



# Variation of ventral color patterns and their association with life history factors in Hong Kong Newts

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## 1. Introduction

Hong Kong Newt (*Paramesotriton hongkongensis*) have unique orange ventral patterns, and it is not known whether they have any fitness implications. In breeding season, newts have been found to return to the stream where they were born to mate and lay eggs (Fu, Karraker & Dudgeon, 2013). Populations from different streams are genetically more distant (Zhang et al. 2011).

It is predicted that individuals from the same stream would have more similar patterns because they are expected to be more genetically related. The association between area of orange patterns and sex, mass, total length, snout-vent length are also explored.

## 2. Methods

- ❖ 265 Photos of Hong Kong Newts taken in October 2019 to February 2020 in 15 sites.
- ❖ Images were resized, aligned using Landmark correspondences plugin, and cropped using Fiji.
- ❖ Patterns were extracted using patRegK function of R package Patternize (Vanbelleghem et al. 2018).
- ❖ The function segments colors by unsupervised color-based image segmentation using K-means clustering, and image alignment using RNiftyReg package (Clayden et al. 2017).
- ❖ Gower's Dissimilarity was computed using gower.dist function from StatMatch (Orazio, 2017).
- ❖ Area of orange patterns in an image were calculated using patArea function in Patternize.

## 3. Results

- ❖ 261 newts' photos were used for analysis, 78 females and 184 males.

Table 1. Pearson's Correlation of 3 body measurements: TL, SVL, Mass.

| Variables                                   | Significance                  |
|---------------------------------------------|-------------------------------|
| SVL (Snout-Vent Length) & TL (Total Length) | $r(259) = 0.749, p < 0.001^*$ |
| SVL & Mass (log scale)                      | $r(259) = 0.788, p < 0.001^*$ |
| Mass (log scale) & TL                       | $r(259) = 0.669, p < 0.001^*$ |

- ❖ Therefore, choose only one of the 3 variables for ANOVA is enough.

### One-way ANOVA

Table 2. Differences of Mass and Area between streams and sex.

| Independent variable | Dependent Variables | Results                             |
|----------------------|---------------------|-------------------------------------|
| Sex                  | Mass                | $F_{(1,258)} = 17.71, p < 0.005^*$  |
| Sex                  | Area (log scale)    | $F_{(1,259)} = 3.734, p = 0.054$    |
| Streams              | Mass                | $F_{(14,245)} = 7.714, p < 0.001^*$ |
| Streams              | Area (log scale)    | $F_{(14,246)} = 9.943, p < 0.001^*$ |

- ❖ Area is different between streams but not sex.

Table 3. Differences of dissimilarity within and between streams.

| Independent variable       | Dependent variable          | Significance                         |
|----------------------------|-----------------------------|--------------------------------------|
| Streams                    | Within group dissimilarity  | $F_{(14,2209)} = 144.4, p < 0.001^*$ |
| Within group dissimilarity | Between group dissimilarity | $F_{(1,2222)} = 0.787, p = 0.375$    |

- ❖ Within group dissimilarity is different between streams, but not different from between group dissimilarity.

Table 4. Linear models for Area as response variable.

| Linear Model            | AIC           | Significant effects |
|-------------------------|---------------|---------------------|
| Mass + Sex + (1 Stream) | AIC=-1402.629 | Sex, $p < 0.05^*$   |
| Mass*Sex + (1 Stream)   | AIC=-1388.57  | NA                  |

- ❖ The model with interaction of Mass and Sex as explanatory variable, and mass and sex without interaction, and Stream as random factor are the models with lowest AIC.

## 4. Discussion

Newts from Hong Kong island and Lantau are in different clusters with some overlap, but not very different from New Territories.

Individuals from the same stream do not have more similar patterns. Dissimilarity varies between groups. Maybe some streams have newts with higher genetic relatedness?

Area also varied between groups. The variation in area might also be due to maybe genetic relatedness or other environmental factors and is yet to be explored.

## 5. Acknowledgements

I want to thank David Chan for helping with data analysis. Dr. Simon Sin, Dr. Anthony Lau, Dr. Yik Hei Sung, David Chan, Emily Poon, Hon Shing Fung, for providing the idea and data collection of this project.

## 6. References

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Figure 1. Variation of newt patterns

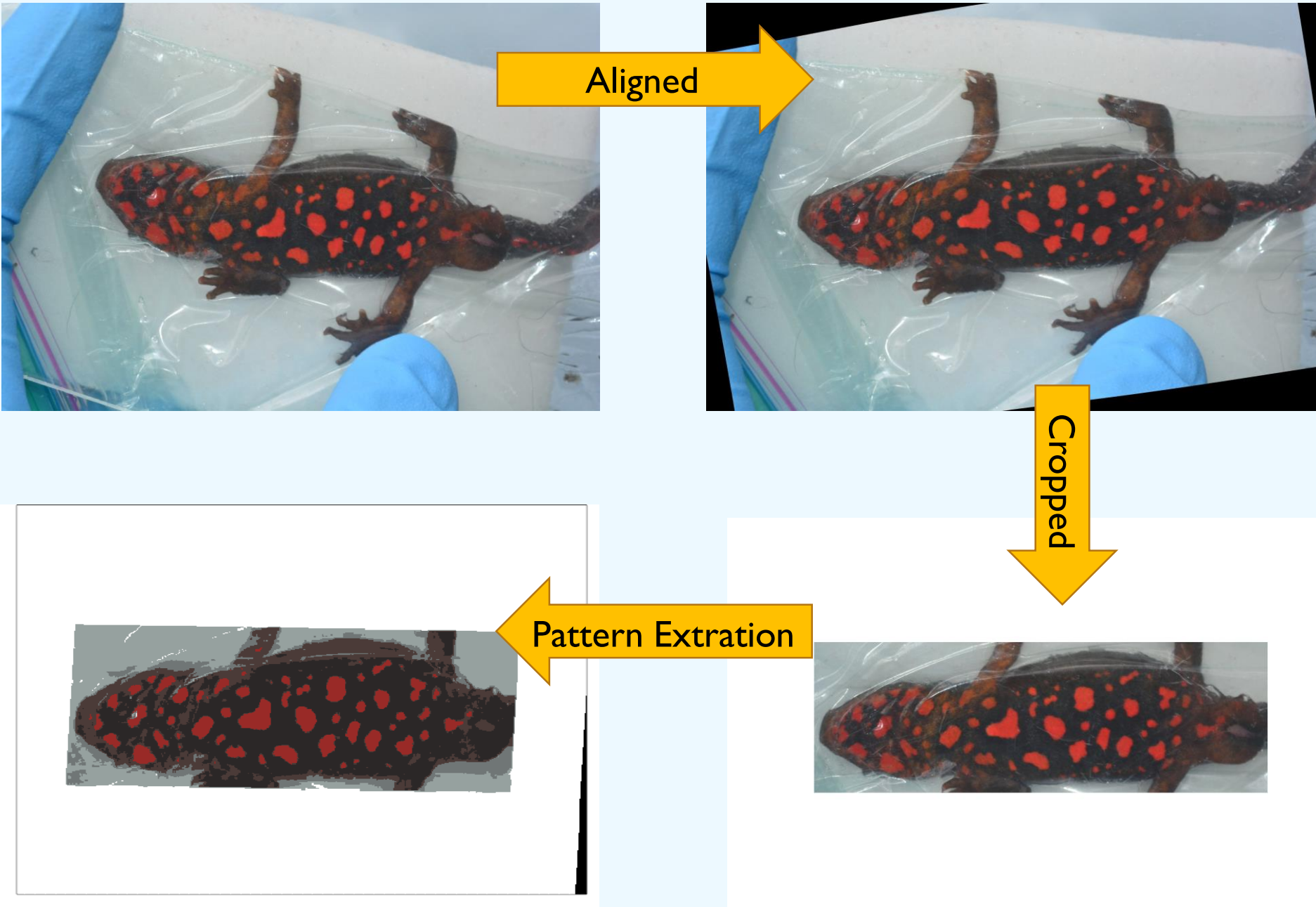


Figure 2. Process of extracting patterns for one image

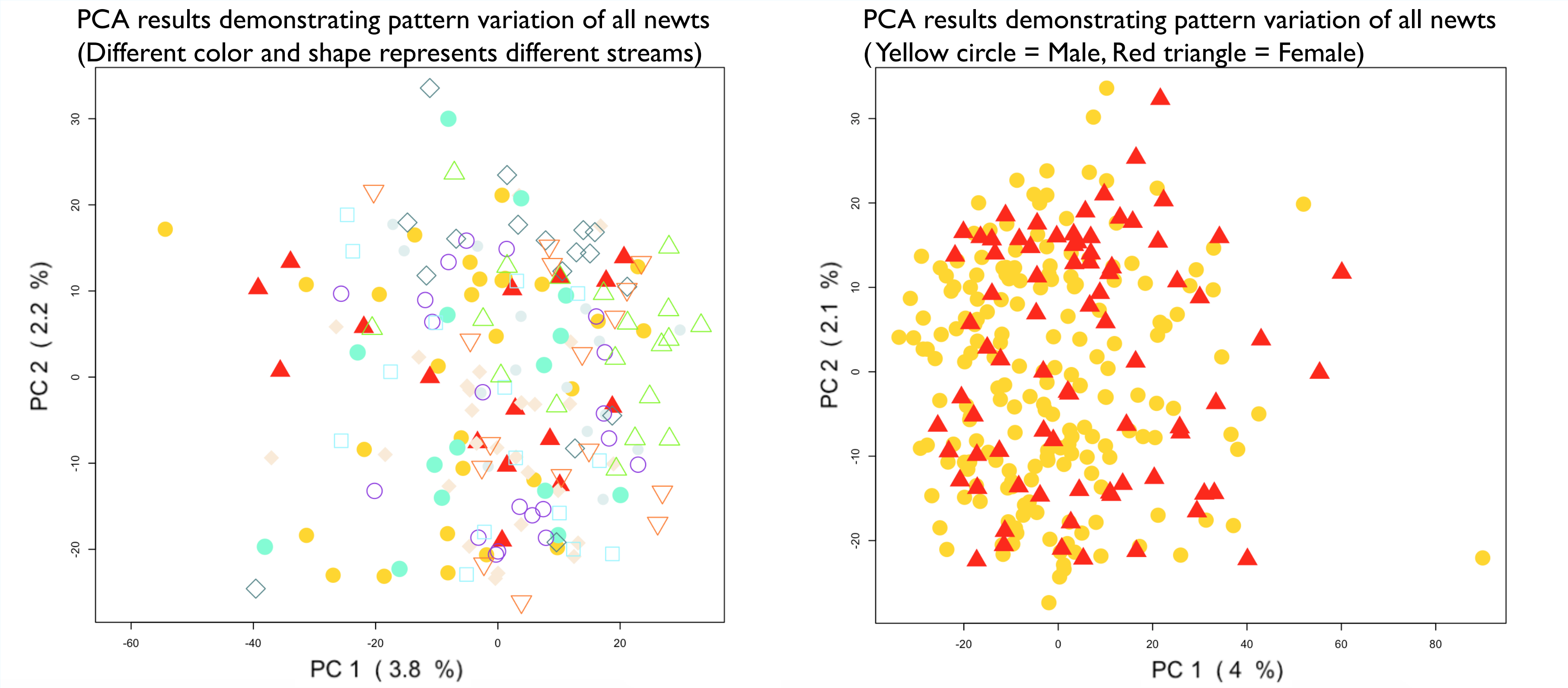


Figure 3a. PCA results for newt patterns by stream or 3b. sex

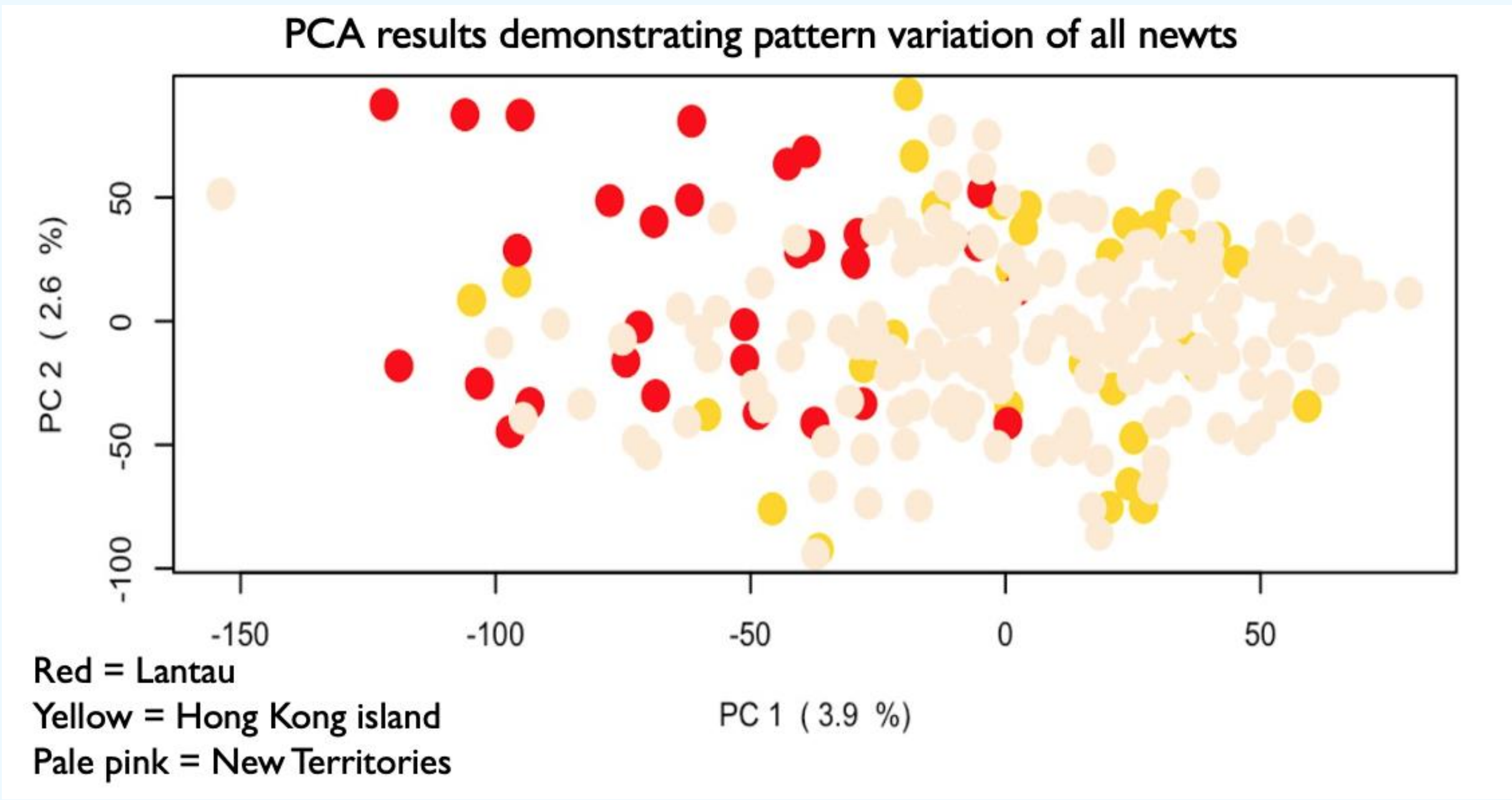


Figure 4. PCA results of newt patterns by region

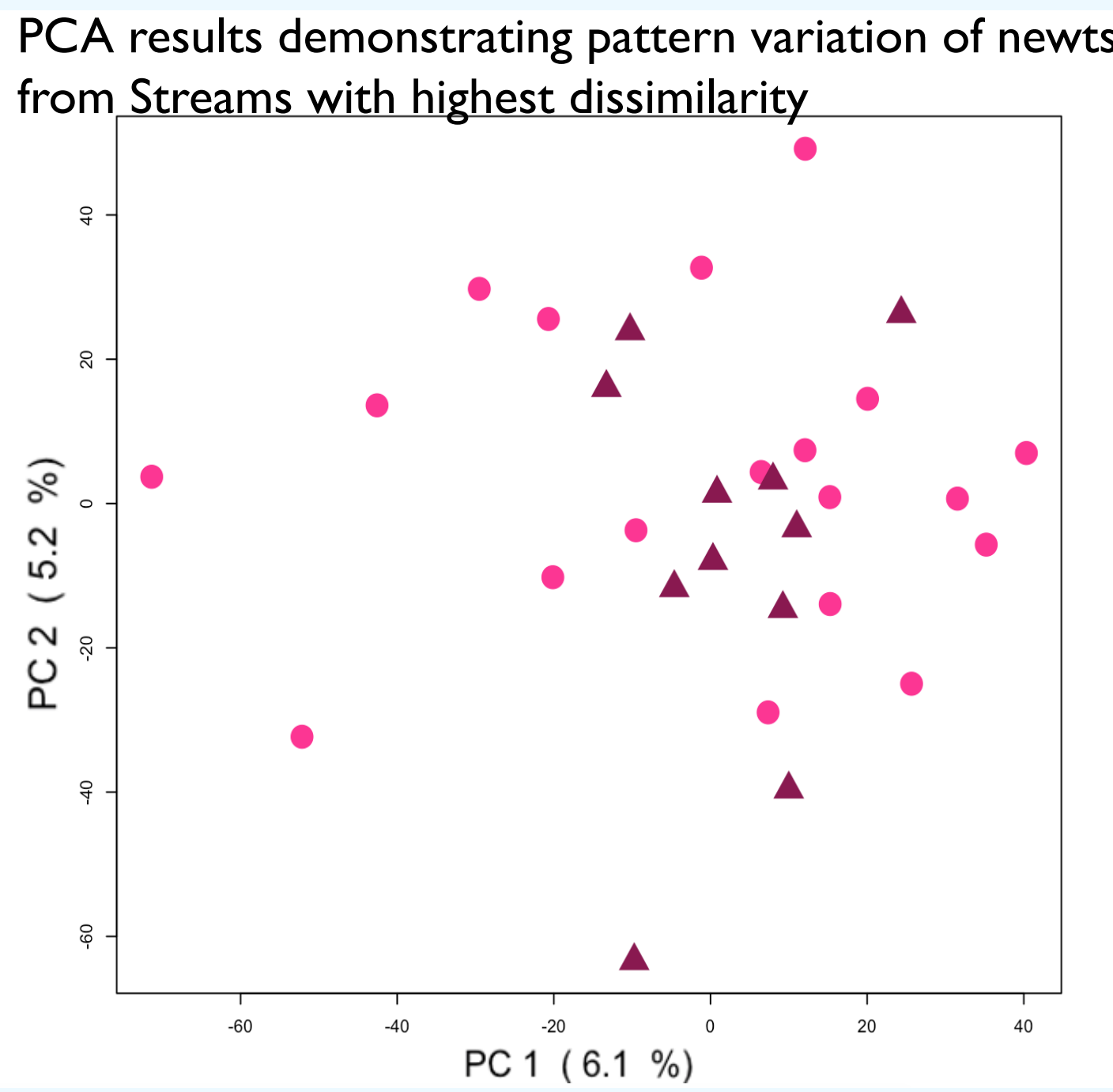


Figure 5. PCA results of SP and WLH stream newts

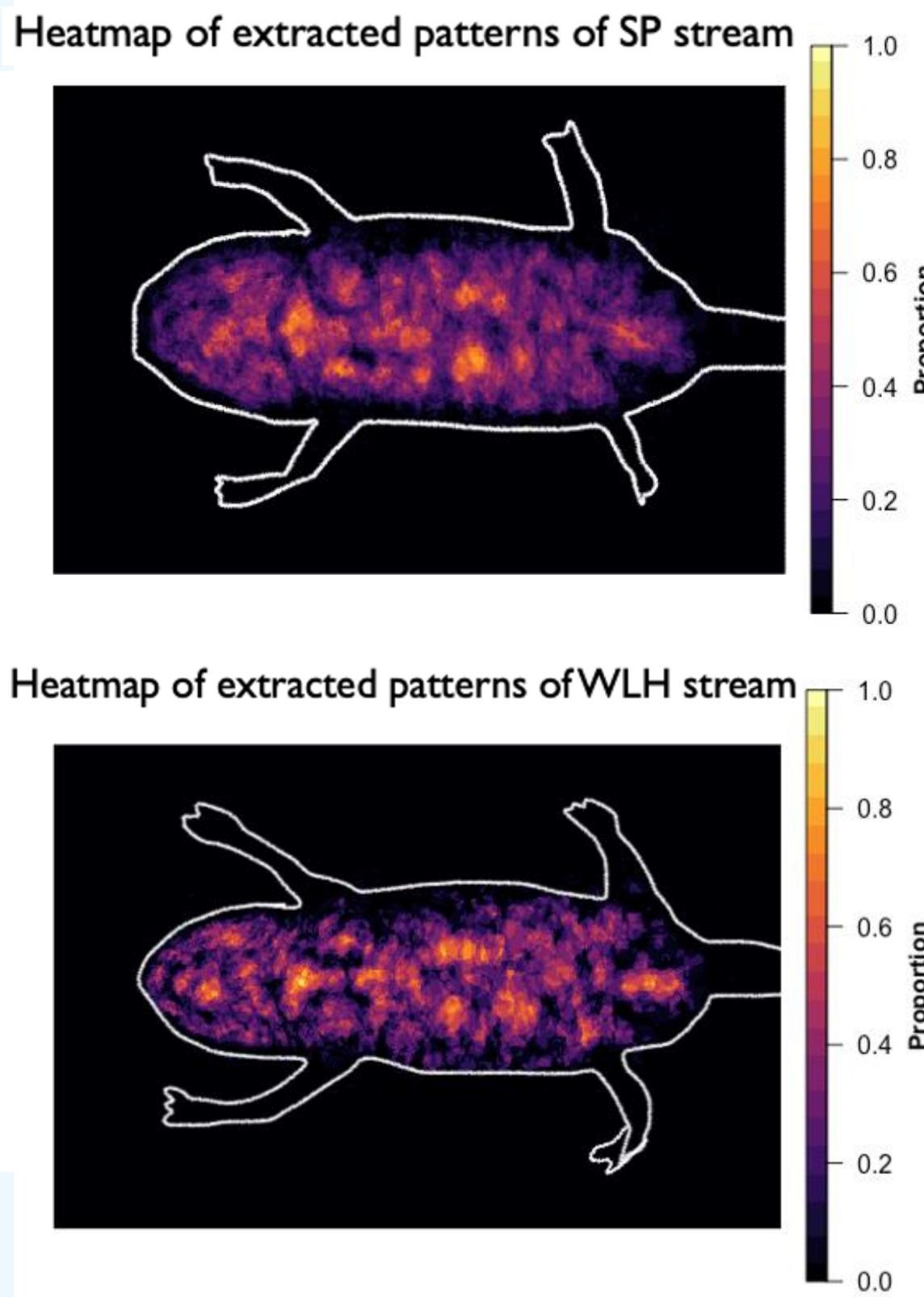


Figure 6. Heatmap of 2 streams of newts with highest mean dissimilarity