

Preface

This document serves as a description for scripts, data, and result files associated with the publication:

Thia et al. (2018) Larval traits show temporally consistent constraints, but are decoupled from post-settlement juvenile growth, in an intertidal fish. *Journal of Animal Ecology*.

All files begin with the prefix: *Thia_2018_JAnimEcol_TraitCov_*.

There are three types of files: *CODE* files contain code used to analyse the data and generate figures. *DATA* files contain data. *RESULTS* contain the results of analysis.

The code is written to run so that all scripts, data, and any result files generated, are in the same directory. Make sure you install the required packages (noted at the start of the scripts).

CODE_Analyses.R

Contains the code for reported analyses.

CODE_Figures.R

Contains the code for data figures.

CODE_Functions_for_Analyses.R

Contains the code for custom functions that are used in the *CODE_Analyses.R* script.

CODE_Functions_for_Figures.R

Contains the code for custom functions that are used in the *CODE_Figures.R* script.

DATA_fish_info.csv

This file contains collection information for fish we obtained otolith traits from.

Variable	Description
id	The individual's ID.
year	The collection year.
month	The collection month.
day	The collection day.
size	The standard length (mm).

DATA_pld_growth.csv

Column heads are each individual fish.

Each row's cell (per column) represents the otolith size for each daily increment.

The first value represents the day 5 of total age or day 3 post-hatch/pre-settlement (dataset doesn't contain first feed check, hatch check, or the 2 embryonic increments); and the last value is the increment prior to the settlement check.

DATA_set_growth.csv

Column heads are each individual fish.

Each row's cell (per column) represents the otolith size for each daily increment.

The first value represents the day 2 post-settlement (1st increment after the settlement check), up to the last easily readable increment. Note that this doesn't include settlement check.

DATA_traits.csv

This files contains the raw otolith trait information. There is missing data.

Variable	Description
id	The individual's ID.
pld	The adjusted number of pelagic days; only the post-hatch days; includes hatch check and settlement check.
age.post.set	The estimated number of days (increments) after settlement.
hatch.size	The distance between the nucleus and hatch check (μm); the 3 rd daily increment, but the 1 st day of post-hatch (pelagic phase).
max.oto.size	The size of the otolith at capture (μm).
set.size	The distance between the nucleus and the settlement check (μm).
age.post.hatch	The number of daily increments post-hatching (pld + age.post.set)

DATA_traits_cleaned.csv

This file contains the cleaned otolith trait information. There is no missing data. Has the same columns as *DATA_traits.csv*, but has additional variables for analysis and plotting.

Variable	Description
id	The individual's ID.
p1d	The adjusted number of pelagic days; only the post-hatch days; includes hatch check and settlement check.
age.post.set	The estimated number of days (increments) after settlement.
hatch.size	The distance between the nucleus and hatch check (μm); the 3 rd daily increment, but the 1 st day of post-hatch (pelagic phase).
max.oto.size	The size of the otolith at capture (μm).
set.size	The distance between the nucleus and the settlement check (μm).
age.post.hatch	The number of daily increments post-hatching (p1d + age.post.set)
set.day4.size	The distance between nucleus and the fourth-day-post-settlement increment (μm).
year	The collection year.
month	The collection month.
day	The collection day.
size	The standard length (mm).
grow.pelagic	The total growth attained in the pelagic phase (μm); the distance between the hatch and settlement check.
grow.set	The total growth attained in the first four days post-settlement (μm); the distance between the settlement check and the fourth-day-post-settlement increment.
year.cols	Hex values for year colours.
hatch.year	The year an individual hatched in.
hatch.month	The month an individual hatch in.
hatch.day	The day an individual hatch on.
hatch.date	A numerical vector that describes the month and day an individual was born on; 1 = 1 December, ending at 90 = 28 February.
season	The breeding season.

RESULTS_GrowthAndSize_Correlations.csv

A pairwise matrix of the correlations between growth and size traits measured in this study (see descriptions for *DATA_traits_cleaned.csv*).

RESULTS_Model_HatchdateBySeason_ANCOVA_NoInteraction.txt

The reduced ANCOVA models for each trait: TRAIT = HATCH DATE + SEASON.

RESULTS_Model_HatchdateBySeason_ANCOVA_WithInteraction.txt

The full ANCOVA models for each trait: TRAIT = HATCH DATE + SEASON + HATCH DATE:SEASON.

RESULTS_PathMods_Coefficients_DirectEffects.csv

The direct effect coefficients from the path models.

Variable	Description
Original	The original β_{DIR} estimate from the data.
Mean.Boot	The mean bootstrap β_{DIR} estimate based on 1,000 replicates.
Std.Error	The standard error around the mean bootstrap β_{DIR} estimate based on 1,000 replicates.
perc.025	The lower 2.5% percentile for bootstrap β_{DIR} estimates based on 1,000 replicates.
perc.975	The upper 97.5% percentile for bootstrap β_{DIR} estimates based on 1,000 replicates.
year	The season sampled, or the pooled dataset.
paths	The path examined, abbreviated as follows: HS = hatch size, LD = larval duration, PG = pelagic growth, SG = post-settlement growth. Interpreted as the first trait affecting the second.
names	A description of the path.

RESULTS_PathMods_Coefficients_TotalEffects.csv

The total effect coefficients from the path models.

Variable	Description
Original	The original β_{TOT} estimate from the data.
Mean.Boot	The mean bootstrap β_{TOT} estimate based on 1,000 replicates.
Std.Error	The standard error around the mean bootstrap β_{TOT} estimate based on 1,000 replicates.
perc.025	The lower 2.5% percentile for bootstrap β_{TOT} estimates based on 1,000 replicates.
perc.975	The upper 97.5% percentile for bootstrap β_{TOT} estimates based on 1,000 replicates.
year	The season sampled, or the pooled dataset.
paths	The path examined, abbreviated as follows: HS = hatch size, LD = larval duration, PG = pelagic growth, SG = post-settlement growth. Interpreted as the first trait affecting the second.
names	A description of the path.

RESULTS_PathMods_Coefficients_TotalEffects.csv

The variation explained in a trait based on all direct and indirect effects of earlier occurring traits.

Variable	Description
R2	The coefficient of determination, R^2 .
year	The season sampled, or the pooled dataset.
traits	The standard error around the mean bootstrap β_{TOT} estimate based on 1,000 replicates.

RESULTS_PathMods_SeasonTests_DirectEffects.csv

Test for significant differences in mean bootstrap estimates (1,000 replicates) of direct effects, β_{DIR} , using Welch's t -test for unequal variance.

Variable	Description
comparison	The two sampling seasons compared.
path	The path examined, abbreviated as follows: HS = hatch size, LD = larval duration, PG = pelagic growth, SG = post-settlement growth. Interpreted as the first trait affecting the second.
t.stat	Welch's t calculated for the difference in means.
df	The associated degrees of freedom.
pval	The associated p -value.

RESULTS_PathMods_SeasonTests_DirectEffects.csv

Test for significant differences in mean bootstrap estimates (1,000 replicates) of total effects, β_{TOT} , using Welch's t -test for unequal variance.

Variable	Description
comparison	The two sampling seasons compared.
path	The path examined, abbreviated as follows: HS = hatch size, LD = larval duration, PG = pelagic growth, SG = post-settlement growth. Interpreted as the first trait affecting the second.
t.stat	Welch's t calculated for the difference in means.
df	The associated degrees of freedom.
pval	The associated p -value.