdom: Animalia, Phylum: Chordata) were included, and classified into one of five vertebrate taxonomic groups: Birds, Reptiles, Mammals, Amphibians, Fish.

## Methods:

Studies were selected for inclusion if they contained data on circulating glucocorticoids (baseline and or stress-induced corticosterone/cortisol) or androgens (testosterone/11-ketotestosterone) that: (i) were from free-living populations, (ii) were collected from adults that had not been subject to an experimental manipulation prior to sampling (e.g., of hormones or the environment), (iii) measured plasma levels, (iv) did not pool data across males and females, or across adults and juveniles, and (v) were reported in or could be converted to a standard unit of measurement (ng/mL). Published values were obtained from text, tables, or supplementary materials, or extracted from published figures using the program Data Thief III. When papers did not directly report the coefficient of variation, it was calculated from the standard deviation or standard error and sample size. Additional information can be found in the associated data paper.

## Dataset Description:

Three files are provided: (1) HormoneBase\_v1.csv, (2) HormoneBase\_references\_v1.csv, (3) HormoneBase\_metadata.pdf

## Table of Variables:

Variable name	Variable definition	Data type/unit
<b>Vert_Group</b>	Taxonomic group (amphibian, bird, fish, mammal, reptile)	String
<b>Genus</b>	Genus	String
<b>Species</b>	Species	String
<b>Common_name</b>	Common name	String
<b>Population_1</b>	Name of first location at which samples were collected (city/region, state/province, country)	String
<b>Population_2</b>	If applicable, name of second location at which samples were collected	String
<b>Population_3</b>	If applicable, name of third location at which samples were collected	String
<b>Latitude</b>	Latitude of primary sampling location	Degrees decimal
<b>Longitude</b>	Longitude of primary sampling location	Degrees decimal
<b>LatLongEst</b>	Were latitude and longitude reported in the paper or estimated by data entry team?	Binary (Reported/Estimated)
<b>Elevation</b>	Elevation at primary sampling location	Numerical (in m)
<b>Years</b>	Year(s) during which study was conducted	Year
<b>Year_1</b>	First year of study	Year
<b>Year_final</b>	Final year of study	Year
<b>Breeding_Cycle</b>	Data collected during breeding, non-breeding, or both	Breeding/Nonbreeding/Breeding, Nonbreeding
<b>Moult</b>	Measurements were collected during molt	Binary (Y/N)
<b>Life_Stage</b>	Life history sub-stage (when provided): Prebreeding, Courtship, Incubation, Copulation, Gravid/Pregnant, Non-Gravid/Pregnant, Laying, Young care, Lactation, Post-breeding, Migration, Torpor, Hibernation, Pre-basic molt. If hormones were measured for a distinct morph or social status, indicated here	String
<b>LifeHistConf</b>	Sampled individuals were confirmed to be in the designated life history stage	Binary (Y/N)
<b>Jan_Sampled</b>	Measures were collected in January	Binary (Y/N)
<b>Feb_Sampled</b>	Measures were collected in February	Binary (Y/N)
<b>Mar_Sampled</b>	Measures were collected in March	Binary (Y/N)
<b>Apr_Sampled</b>	Measures were collected in April	Binary (Y/N)
<b>May_Sampled</b>	Measures were collected in May	Binary (Y/N)
<b>June_Sampled</b>	Measures were collected in June	Binary (Y/N)
<b>July_Sampled</b>	Measures were collected in July	Binary (Y/N)
<b>Aug_Sampled</b>	Measures were collected in August	Binary (Y/N)

<b>Sept_Sampled</b>	Measures were collected in September	Binary (Y/N)
<b>Oct_Sampled</b>	Measures were collected in October	Binary (Y/N)
<b>Nov_Sampled</b>	Measures were collected in November	Binary (Y/N)
<b>Dec_Sampled</b>	Measures were collected in December	Binary (Y/N)
<b>Time_min</b>	Beginning of sampling window	Time (24h:min)
<b>Time_max</b>	End of sampling window	Time (24h:min)
<b>CaptureMethod</b>	Method of capture	String
<b>SampleMethod</b>	Sampling active (known time to sampling, no attractants), passive (captured for unknown period before sampling), or attractant (captured with aid of playback, baited traps, etc.)	Active, Passive, Attractant
<b>MaxLatency_A</b>	Maximum sampling latency for androgens	Numerical (min)
<b>MaxLatency_Cort</b>	Maximum sampling latency for baseline glucocorticoids	Numerical (min)
<b>LateStressCort</b>	Latency between capture and stress-induced sample	Numerical (min)
<b>StressorType</b>	Type of stressor applied (baseline to stress-induced)	String
<b>MajorStressPop</b>	Major stressor experienced by population (if relevant)	String
<b>Method</b>	Assay method	String
<b>A_AntibodyKit</b>	Kit or antibody used for androgen assays	String
<b>Cort_AntibodyKit</b>	Kit or antibody used for cort assays	String
<b>CORT</b>	Glucocorticoid measured	Binary (corticosterone/ cortisol)
<b>Androgen</b>	Androgen measured	Binary (testosterone/ 11-ketotestosterone)
<b>M_A_Mean</b>	Males - mean androgen concentration	Numerical (ng/mL)
<b>M_A_SE</b>	Males - Standard error of androgens	Numerical
<b>M_A_CV</b>	Males - Coefficient of variation in androgens	Numerical
<b>M_A_N</b>	Males - Sample size for androgens	Numerical
<b>M_A_Min</b>	Males - Minimum reported androgen value	Numerical (ng/mL)
<b>M_A_Max</b>	Males - Maximum reported androgen value	Numerical (ng/mL)
<b>M_A_RemoveOutlier</b>	Males - Were androgen outliers removed?	Binary (Y/N)
<b>F_A_Mean</b>	Females - Mean androgen concentration	Numerical (ng/mL)
<b>F_A_SE</b>	Females - Standard error of androgens	Numerical
<b>F_A_CV</b>	Females - Coefficient of variation in androgens	Numerical
<b>F_A_N</b>	Females - Sample size for androgens	Numerical
<b>F_A_Min</b>	Females - Minimum reported androgen value	Numerical (ng/mL)
<b>F_A_Max</b>	Females - Maximum reported androgen value	Numerical (ng/mL)
<b>F_A_RemoveOutlier</b>	Females - Were androgen outliers removed?	Binary (Y/N)
<b>M_BC_Mean</b>	Males - mean baseline cort concentration	Numerical (ng/mL)
<b>M_BC_SE</b>	Males - Standard error of baseline cort	Numerical
<b>M_BC_CV</b>	Males - Coefficient of variation in baseline cort	Numerical
<b>M_BC_N</b>	Males - Sample size for baseline cort	Numerical
<b>M_BC_Min</b>	Males - Minimum reported value of baseline cort	Numerical (ng/mL)
<b>M_BC_Max</b>	Males - Maximum reported value of baseline cort	Numerical (ng/mL)
<b>M_BC_RemoveOutlier</b>	Males - Were baseline cort outliers removed?	Binary (Y/N)
<b>F_BC_Mean</b>	Females - Mean baseline cort concentration	Numerical (ng/mL)
<b>F_BC_SE</b>	Females - Standard error of baseline cort	Numerical
<b>F_BC_CV</b>	Females - Coefficient of variation in baseline cort	Numerical
<b>F_BC_N</b>	Females - Sample size for baseline cort	Numerical
<b>F_BC_Min</b>	Females - Minimum reported value of baseline cort	Numerical (ng/mL)
<b>F_BC_Max</b>	Females - Maximum reported value of baseline cort	Numerical (ng/mL)
<b>F_BC_RemoveOutlier</b>	Females - Were baseline cort outliers removed?	Binary (Y/N)
<b>M_SC_Mean</b>	Males - Mean stress-induced cort concentration	Numerical (ng/mL)
<b>M_SC_SE</b>	Males - Standard error of stress-induced cort	Numerical
<b>M_SC_CV</b>	Males - Coefficient of variation in stress-induced cort	Numerical
<b>M_SC_N</b>	Males - Sample size for stress-induced cort	Numerical
<b>M_SC_Min</b>	Males - Minimum reported value of stress-induced cort	Numerical (ng/mL)
<b>M_SC_Max</b>	Males - Maximum reported value of stress-induced cort	Numerical (ng/mL)
<b>M_SC_RemoveOutlier</b>	Males - Were stress-induced cort outliers removed?	Binary (Y/N)
<b>F_SC_Mean</b>	Females - Mean stress-induced cort concentration	Numerical (ng/mL)
<b>F_SC_SE</b>	Females - Standard error of stress-induced cort	Numerical
<b>F_SC_CV</b>	Females - Coefficient of variation in stress-induced cort	Numerical
<b>F_SC_N</b>	Females - Sample size for stress-induced cort	Numerical

<b>F_SC_Min</b>	Females - Minimum reported value of stress-induced cort	Numerical (ng/mL)
<b>F_SC_Max</b>	Females - Maximum reported value of stress-induced cort	Numerical (ng/mL)
<b>F_SC_RemoveOutlier</b>	Females – Were stress-induced cort outliers removed?	Binary (Y/N)
<b>OutlierCriteria</b>	Criteria for removing outliers	String
<b>Notes</b>	Notes on data	String
<b>Lab_ID</b>	PI of lab where assays conducted, if specified; if unspecified, arbitrarily assigned to one of the collaborating endocrine labs	String
<b>Ref_ID</b>	Reference to data source	Code