



hatchR: A tool set to predict when fish hatch and emerge

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hatchR

hatchR is a software ecosystem for predicting fish developmental phenology using statistical models. It offers three primary applications:

1. Basic summarization, plotting, and data checks for water temperature data.
2. Access published parameterizations for salmonid developmental models or build your own custom parameterizations for any species with user provided data.
3. Predict hatch and/or emergence timing across ambient temperatures from common data sources such as HOBO loggers.

hatchR is deployed in two formats. First, it can be downloaded as a R package. Secondly, for users not familiar with R, it can also be accessed as a web app built in Shiny as a point-and-click tool.

To predict phenology, you need daily average temperatures over incubation (or data that can be summarized as such) and spawn timing.

hatchR's workflow

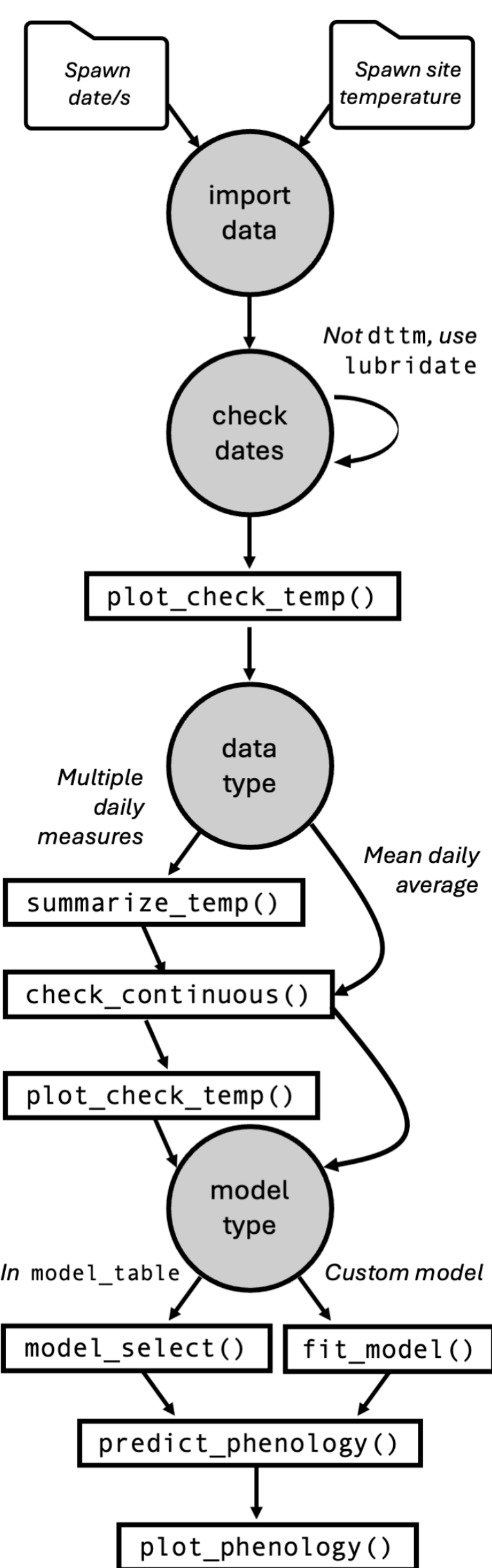


Figure 1: hatchR workflow. Processes are presented as filled circles, functions as plain text rectangles, and decisions as italicized text.

Included & custom models

hatchR includes numerous parameterizations for salmonids because the original models were built from aquaculture studies with salmon. Those models are included in `model_table` and include all North American Pacific Salmon (*Oncorhynchus spp.*) and Bull Trout (*Salvelinus confluentus*).

Table 1: Two example rows (of 51) from `model_table`.

author	species	expression
Beacham and Murray 1990	sockeye	1 / exp(6.727 - log(x + 2.394))
Beacham and Murray 1990	pink odd	1 / exp(6.663 - log(x + 2.557))

Alternatively, you can build custom models with experimental data. Here we demonstrate with Channel Catfish (*Ictalurus punctatus*).

```
# make catfish data object for function
catfish <- matrix(NA, 3, 2) |> data.frame()
colnames(catfish) <- c("days", "temp_C")
catfish$days <- c(16,21,26) # days to hatch
catfish$temp_C <- c(22,10,7) # exp. temperatures

# fit model
cat_mod <- fit_model(
  temp = catfish$temp_C,
  days = catfish$days,
  species = "catfish",
  development_type = "hatch")
```

To further demonstrate this approach we parameterize models (not shown) for Smallmouth Bass (*Micropterus dolomieu*) and Lake Sturgeon (*Acipenser fulvescens*) and apply the models to a temperature regime with mean temperature 16 °C.

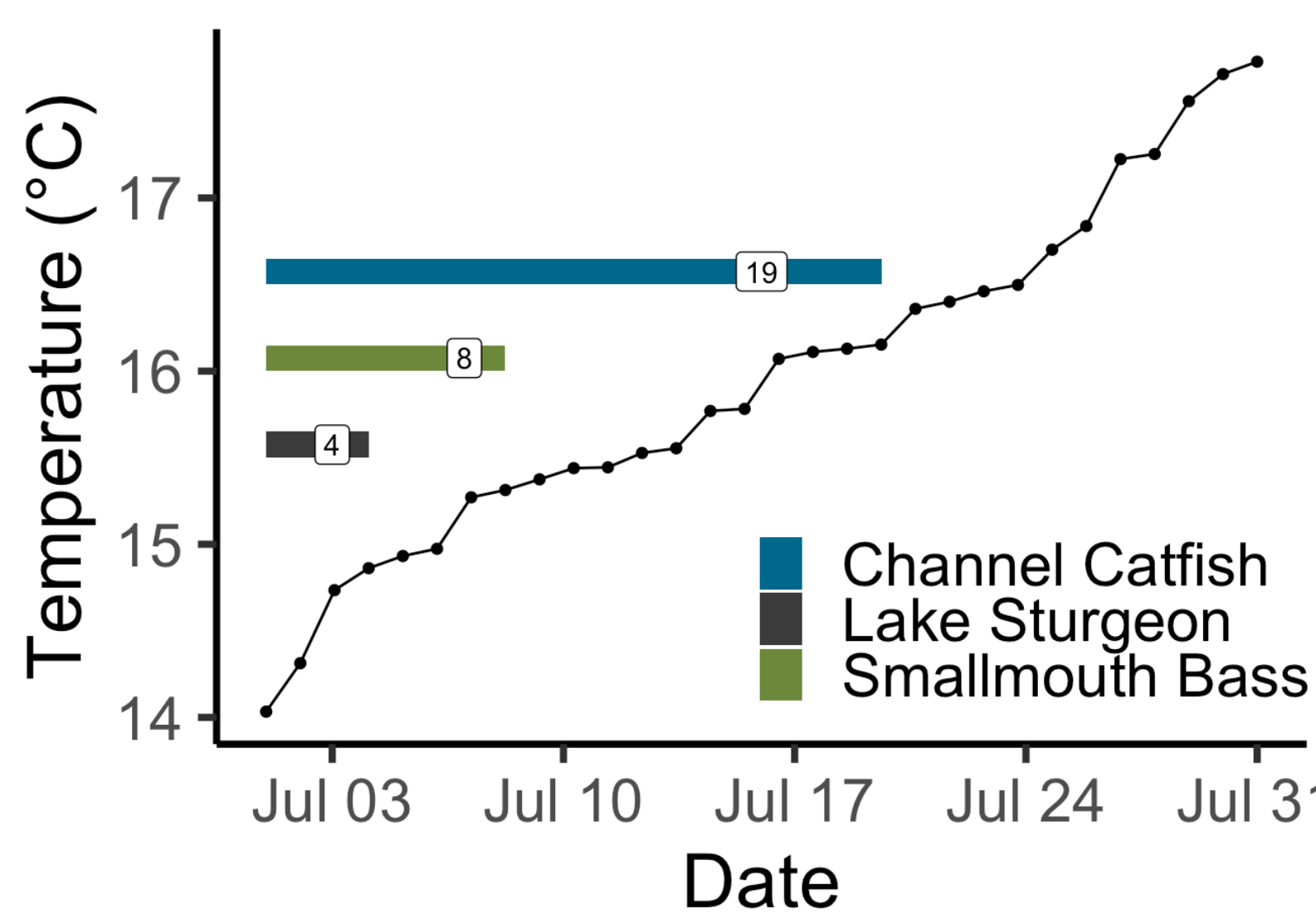


Figure 2: Predicted days to hatch using custom parameterizations for three warmwater species with mean 16 °C thermal regime.

Basic prediction

As a case study for a basic application we'll use our included data set of `crooked_river` and an example with Bull Trout.

Let's assume the forest manager wants to do some roadwork upstream of a Bull Trout spawning reach in Crooked River starting **July 1**. They engage the forest biologist who knows Bull Trout, which are sensitive to sediment, will be finished spawning there by **September 30**. They can then predict if fish are likely to have emerged from the gravel by July (using the 2014-2015 spawn year).

```
# get model from model_table
bull_trout_emerge <- model_select(
  author = "Austin et al. 2019",
  species = "bull trout",
  model = "MM",
  development_type = "emerge")

# predict phenology assuming Sept. 30th as spawn
crooked_river_emerge <- predict_phenology(
  data = crooked_river,
  dates = date,
  temperature = temp_C,
  spawn.date = "2014-09-30",
  model = bull_trout_emerge)

#predicted days to emerge
crooked_river_emerge$days_to_develop
```

[1] 204

Our model predicts Bull Trout will emerge 204 days after September 30th, which is April 22 or well before the July 1 date of road construction.

Advanced prediction

The power of **hatchR** is fully realized when we combine multiple variables for iterating the **hatchR** function, `predict_phenology()`. We'll use 139 putative Bull Trout populations spread across Idaho to demonstrate combining predictions across sites, years, and spawn dates. We will use the included `idaho` data set, with which we will do some filtering (not shown) and then predict hatch timing assuming fish spawn September 1, 15, and 30 (Early, Peak, Late) at each site in each of the four continuous years of temperature data (1668 parameter combinations).

We present an abridged demonstration automating across our parameter set:

```
# predict hatch time across variable combinations
hatch_res <- isaak_summ_bt |>
  mutate(dev_period = map2(
    summ_obj, spawn_dates,
    predict_phenology,
    temperature = daily_temp,
    model = bt_hatch,
    dates = date) |>
    map_df("dev.period") |>
    list()) |>
  select(site, dev_period) |>
  unnest(cols = c(dev_period)) |>
  mutate(days_to_hatch = stop - start)
```

We can then plot those results (code not shown) to visualize phenology across our variable set.

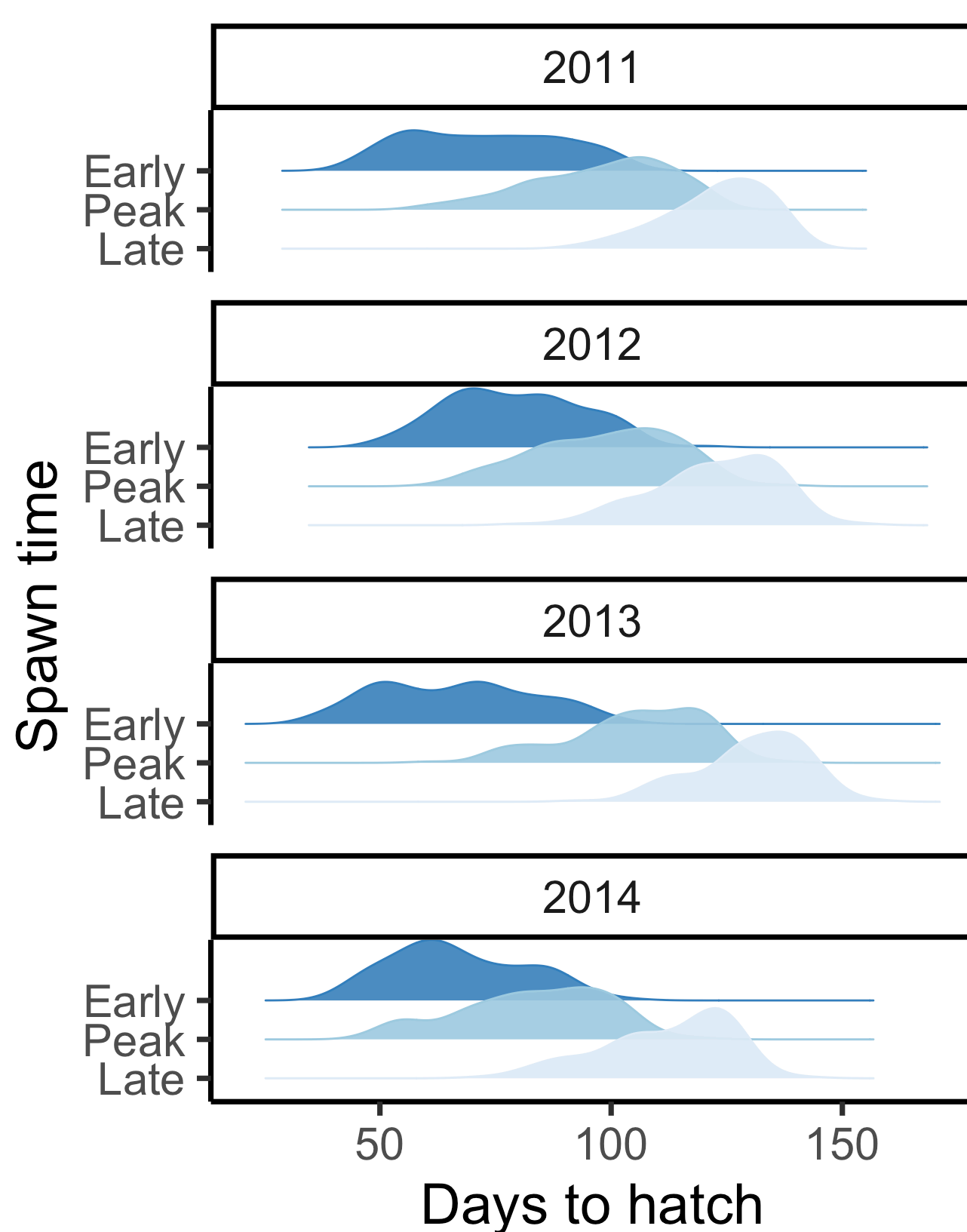


Figure 3: Predicted hatch timing for 139 putative Bull Trout sites for three spawning periods.

Conclusion

hatchR includes extensive documentation for these and other examples. To fully explore **hatchR** or try out the **Basic prediction** example in Shiny (*scroll pages down on mobile devices*), we recommend visiting the Shiny and package websites.



Figure 4: Shiny App (left), Website (Right)