

Supplementary material

Appendix 1

Download Appendix 2

Table A1: Model selection results for the Californian population for models with different random-effect structures. The fixed effect structure was a three-parameter logistic model. In the top model the correlation between the two nestling-level random effects was constrained to be zero, as indicated by an asterisk.

Random effect structure		Δ AIC	AIC	$\log(\mathcal{L})$	Total number of parameters	Number of random-effect parameters
Nest level	Nestling level					
<i>A</i>	<i>A</i> and <i>I</i> *	0.00	381.23	-183.61	7	3
<i>A</i>	<i>A</i> and <i>I</i>	1.77	383.00	-183.50	8	4
-	<i>A</i> and <i>I</i>	3.70	384.93	-185.47	7	3
<i>A</i>	<i>A</i>	4.49	385.72	-186.86	6	2
<i>A</i> and <i>I</i>	<i>A</i> and <i>I</i>	4.54	385.77	-182.89	10	6
-	<i>A</i>	6.57	387.80	-188.90	5	1
-	<i>A</i> and <i>K</i>	10.58	391.81	-188.91	7	3
-	<i>A</i> , <i>K</i> , and <i>I</i>	22.93	404.16	-192.08	10	6
-	<i>I</i>	30.55	411.78	-200.89	5	1
<i>I</i>	<i>I</i>	31.05	412.28	-200.14	6	2
<i>A</i>	-	40.37	421.60	-205.80	5	1
<i>A</i> and <i>K</i>	-	42.76	423.99	-205.00	7	3
<i>A</i> and <i>I</i>	-	43.05	424.28	-205.14	7	3
<i>K</i> and <i>I</i>	-	45.81	427.04	-206.52	7	3
<i>I</i>	-	53.44	434.67	-212.34	5	1
-	-	86.21	467.44	-229.72	4	0
<i>K</i>	-	86.62	467.85	-228.93	5	1
-	<i>K</i>	88.16	469.39	-229.69	5	1
<i>K</i>	<i>K</i>	88.62	469.85	-228.92	6	2

Table A2: Model selection results for the Alaskan population, where all models included fixed differences in each parameter between younger and older nestlings. In the top models, the correlation between random effects within the nest and/or nestling level was constrained to be zero; this constraint is indicated with an asterisk.

Random effect structure		Δ AIC	AIC	$\log(\mathcal{L})$	Total number of parameters	Number of random-effect parameters
Nest level	Nestling level					
<i>A</i> and <i>I</i> *	<i>A</i> and <i>I</i> *	0	728.93	-353.47	11	4
<i>A</i> and <i>I</i> *	<i>A</i> and <i>I</i>	1.89	730.82	-353.41	12	5
<i>A</i> and <i>I</i>	<i>A</i> and <i>I</i> *	1.94	730.87	-353.44	12	5
<i>A</i> and <i>I</i>	<i>A</i> and <i>I</i>	3.80	732.73	-353.37	13	6
<i>A</i> and <i>K</i>	<i>A</i> and <i>K</i>	62.24	791.18	-382.59	13	6
-	<i>A</i> and <i>I</i>	69.98	798.91	-389.46	10	3
<i>A</i>	<i>A</i>	89.32	818.25	-400.13	9	2
<i>I</i>	<i>I</i>	123.18	852.11	-417.06	9	2
-	<i>A</i>	145.39	874.32	-429.16	8	1
-	<i>I</i>	168.68	897.61	-440.8	8	1
<i>A</i> and <i>I</i>	-	229.85	958.78	-469.39	10	3
<i>I</i>	-	250.93	979.87	-481.93	8	1
<i>A</i>	-	267.38	996.31	-490.15	8	1
<i>K</i>	-	529.64	1258.57	-621.29	8	1
<i>K</i>	<i>K</i>	531.64	1260.57	-621.28	9	2
-	-	544.80	1273.73	-629.86	7	0
-	<i>K</i>	546.80	1275.73	-629.86	8	1

Table A3: Model selection results for models testing for fixed differences in the growth rate constant, the inflection point, and the asymptotic mass between populations breeding in Alaska and California. All models included a fixed effect that shifted the inflection point for younger nestlings; this effect did not differ between populations.

Random effect structure		Δ AIC	AIC	$\log(\mathcal{L})$	Total number of parameters	Number of random-effect parameters
Nest level	Nestling level					
<i>A</i> and <i>I</i>	<i>A</i> and <i>I</i>	0.00	1125.58	-548.79	14	6
<i>A</i>	<i>A</i>	63.34	1188.92	-584.46	10	2
-	<i>A</i> and <i>I</i>	85.48	1211.06	-594.53	11	3
-	<i>A</i>	132.38	1257.96	-619.98	9	1
-	<i>A</i> and <i>K</i>	136.38	1261.96	-619.98	11	3
<i>I</i>	<i>I</i>	155.62	1281.20	-630.60	10	2
<i>A</i> and <i>I</i>	-	199.88	1325.46	-651.73	11	3
<i>K</i> and <i>I</i>	-	202.15	1327.73	-652.87	11	3
-	<i>I</i>	214.19	1339.77	-660.88	9	1
<i>A</i> and <i>K</i>	-	230.68	1356.26	-667.13	11	3
<i>A</i>	-	235.24	1360.82	-671.41	9	1
<i>I</i>	-	240.91	1366.49	-674.24	9	1
<i>K</i>	-	545.11	1670.69	-826.34	9	1
<i>K</i>	<i>K</i>	547.10	1672.68	-826.34	10	2
-	-	561.42	1687.00	-835.50	8	0
-	<i>K</i>	563.42	1689.00	-835.50	9	1

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```
# R CODE FOR ORANGE-CROWNED WARBLER NESTLING GROWTH ANALYSIS
# Note that when analyzing new datasets with a nested sampling structure (e.g. nestlings within
  nests), the data should be formatted so that each individual ID is unique. For example, use the
  format Nest1_Nestling1, rather than having the ID Nestling1 reused for birds in different nests.
```

```
# Import data
```

```
NTgrowth = read.csv("Sofaer_etal_Appendix2_OCWAGrowthData.csv")
```

```
NTgrowth$Age = NTgrowth$Age_Oldest
```

```
# Create two new dataframes containing data from the Alaskan and Californian population
```

```
AKgrowth = subset(NTgrowth, NTgrowth$site == 1)
```

```
CAGrowth = subset(NTgrowth, NTgrowth$site == 0)
```

```
# Load nlme package
```

```
require(nlme)
```

```
#####
```

```
# Analysis of growth trajectories in a single population
```

```
#####
```

```
# Goal is to fit: weight = A/(1+exp(-K*(t-I))). Note that in the manuscript and below I have
  incorporated the negative sign on K into the parentheses, rather than using this standard format
# A = Asym = asymptotic mass (grams), K = growth rate constant, I = xmid = inflection point
  (days), t = Age (days)
```

```
# Define a logistic function.
```

```
OnePop = function(Age, Asym, xmid, K){
  Asym/(1 + exp((xmid - Age)*K))
}
```

```
# Calculate the derivatives of the function
```

```
DerivOnePop = deriv(body(OnePop)[[2]], namevec = c("Asym", "xmid", "K"), function.arg=
  OnePop)
```

```
# Starting values; these can be estimates from nls (i.e. a model without random effects), or from
  previous studies
```

```
startOnePop = c(Asym = 9, xmid = 3, K = .5)
```

```
# Example model syntax for the Alaskan population
```

```
# Fixed effect only model using gnls() in nlme package
```

```
OnePop_NoRE_gnls = gnls(weight_g ~ Asym/(1 + exp((xmid - Age)*K)), data = AKgrowth,
  start = startOnePop)
```

```
summary(OnePop_NoRE_gnls)
```

```
# Example syntax for models with one random effect (either Nest or Nestling) on one parameter
```

```
# Model with nest-level random effect on the asymptotic mass
```

```
OnePop_A_Nest = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data = AKgrowth,
```

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```
fixed = Asym + xmid + K ~ 1, random = Asym ~ 1 | Nest_ID, start = startOnePop)
summary(OnePop_A_Nest)
```

```
# Model with nestling-level random effect on the inflection point
OnePop_i_Nestling = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data = AKgrowth,
  fixed = Asym + xmid + K ~ 1, random = xmid ~ 1 | Nestling_ID, start = startOnePop)
summary(OnePop_i_Nestling)
```

```
# Example syntax for models with both levels of random effects (Nest and Nestling) on a single
  parameter. Note that Nestling_ID is nested within Nest_ID.
```

```
# Model with nest- and nestling-level random effects on the inflection point
OnePop_i_NestNestling = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data =
  AKgrowth, fixed = Asym + xmid + K ~ 1, random = xmid ~ 1 | Nest_ID/Nestling_ID, start =
  startOnePop)
summary(OnePop_i_NestNestling)
```

```
# Example syntax for models with one level of random effect on multiple parameters. By default,
  nlme allows for covariance between parameters.
```

```
# Model with nestling-level random effects on the asymptotic mass and the inflection point
OnePop_Ai_Nestling = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data =
  AKgrowth, fixed = Asym + xmid + K ~ 1, random = Asym + xmid ~ 1 | Nestling_ID, start =
  startOnePop)
summary(OnePop_Ai_Nestling)
```

```
# Example syntax for models with both levels of random effects on multiple parameters.
```

```
# Model with nest- and nestling-level random effects on the asymptotic mass and the inflection
  point
```

```
OnePop_Ai_NestNestling = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data =
  AKgrowth, fixed = Asym + xmid + K ~ 1, random = Asym + xmid ~ 1 | Nest_ID/Nestling_ID,
  start = startOnePop)
summary(OnePop_Ai_NestNestling)
```

```
# For confidence intervals on the random effect standard deviations and correlations:
```

```
intervals(OnePop_Ai_NestNestling, which = "var-cov")
```

```
### Constraining covariance between random effects to be zero ###
```

```
# Any model's syntax can allow for covariance between random effect parameters within a level
  (with the default symmetrical matrix), or can be modified for zero covariance (by specifying a
  diagonal matrix).
```

```
# With covariance: Nestling_ID = pdSymm(Asym + xmid ~ 1))
```

```
# Zero covariance: Nestling_ID = pdDiag(Asym + xmid ~ 1))
```

```
# Need to group data:
```

```
GroupedNestNestling_AKGrowth = groupedData(weight_g ~ Age | Nest_ID/Nestling_ID, data =
  AKgrowth)
```

```
# Model without a correlation between random effects at the nest level, with a correlation at the
```

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```
nestling level
AK_AiNestNestling_noCorrNest = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data =
  GroupedNestNestling_AKGrowth, fixed = Asym + xmid + K ~ 1, random = list(Nest_ID =
  pdDiag(Asym + xmid ~ 1), Nestling_ID = pdSymm(Asym + xmid ~ 1)), start = startOnePop)
summary(AK_AiNestNestling_noCorrNest)

# Model without a correlation at either nest or nestling levels
AK_AiNestNestling_noCorrBoth = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data
  = GroupedNestNestling_AKGrowth, fixed = Asym + xmid + K ~ 1, random = list(Nest_ID =
  pdDiag(Asym + xmid ~ 1), Nestling_ID = pdDiag(Asym + xmid ~ 1)), start = startOnePop)
summary(AK_AiNestNestling_noCorrBoth)
# For confidence intervals on the random effect standard deviations:
intervals(AK_AiNestNestling_noCorrBoth, which = "var-cov")

##### Different random effect structure at each level #####
# Top-ranked model of CA data had different random effect structure at nest and nestling levels:
# Need to group data:
GroupedNestNestling_CAGrowth = groupedData(weight_g ~ Age | Nest_ID/Nestling_ID, data =
  CAgrowth)

# Model with nest-level random effect on the asymptotic mass, nestling-level random effect on
  both the asymptotic mass and the inflection point (no correlation)
CA_ANest_AiNestlingNoCorr = nlme(weight_g ~ DerivOnePop(Age, Asym, xmid, K), data =
  GroupedNestNestling_CAGrowth, fixed = Asym + xmid + K ~ 1, random = list(Nest_ID =
  pdDiag(Asym ~ 1), Nestling_ID = pdDiag(Asym + xmid ~ 1)), start = startOnePop)
summary(CA_ANest_AiNestlingNoCorr)

##### Example syntax for producing diagnostic plots #####
# "." references the fitted object

# Example code based on top AK model:
plot(AK_AiNestNestling_noCovBoth) # plot residuals vs. fitted values
plot(AK_AiNestNestling_noCovBoth, resid(., type = "p") ~ fitted(.) | Younger_1ifknown) #
  residuals vs. fitted by group - use to compare residuals of older/younger birds, populations

# observed vs. fitted values
plot(AK_AiNestNestling_noCovBoth, weight_g ~ fitted())
plot(AK_AiNestNestling_noCovBoth, weight_g ~ fitted(.) | Nest_ID) # separately by nest

# normal plots of residuals
qqnorm(AK_AiNestNestling_noCovBoth, ~ resid(., type = "p"))
qqnorm(AK_AiNestNestling_noCovBoth, ~ resid(., type = "p") | Younger_1ifknown)

# Check assumption that random effects are normally distributed
ranef(AK_AiNestNestling_noCovBoth, level = "Nest_ID") # this is how to access the 'BLUPs'
```

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```
qqnorm(AK_AiNestNestling_noCovBoth, ~ ranef(., level = "Nest_ID"))
qqnorm(AK_AiNestNestling_noCovBoth, ~ ranef(., level = "Nestling_ID"))

# residuals by group (i.e. by nest):
plot(AK_AiNestNestling_noCovBoth, Nest_ID ~ resid(., type = "p"), abline = 0)

#####
#           Incorporating asynchronous hatching
#####
# Goal is to add a fixed effect that shifts the inflection point for asynchronously hatched
# nestlings, and fixed effects that test for a difference in the growth rate constant and the
# asymptotic mass

# Younger_1ifknown is coded as a 1 for nestlings that were known to have hatched after their
# nestmates (i.e. runts), and as a 0 for all other nestlings. Defined as Xr in manuscript text (eqn 3)

# function including fixed effects of asynchronous hatching on xmid, K, and Asym
OnePopRuntAIK = function(Age, Younger_1ifknown, Asym, xmid, K, Irunt, Krunt, Arunt){
  (Asym + Arunt*Younger_1ifknown)/(1 + exp((xmid+Irunt*Younger_1ifknown -
  Age)*(K+Krunt*Younger_1ifknown)))
}

# Calculate derivatives:
DerivOnePopRuntAIK = deriv(body(OnePopRuntAIK)[[2]], namevec = c("Asym", "xmid", "K",
" Irunt", "Krunt", "Arunt"), function.arg= OnePopRuntAIK)

# Starting values:
startOnePopRuntAIK = c(Asym = 9, xmid = 3, K = .5, Irunt = 0, Krunt = 0, Arunt = 0)

# Model without random effects
OnePopRUNT_gnls = gnls(weight_g ~ DerivOnePopRuntAIK(Age, Younger_1ifknown, Asym,
xmid, K, Irunt, Krunt, Arunt), data = AKgrowth, start = startOnePopRuntAIK)
summary(OnePopRUNT_gnls)

# Syntax for running models mirrors syntax shown above, with updated fixed-effect function
# Top-ranked model: Random effects of nest and nestling on the asymptotic mass and the
# inflection point with no correlation between random effects (see above for code creating
# grouped data)
OnePopRunt_Ai_NestNestling_NoCorrBoth = nlme(weight_g ~ DerivOnePopRuntAIK(Age,
Younger_1ifknown, Asym, xmid, K, Irunt, Krunt, Arunt), data =
GroupedNestNestling_AKGrowth, fixed = Asym + xmid + K + Irunt + Krunt + Arunt ~ 1,
random = list(Nest_ID = pdDiag(Asym + xmid ~ 1), Nestling_ID = pdDiag(Asym + xmid ~ 1)),
start = startOnePopRuntAIK)
summary(OnePopRunt_Ai_NestNestling_NoCorrBoth)
intervals(OnePopRunt_Ai_NestNestling_NoCorrBoth, which = "var-cov")
```


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```
#####  
# Comparison of growth trajectories between two populations  
#####  
# Goal is to test for differences in the three logistic growth parameters between two populations.  
# Model included a fixed runt effect on the inflection point that does not differ between  
# populations (called runt)  
  
# Function including differences between populations and a runt effect on the inflection point  
SiteAKiRUNT = function(Age, site, Younger_1ifknown, Asym, xmid, K, Kdiff, middiff, Adiff,  
  runt){  
  (Asym + Adiff*site)/(1 + exp(((xmid+middiff*site+runt*Younger_1ifknown) -  
  Age)*(K+Kdiff*site)))  
  }  
  
# Calculate derivatives:  
SiteAKiRUNTderiv = deriv(body(SiteAKiRUNT)[[2]], namevec = c("Asym", "xmid", "K",  
  "Kdiff", "middiff", "Adiff", "runt"), function.arg= SiteAKiRUNT)  
  
# Starting values:  
startsiteAKiRUNT = c(Asym = 9, xmid = 3, K = .5, Kdiff=0, middiff=0, Adiff = 0, runt = 0)  
  
# Model without random effects  
SiteAKiRUNT_noRE_gnls = gnls(weight_g ~ SiteAKiRUNTderiv(Age, site,  
  Younger_1ifknown, Asym, xmid, K, Kdiff, middiff, Adiff, runt), data = NTgrowth, start =  
  startsiteAKiRUNT)  
summary(SiteAKiRUNT_noRE_gnls)  
  
# Syntax for running models mirrors syntax shown above, with updated fixed-effect function  
# Top-ranked model: Random effects of nest and nestling on the asymptotic mass and the  
# inflection point  
SiteAKiRUNT_Ai_NestNestling = nlme(weight_g ~ SiteAKiRUNTderiv(Age, site,  
  Younger_1ifknown, Asym, xmid, K, Kdiff, middiff, Adiff, runt), fixed = Asym + xmid + K +  
  Kdiff + middiff + Adiff + runt ~ 1, random = Asym + xmid ~ 1 | Nest_ID/Nestling_ID, data =  
  NTgrowth, start = startsiteAKiRUNT)  
summary(SiteAKiRUNT_Ai_NestNestling)  
  
#####  
#           Example syntax for lme4 package  
#####  
# Note that you will want to quit and restart R when switching between nlme and lme4  
# As of early 2012, there appeared to be some issues with AIC output from lme4. Specifically,  
# adding a random effect for which the random effect standard deviation was estimated as zero  
# could lower the AIC value. Look for these issues and confirm that they have been resolved  
# before using nonlinear mixed models in lme4 in your research.
```

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```
require(lme4)
```

```
# To use lme4, define the fixed-effect function, its derivatives, and the starting values as in nlme
```

```
# Example syntax for model from the Alaskan population with nest- and nestling-level random effects on the asymptotic mass and the inflection point, allowing for covariance between random effects at each level:
```

```
OnePop_Ai_NestNestling_lme4 = nlmer(weight_g ~ DerivOnePop(Age, Asym, xmid, K) ~ (Asym + xmid | Nest_ID) + (Asym + xmid | Nestling_ID), data = AKgrowth, start = startOnePop, verbose = TRUE)
```

```
summary(OnePop_Ai_NestNestling_lme4)
```

```
# Example syntax for the model that does not allow for covariance between random effects at the nest level
```

```
OnePop_Ai_NestNestling_noCovNest_lme4 = nlmer(weight_g ~ DerivOnePop(Age, Asym, xmid, K) ~ (Asym | Nest_ID) + (xmid | Nest_ID) + (Asym + xmid | Nestling_ID), data = AKgrowth, start = startOnePop, verbose = TRUE)
```

```
summary(OnePop_Ai_NestNestling_noCovNest_lme4)
```