

# hatchR

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## Introduction

**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 in *wild* environments from common data sources such as HOBO loggers.

**hatchR** is deployed in two formats. First, it can be downloaded as an 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 development (or data that can be summarized as such) and spawn timing.

## Using hatchR

**hatchR can be accessed two ways:**

### R package

**hatchR** can be downloaded from CRAN and used in the R programming language for full functionality. The **hatchR** website provides numerous Articles on basic to advanced use.



A toolset to predict when fish hatch and emerge in the wild



### Shiny app

**hatchR** can be accessed in a point-and-click interface via Shiny. The app loads in your browser and provides much of the functionality of the R package but is less flexible.



## Workflow

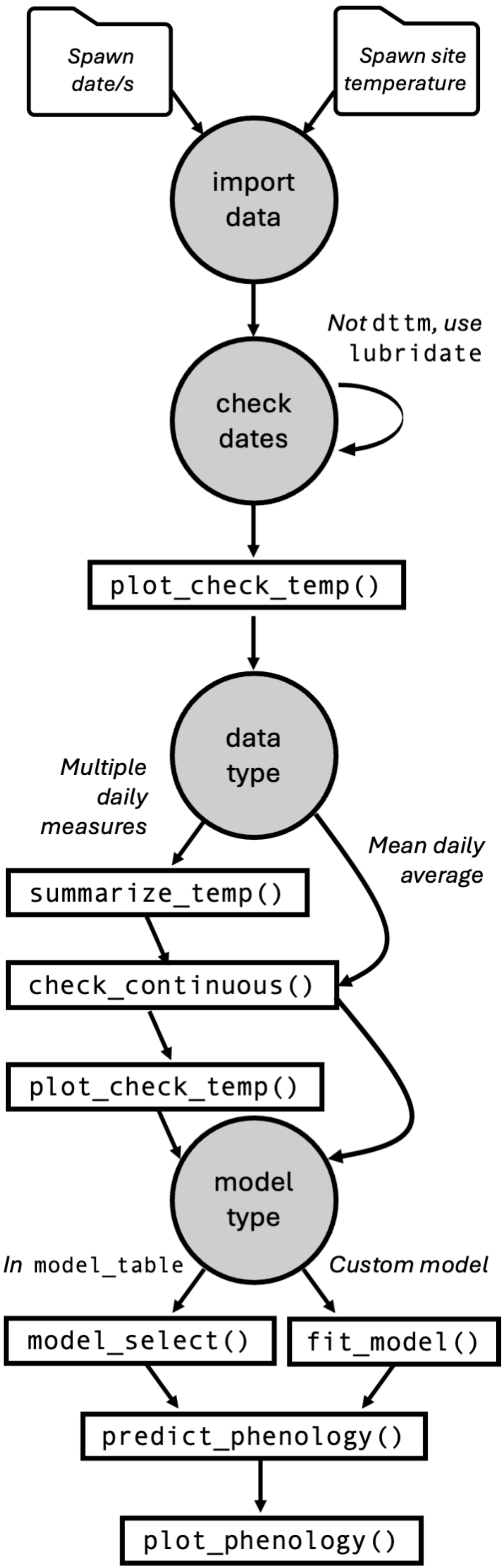


Figure 1: **hatchR** workflow. Processes are presented as filled circles, functions as plain text rectangles, and decisions as italicized text.