test

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source("scripts/04\_divesummary.R") library(dplyr) library(knitr)

# ' ---

# ' title: test

# '

# ' Annual Report for Gratuitous Permit No. FBP-0079-14

# ' author: Michelle Stuart

# ' date: #' 2018-03-13

# ' output:

# ' word\_document:

# ' fig\_width: 5

# ' fig\_height: 5

# ' fig\_caption: true

# ' ---

# ' ### Introduction

# ' Under the project “Effects of low population density on reef fish

# ' connectivity,” we conducted fieldwork and collected anemonefish samples in

# ' Leyte from May 1 to June 16, 2016. The primary objective was to collect

# ' tissue samples (fin clips) from individuals of Amphiprion clarkii at each of

# ' #' #'

13 locations. In this season, we sampled

13 sites in Albuera and Bay Bay City, Leyte. #' We are now beginning laboratory analysis of the collected specimens. We are #' using genotyping-by-sequencing methods to genotype each specimen at a number #' of Single Nucleotide Polymorphisms (SNPs). This will allow us to match #' parents and offspring and to identify when we recapture the same fish in a #' different field season. This information will allow us to determine whether #' small populations are self-persistent or whether they rely on surrounding #' populations for persistence (network persistence).

# '### Inventory

# ' Note: All samples are tissue clips from the caudal fin.

# generate a table for the bfar report

# in the field, load 2017 dive data from saved database

dive <- read.csv("data/diveinfo.csv", stringsAsFactors = F) %>% filter(grepl("2017", date)) %>% select(dive\_table\_id, site, municipality) # in the field, load the anemones that correspond to those dives anem <- read.csv("data/anemones.csv", stringsAsFactors = F) %>% filter(dive\_table\_id %in% diveanem\_table\_id, !is.na(fin\_id), fin\_id != "NULL") %>% select(fish\_table\_id, anem\_table\_id, fin\_id) fish <- left\_join(fish, anem, by = "anem\_table\_id") rm(anem) bfar <- fish %>% group\_by(site, municipality) %>% summarise(samples = n()) bfar <- bfar %>% mutate(Province = "Leyte") %>% rename(Municipality = municipality, Site = site, Samples = samples) %>% select(Province, Municipality, Site, Samples)

# ' ### Map of the sites on the west coast of Leyte

map\_path <- "data/leyte\_map.png" include\_graphics(map\_path)