Data Development and Analysis Pathways for Marine Mammals and Turtles: Creating a User Interface Sarina Fernandez^{1,2}, Warren Asfazadour^{2,3}, Eric Archer⁴ and Lisa Komoroske⁴ ¹ California Polytechnic State University, San Luis Obispo, CA ² STAR Program, San Luis Obispo, CA ³ Boston University, Boston, MA⁴ NOAA Southwest Fisheries Science Center, La Jolla, CA

Introduction

- containing functions for summarizing genetic data and analyzing population structure.

Creating a shiny User Interface

The user interface script controls the layout of the app.

The first step of creating a shiny user interface is loading the shiny package.



Some important general commands include: fluidPage: allows the app to adjust automatically to the user's browser window size

helpText: provides users with general directions for using the app

Widgets are web elements that users interact with in order to communicate with the app. Here are some examples of widgets and the code that creates them within this app:

File inputs allow users to upload their raw data.



Acknowledgements

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• Researchers are in need of user-friendly tools to help streamline data analysis for ongoing genomics projects. Using shiny⁴, an R package that provides a framework for developing web applications, we created a web application for strataG^{1,2}, an R package

Using the strataG shiny Application

Running a shiny app requires two R scripts: the server³ and the user interface. The server code is essentially the brains of the app. It contains all of the strataG functions that analyze the genetic data and it interprets the inputs from each widget in the user interface.

When both a server and user interface file are open in RStudio, the user will have the option to click a "Run App" button which will open the app in a new window.

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The raw data is uploaded on the first tab and used to create a *gtypes object* that can then be analyzed by functions of strataG on the subsequent tabs.

The QA/QC tab allows users to run a variety of quality control summary functions on their genetic data. This important step helps users ensure that their data is as error-free as possible prior to downstream analyses.

Users can run a number of statistical tests to analyze the population structure of their data on the final tab.

All outputs generated by the app's functions can be saved in .csv format to any directory that the user specifies.



