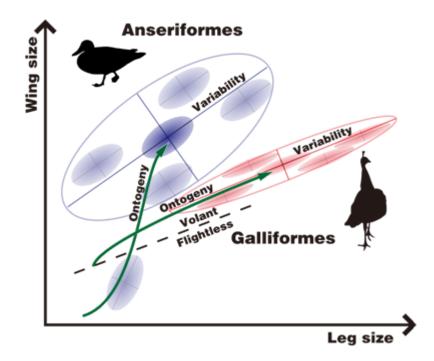
# Clade-specific evolutionary diversification along ontogenetic major axes in avian limb skeleton





Junya Watanabe (Kyoto Univ., Japan)

# **Integration and Evolutionary Bias**

• Phenotypic integration can bias evolution

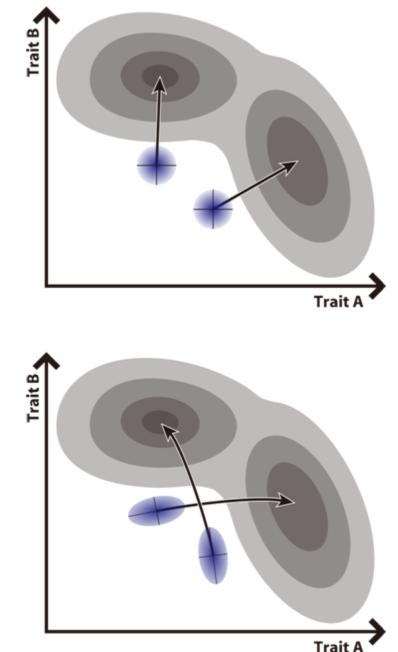
(e.g., Cheverud, 1982; Steppan et al., 2002; Armbruster et al., 2014; Goswami et al., 2015)

### Ex.:

Genetic covariation of traits as genetic lines of least resistance (Schluter, 1996)

- Different levels of integration:
  - Static
  - Ontogenetic
  - Evolutionary etc. (Klingenberg, 2014)

# How are different levels of integration related?



# **Integration and Evolutionary Bias**

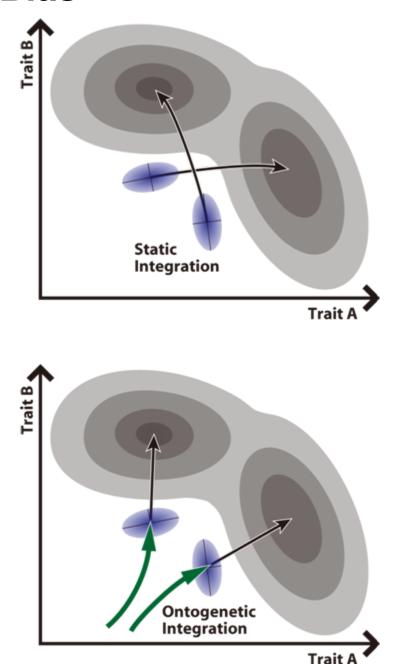
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(e.g., Cheverud, 1982; Steppan et al., 2002; Armbruster et al., 2014; Goswami et al., 2015)

## Ex.:

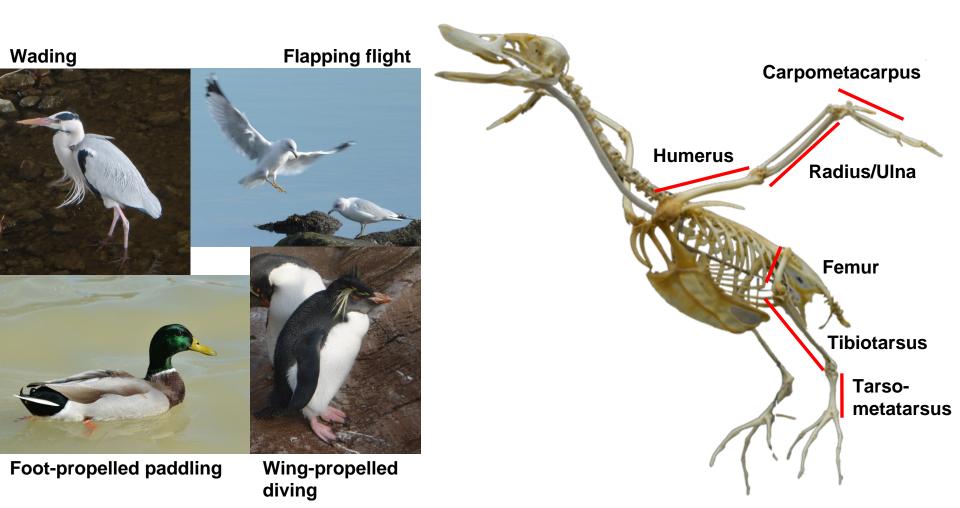
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- How are different levels of integration related?



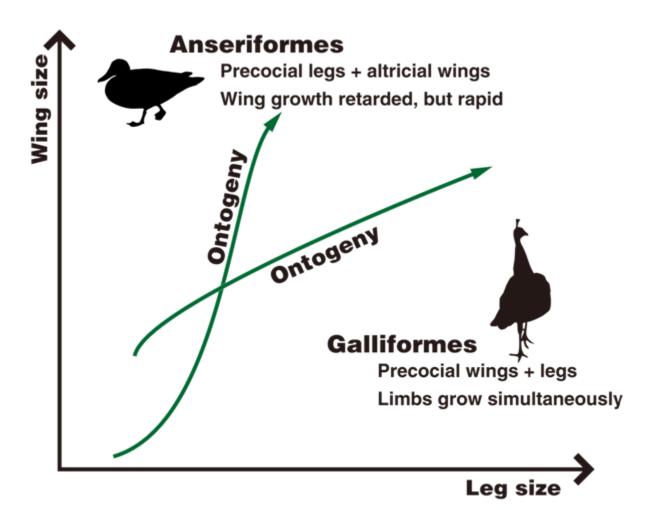
# **Avian Limb Skeleton**

- Enables various locomotion, with suitable proportion (e.g., Raikow, 1970, 1985; Storer, 1971; Gatesy & Middleton, 1997; Middleton & Gatesy, 2000)
- Functional signals have been well documented (e.g., Zeffer et al., 2003; Nudds et al., 2007; Hinić-Frlog & Motani, 2010; Watanabe, 2017)



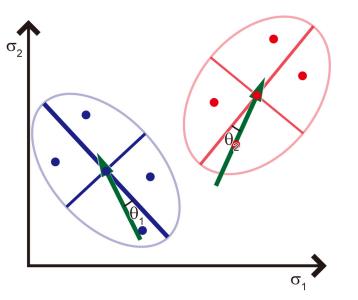
# **Ontogeny of Avian Limbs**

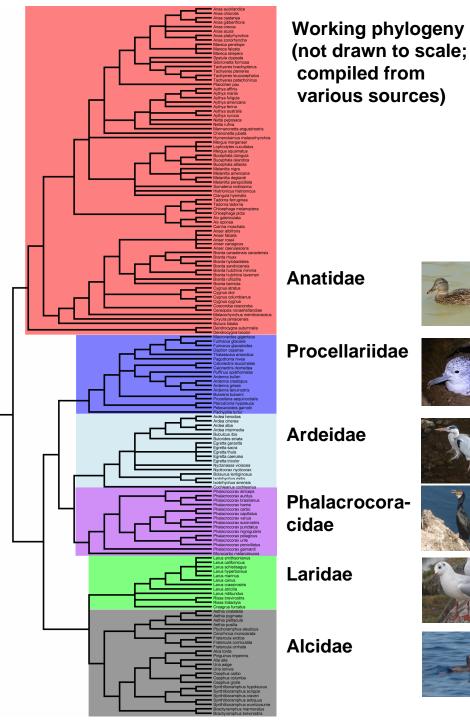
- Highly integrated postnatal ontogeny (Cane, 1993)
- Diverse ontogenetic trajectories among clades (Heers & Dial, 2015)
- Clade-specific ontogeny bias evolutionary variability?



# **Study Design**

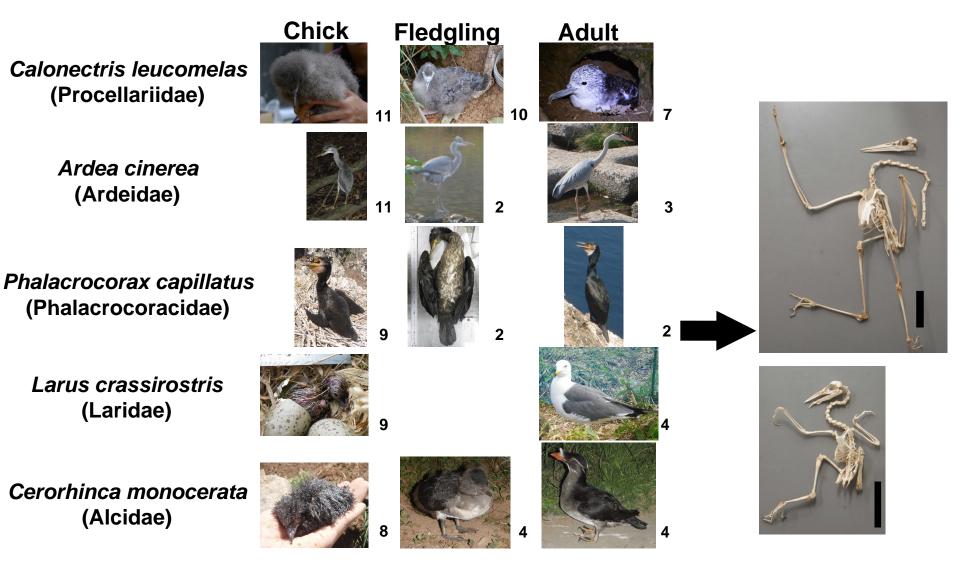
- Compared evolutionary variability and ontogenetic trajectory in 6 avian families
- Ontogenetic trajectory of each family is represented by one selected species
- Included length of 6 limb bones
- Major axes of variation extracted by PCA/pPCA with size-corrected data





# **Collection of Ontogenetic Series**

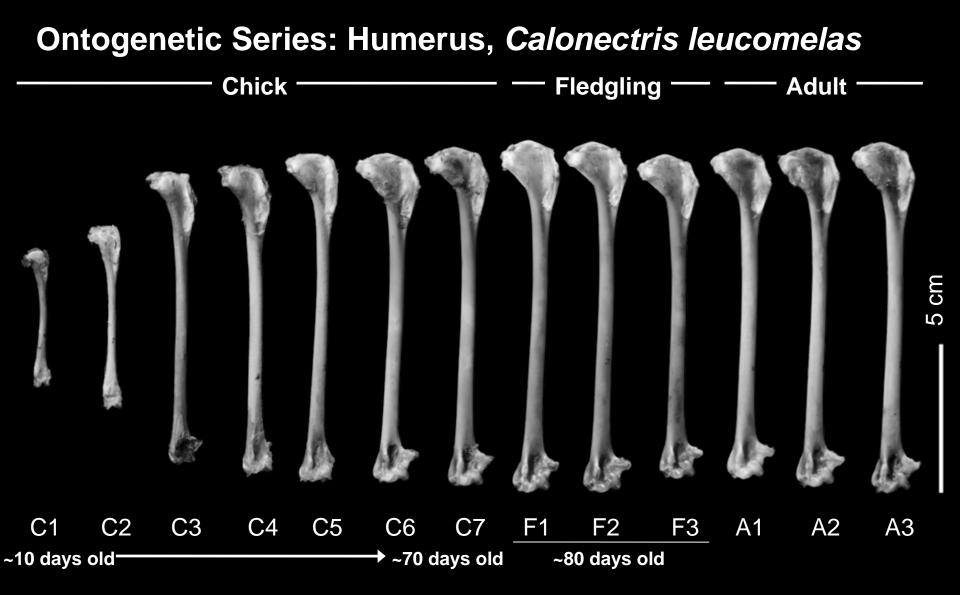
- Conducted fieldworks in breeding colonies
- Prepared series of specimens of known ontogenetic stages











Limb bones reach their adult size before/around fledging

# **Data Acquisition**

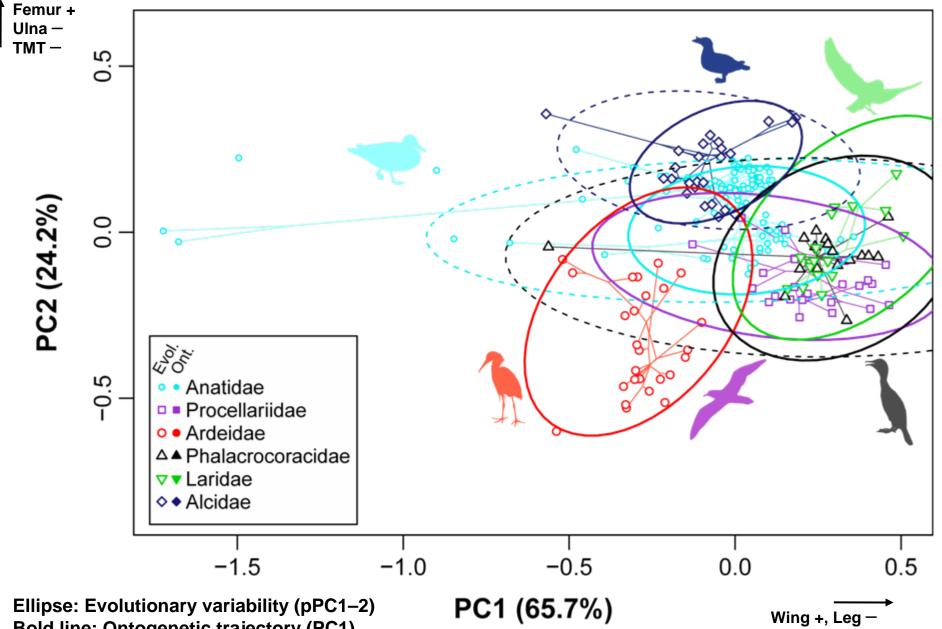
- Ontogenetic dataset:
  - Pooled data of chicks + juveniles
  - Data for Anas platyrhynchos were taken from the literature (Dial & Carrier, 2012)
- Evolutionary dataset:

Species means from museum specimens (both modern and fossil, only adults were included):

- Anatidae 109 spp. (1127 ind.)
- Procellariidae 25 spp. (344 ind.)
- Ardeidae 26 spp. (202 ind.)
- Phalacrocoracidae 17 spp. (298 ind.)
- Laridae 17 spp. (148 ind.)
- Alcidae 25 spp. (582 ind.)
- Isometric size was removed before analyses (Burnaby, 1966)

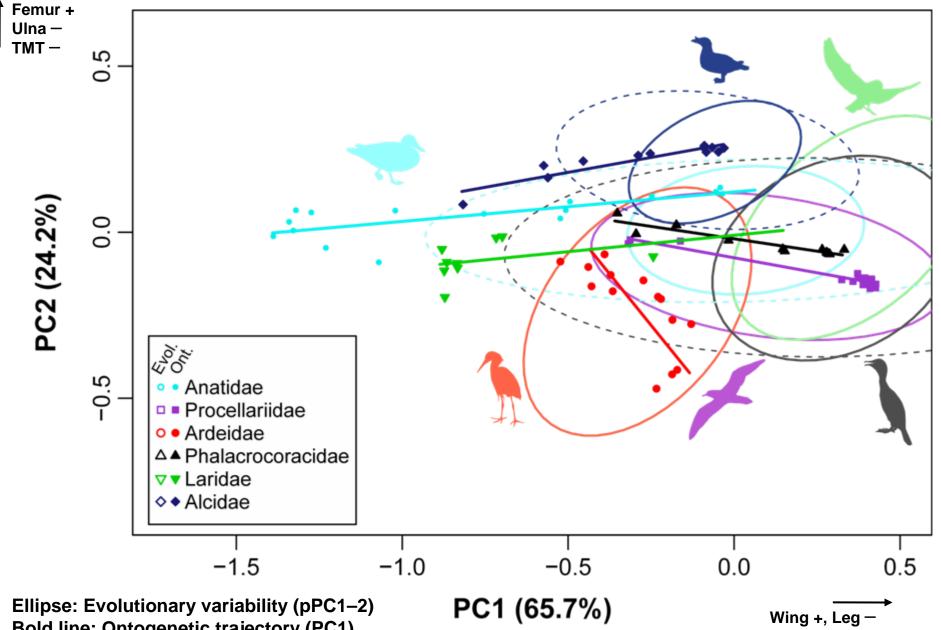


# **Results: Shape Variation Patterns**



**Bold line: Ontogenetic trajectory (PC1)** 

# **Results: Shape Variation Patterns**



**Bold line: Ontogenetic trajectory (PC1)** 

# **Results: Difference between Ontogenetic PC1s**

# Upper triangle: *p*-values (Red: significant difference)

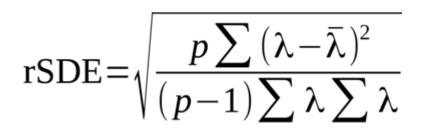
Anatidae	0.00	0.00	0.00	0.01	0.07
0.95	Procellariidae	0.05	0.10	0.09	0.00
0.48	0.71	Ardeidae	0.01	0.01	0.01
0.96	0.98	0.69	Phalàcro- coracidae	0.01	0.00
0.96	0.88	0.40	0.93	Laridae	0.00
0.99	0.93	0.45	0.94	0.94	Alcidae

#### **Lower triangle:** $\cos \theta$ (Darker blue: more similar)

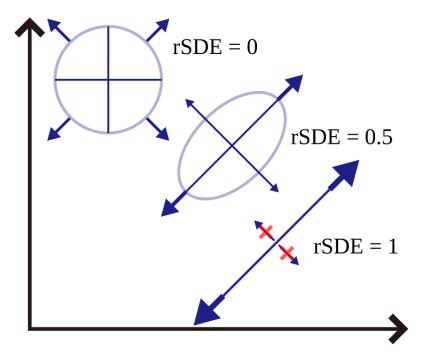
- Calculated angles
  between ontogenetic PC1s
- Mean angle: 25.8°
  Range: 8.5°–66.6°
- Tested differences with permutations (10,000 times each), with correction of False Discovery Rate
- Significant differences in most combinations
- Ontogenetic trajectories are diverse among families

# rSDE: Strength of Bias

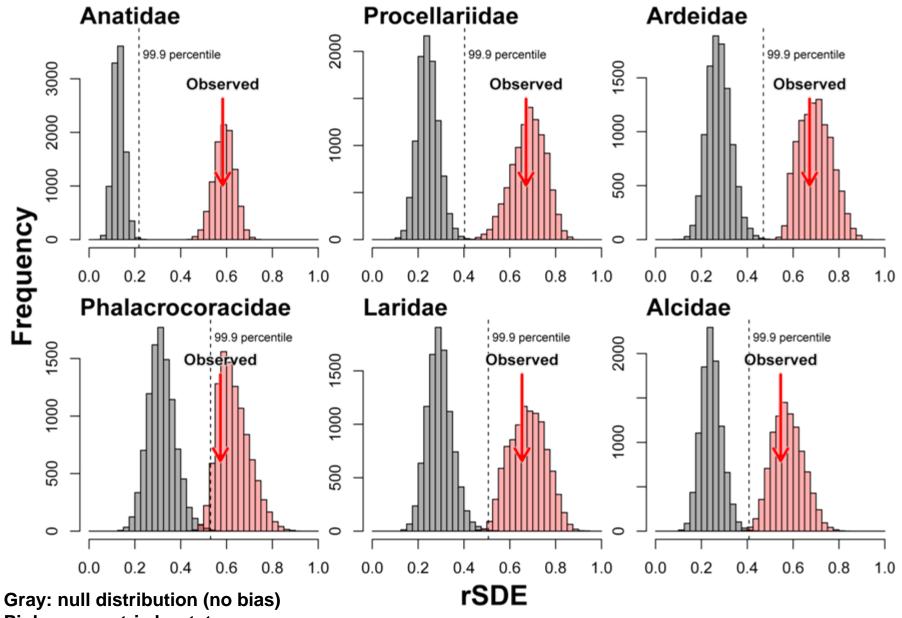
- Regularized standard deviation of eigenvalues (rSDE):
  - An index of matrix shape (Palvicev et al., 2009; Haber, 2011)
  - Provides a measure of anisotropy of Cov.-matrix
  - Takes a value from 0 (no bias) to 1 (absolute bias)
- Observed values were compared with null distributions obtained by simulated BM evolution on working phylos



- *p*: Number of eigenvalues
- $\lambda$ : Eigenvalues
- $\boldsymbol{\Sigma} :$  Mean of eigenvalues

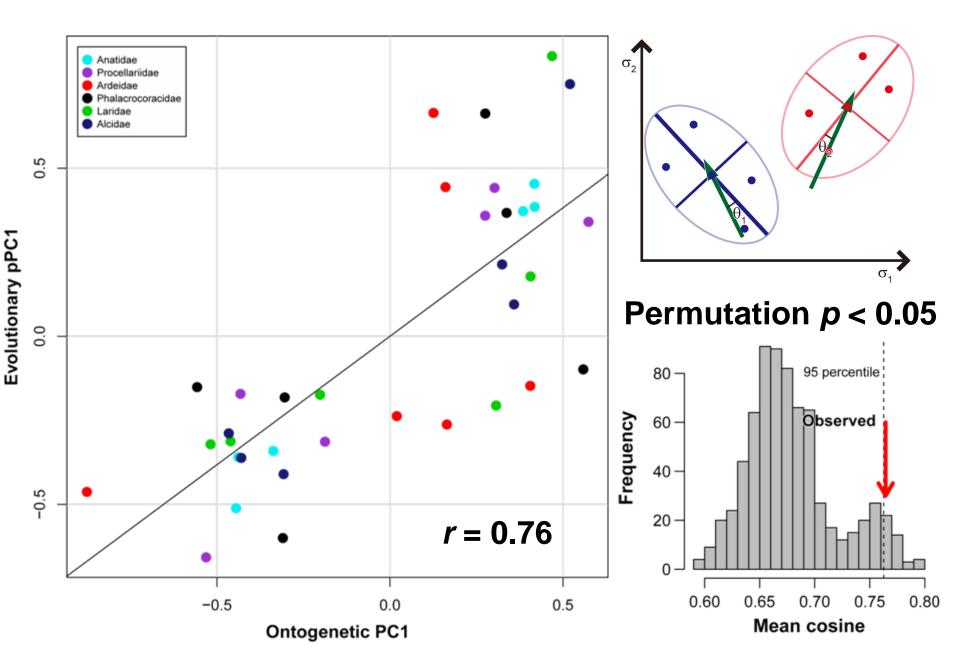


# **Results: rSDE**



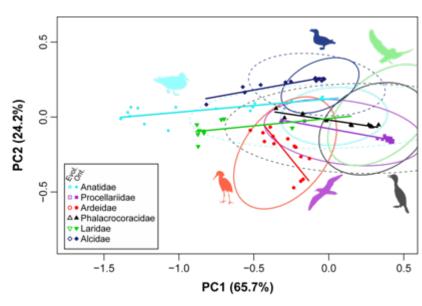
Pink: parametric bootstrap

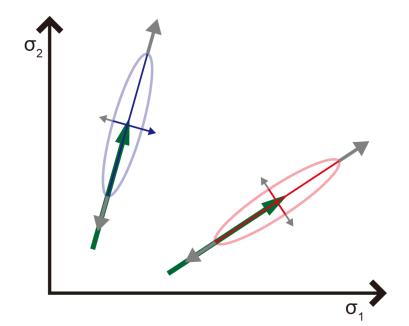
# **Results: Evolutionary vs. Ontogenetic PC1s**



# Discussion

- Evolutionary variation is concentrated in the major axis of ontogeny
- Bias of evolutionary variability by ontogenetic integration (lines of least resistance)
- > Bias is clade-specific
- Strong ontogenetic integration of avian skeleton could be a cause
- Main driving forces of divergence (selection/drift) remain elusive at this scale



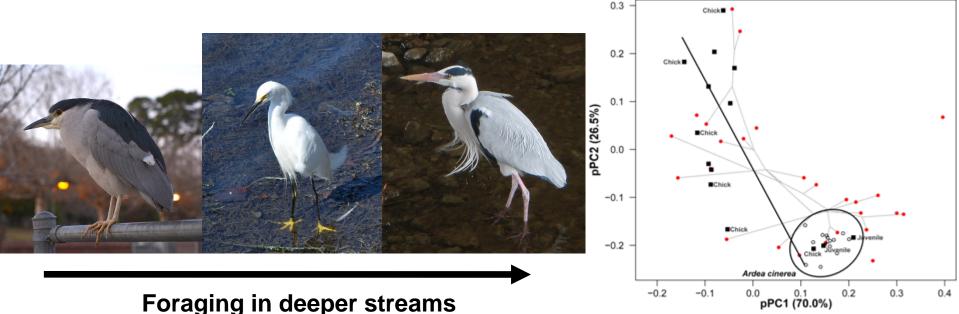


# **Implications for Evolutionary Diversification**

 Differences in ontogenetic integration patterns might explain clade-specific patterns of evolutionary diversification

### Ex.:

- **Diversity of leg length in Ardeidae** In Ardeidae, leg length corresponds to main foraging habitat Highly variable even among close relatives (Boev, 1988, 1989)
- Characteristic ontogeny of the family may have facilitated the diversification



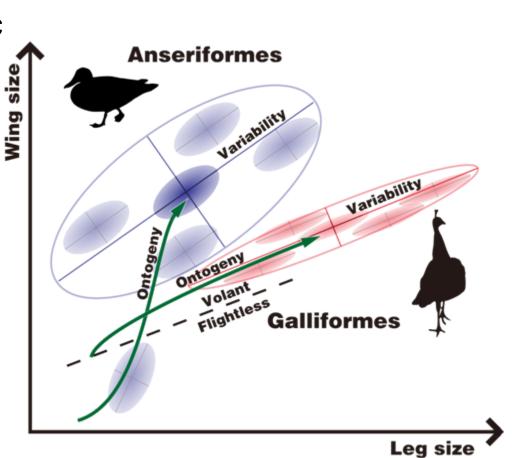
# **Implications for Evolutionary Diversification**

# Murray & Vickers-Rich (2004):

Clade-specific propensity for flightlessness might result from differences in ontogenetic trajectories?

# This study:

- Clade-specific ontogenetic trajectory may bias evolutionary variability
- Ontogenetic basis for flightlessness

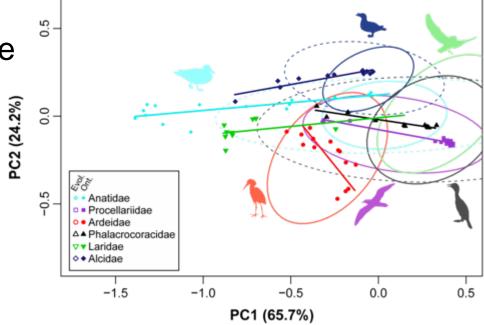


# Summary

- Relationship between ontogenetic trajectory and evolutionary variability was examined in 6 families
- Clade-specific ontogenetic trajectories seem to bias evolutionary variability
- Such bias might explain differences in evolutionary diversification patterns in avian clades

# Ex:

Long-leggedenss in Ardeidae Flightlessness in Anatidae



# Acknowledgements

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# **Size-correction**

- Variation patterns in the shape space is examined
- Log-transformed variables were projected onto the shape hyperplane perpendicular to the isometric size axis with Burnaby's (1966) method

