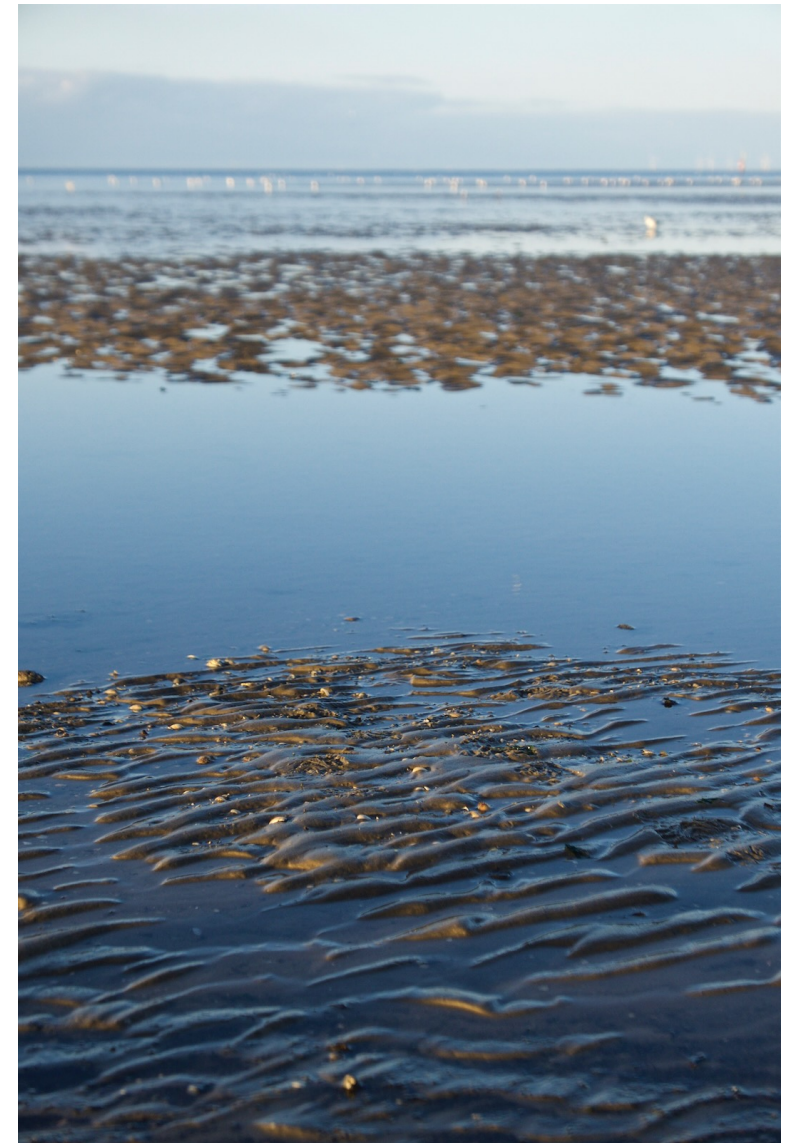# Exercises in Marine Ecological Genetics

05. Isolation by distance

- Correlate geographic and genetic distance

- Test for isolation by distance

- Deepen your understanding of tidyverse / ggplot

Martin Helmkampf

Carl von Ossietzky
Universität
Oldenburg

Download course materials using git

Go to project directory and check contents

```
cd dir              # e.g. Documents/meg23_exercises
ls -l                           # -l: long format
```

```
📁  meg23_exercises
    ├── local
    └── meg23_repo
            ├── code
            ├── data
            ├── other
            └── slides
```

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05. Isolation by distance

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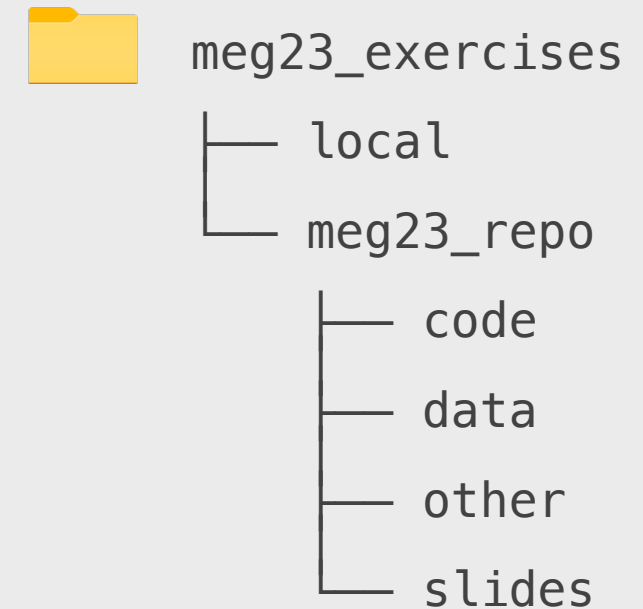Oldenburg

Download course materials using git

Go to project directory and check contents

```
cd dir          # e.g. Documents/meg23_exercises
ls -l                           # -l: long format
```

Update course repository

```
cd meg23_repo
git pull
```

```
meg23_exercises
├── local
└── meg23_repo
    ├── code
    ├── data
    ├── other
    └── slides
```

Please do not save over files in the course repository. Instead, save your own scripts to the local subdirectory (including copies of course scripts you would like to edit), e.g with

```
cp code/05_ibd.R ../local/05_ibd_lc.R          # cp [source] [destination]
```

Exercises in Marine Ecological Genetics
05. Isolation by distance

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In case of an error message …

Delete old repository and re-download from GitHub

```
rm -rf meg23_repo

git clone https://github.com/mhelmkampf/meg23_repo.git
```

Exercises in Marine Ecological Genetics
05. Isolation by distance

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Oldenburg

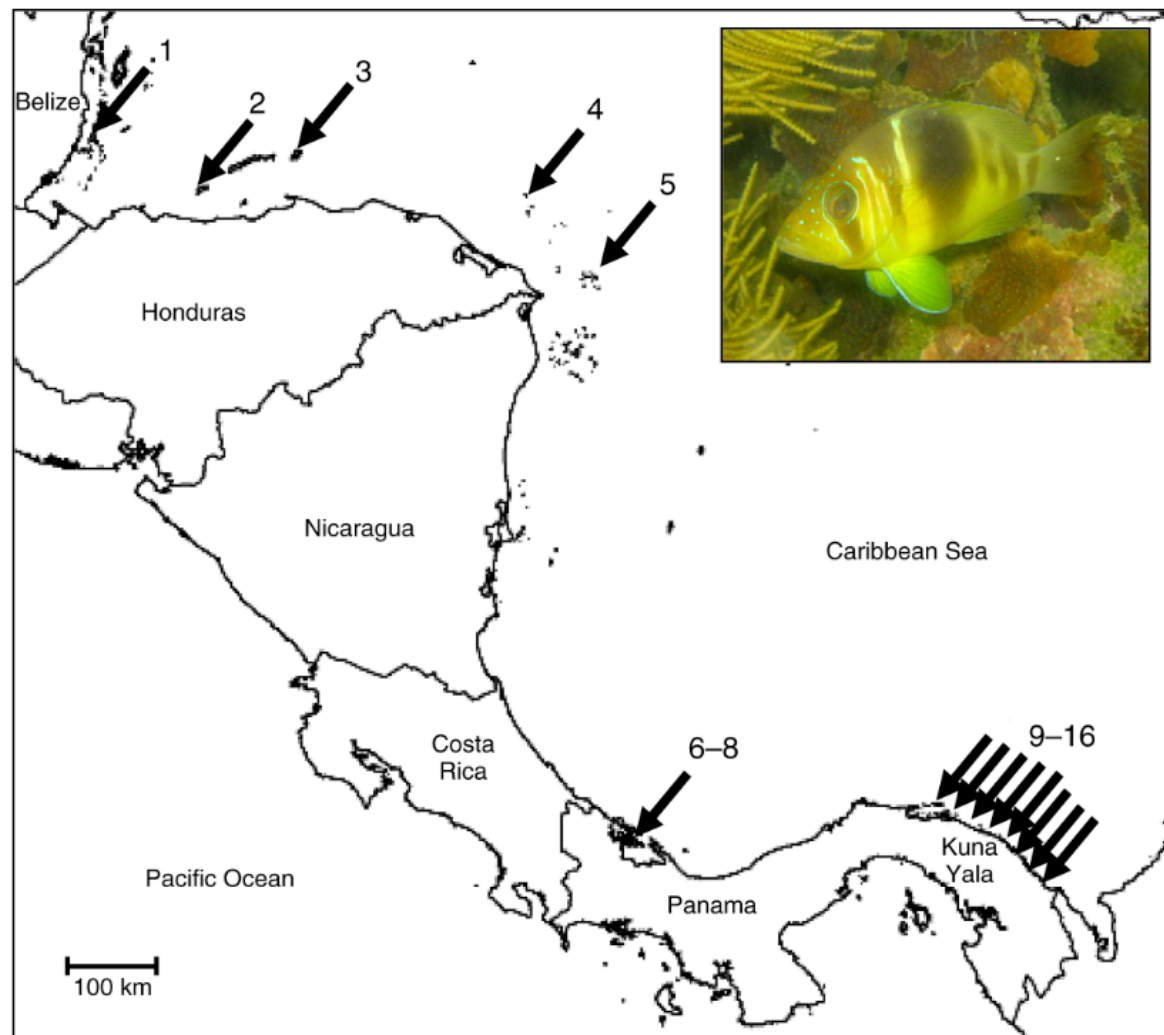# New R concepts: tidyverse and ggplot

Tidyverse pipes

```
x <- df %>%        # assign to new object (copy)

  mutate() %>%     # 1st operation

  arrange() %>%    # 2nd operation

  select()         # 3rd operation
```

Basic ggplot syntax

```
ggplot(data = df, aes(x = var1, y = var2)) +  # mapping variables

  geom_bar() +     # geometric shapes representing the data

  labs() +         # set plot and axis labels

  guides() +       # customize plot legend

  theme()          # customize non-data, e.g. fonts, gridlines
```

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05. Isolation by distance

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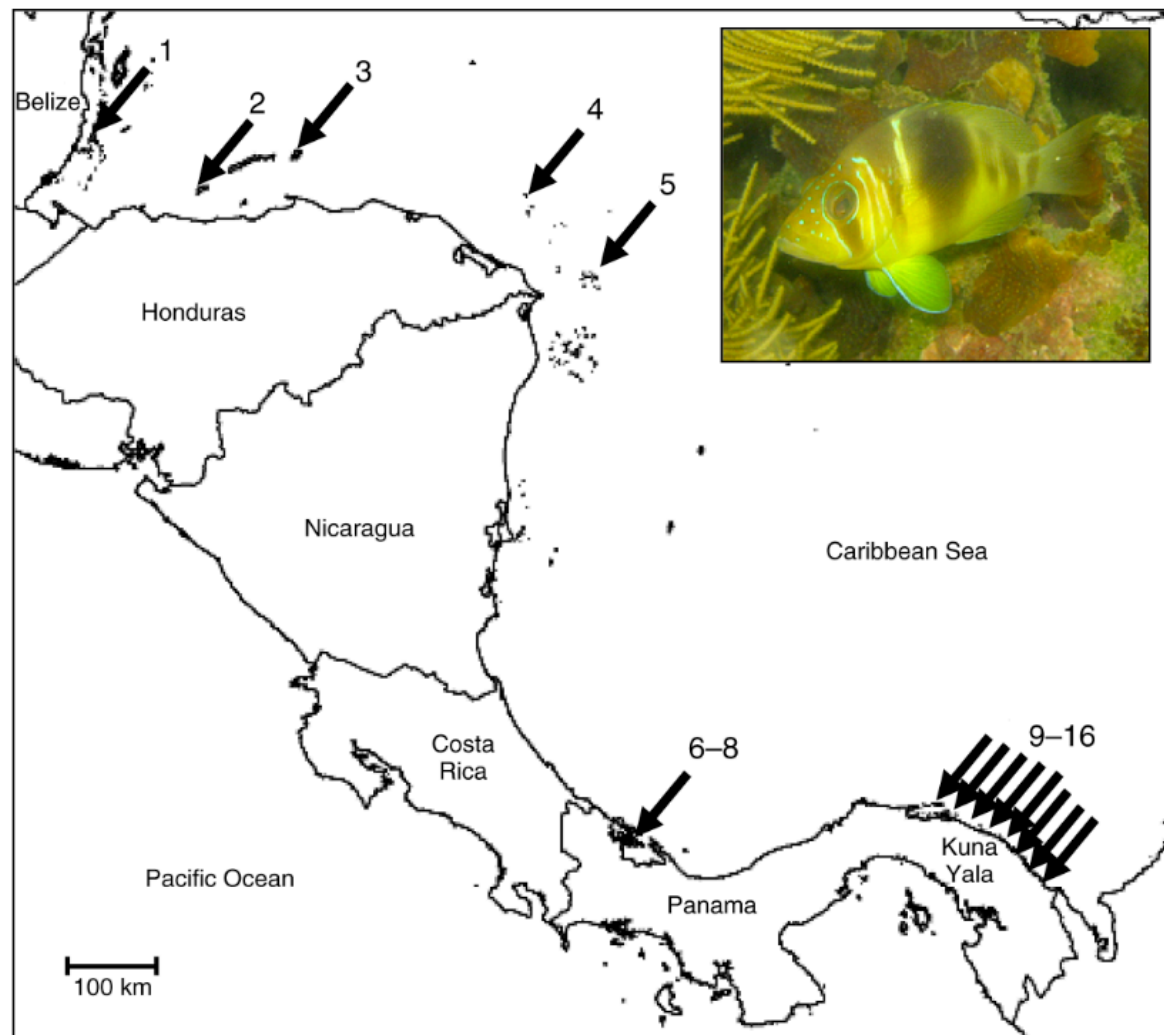
Barred hamlet (*H. puella*) microsatellite dataset

Estimating dispersal from genetic isolation by distance in a coral reef fish (*Hypoplectrus puella*)

OSCAR PUEBLA,[1,2,3] ELDREDGE BERMINGHAM,[1,2] AND FRÉDÉRIC GUICHARD[2]

- 10 highly variable microsatellite loci

- 854 individuals

- 15 Caribbean locations

- Spatial scales from 10 km to > 3000 km

Exercises in Marine Ecological Genetics

05. Isolation by distance

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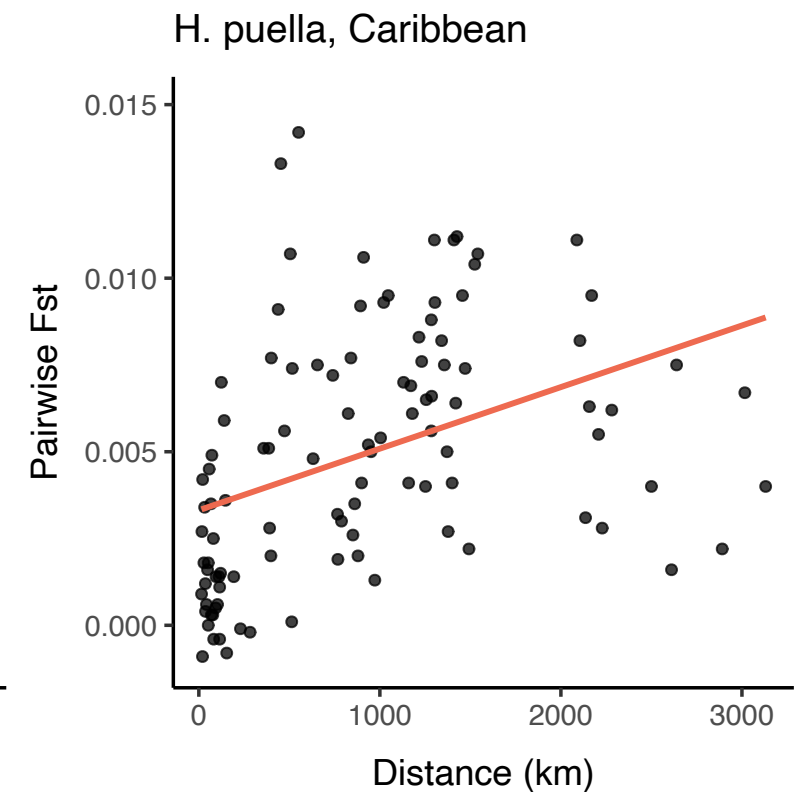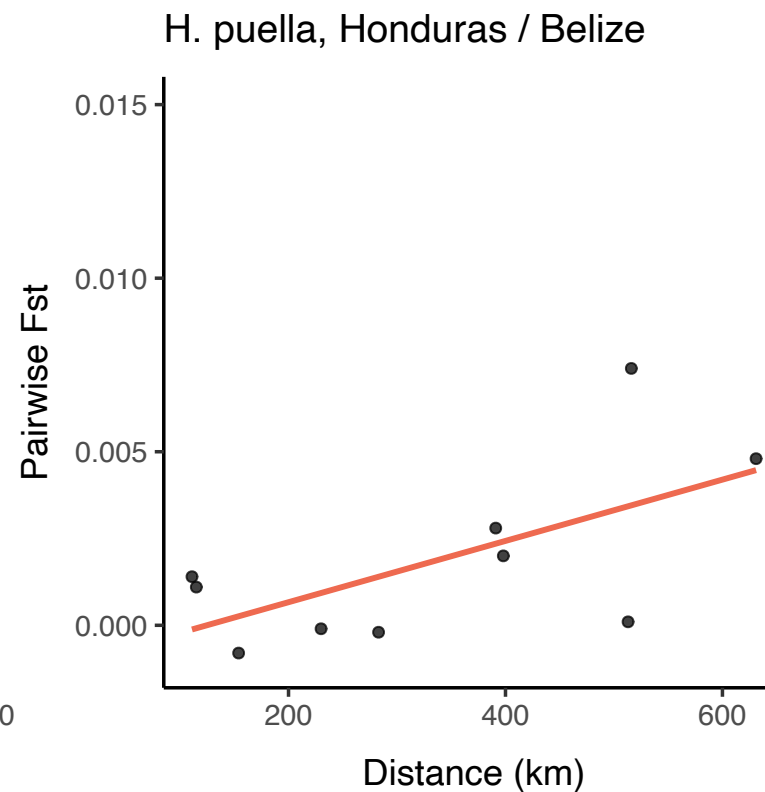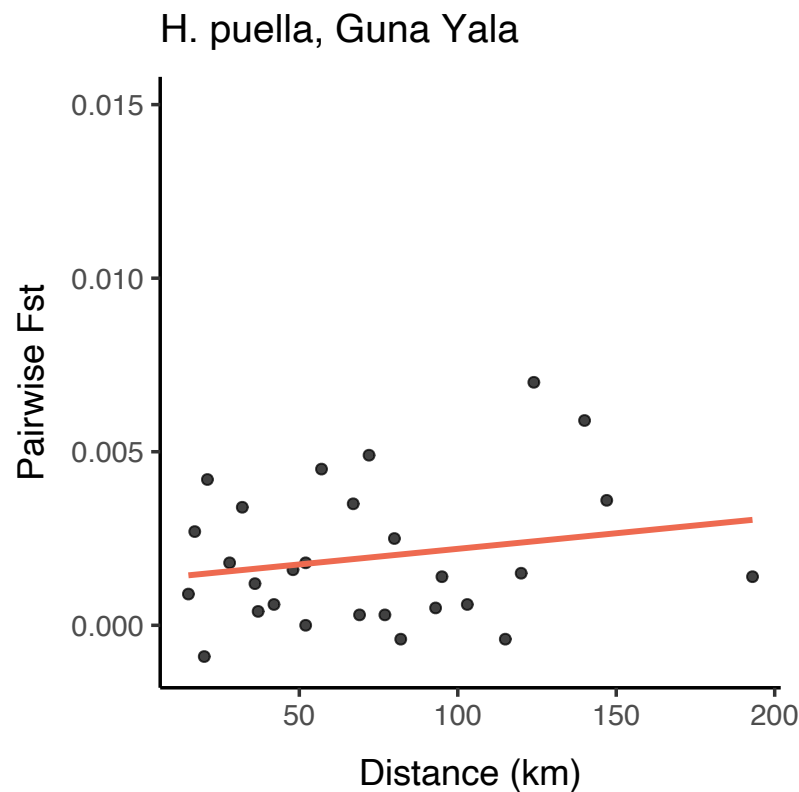
Barred hamlet (*H. puella*) microsatellite dataset

Estimating dispersal from genetic isolation by distance in a coral reef fish (*Hypoplectrus puella*)

OSCAR PUEBLA,[1,2,3] ELDREDGE BERMINGHAM,[1,2] AND FRÉDÉRIC GUICHARD[2]

- Is there evidence for isolation by distance in the dataset?

- At what geographic scale does isolation by distance emerge?

- How can we test for isolation by distance?

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Exercises in Marine Ecological Genetics
05. Isolation by distance

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At what scale does isolation by distance emerge?

Test	Guna Yala	Honduras / Belize	Caribbean
Regression	$R^2 < 0.01$, $p = 0.31$	$R^2 < 0.32$, $p = 0.05$	$R^2 = 0.15$, $p < 0.0001$
Mantel	?	$p \sim 0.25$	$p < 0.05$

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At what scale does isolation by distance emerge?

H. puella, Guna Yala · H. puella, Honduras / Belize · H. puella, Caribbean
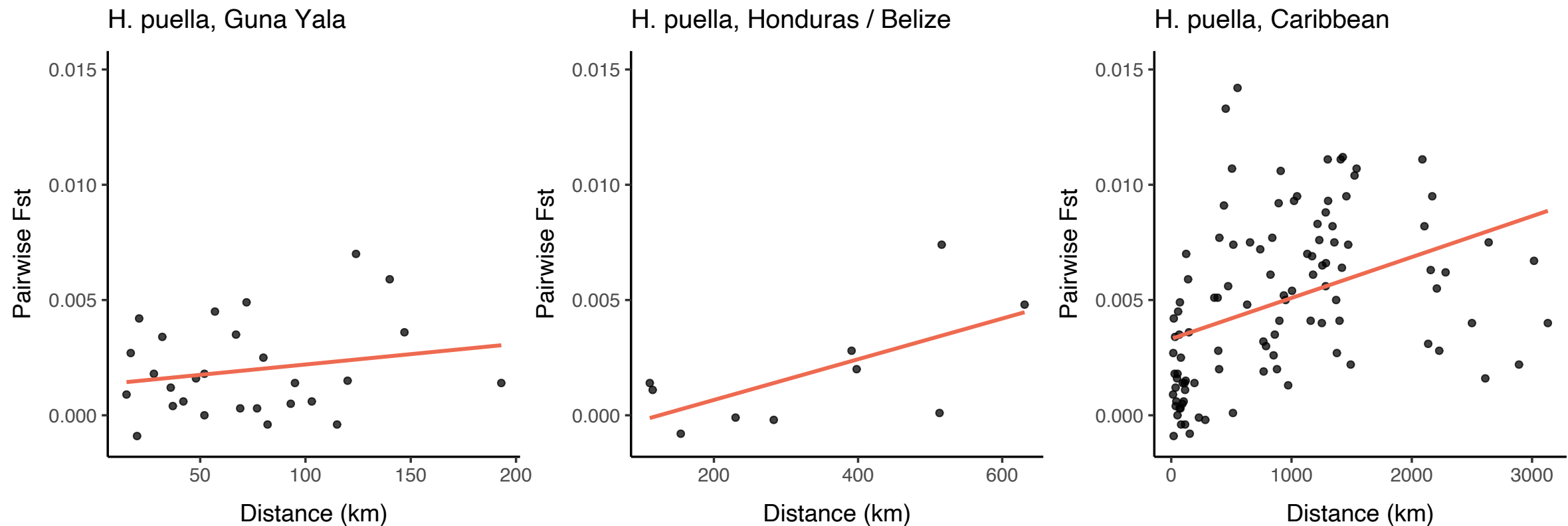
- There is evidence for isolation by distance in the dataset

- Isolation by distance is observable at medium (> 100 km) to larger scales (> 1000 km)

- We can test this with the Mantel test for similarity of two matrices

Exercises in Marine Ecological Genetics
05. Isolation by distance

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We used 10 hypervariable DNA markers to genotype 854 fish from 15 locations, and our results establish that IBD in *H. puella* emerges at a spatial scale of 175 km and is preserved up to the regional scale (3200 km). Assuming a normal or a Laplace dispersal function, our data are consistent with mean dispersal distances in *H. puella* that range between 2 and 14 km. Such small mean dispersal distances is a surprising result given the three-week pelagic larval duration of *H. puella* and the low level of genetic structure at the Caribbean scale (Wright's fixation index, F_{ST}, estimate = 0.005). Our data reinforce the

Low levels of genetic structure over large geographic areas such as the ones reported in this study do not even necessarily imply long-distance (i.e., between nonadjacent populations) dispersal; they can result from stepping-stone (i.e., between adjacent populations) migration exclusively (Rousset 2004).

— Puebla et al. 2009, *Ecology*

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05. Isolation by distance

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Course outline

May be subject to change

Class	Date	Topics	Script
01	Apr 14	Introduction, software installation	01_intro.R
02	Apr 21	Hardy-Weinberg equilibrium	02_hwe.R
03	Apr 28	Genetic drift and effective population size	03_drift.R
04	May 05	Population structure and gene flow	04_structure.R
05	May 12	Isolation by distance (lecture online, exercises in person)	05_ibd.R
–	May 19	Himmelfahrt break	–
06	May 26	Whole-genome sequencing and genome assembly	06_genseq.sh
07	Jun 02	Genotyping, SNPs and population genomics	07_snps.R
08	Jun 09	Recombination and linkage disequilibrium	08_linkage.R
–	Jun 16	Student presentations	–
09	Jun 23	Selection and mutation	09_selection.R
10	Jun 30	DNA barcoding	10_barcode.sh
11	Jul 07	Metabarcoding	11_meta.sh
–	Jul 14	To be determined	–

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Exercises in Marine Ecological Genetics

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