# Aggregating Chinook Stocks for Harvest Management and Improved Genetic Stock Identification

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# Why Aggregate Stocks?
## (as it relates to a mixed-stock fishery)

- Fishery Management
  - Use of CWT and Indicator Stocks
  - Simplifies analyses/models or reporting
  - Incomplete information

- Genetic Stock Identification
  - Stock $\neq$ Population
  - Lack of power to differentiate genetically distinct stocks

# Assumptions

(for applying fishery-based information from one or several stocks in an aggregate to other stocks in an aggregate)

- Other stocks in the aggregate occur in the mixed-stock fishery

- Data from known stocks in aggregate (e.g., exploitation rates) are indeed applicable to the unknown stocks in the aggregate
  = "*Gorilla Assumption*"

## So . . . given

1. There is a need to aggregate stocks
2. Management utility of the aggregations rests on assumptions that are difficult to test

## You can . . .

1. Not aggregate
2. Aggregate in such a way that provides "high confidence" that assumptions are correct
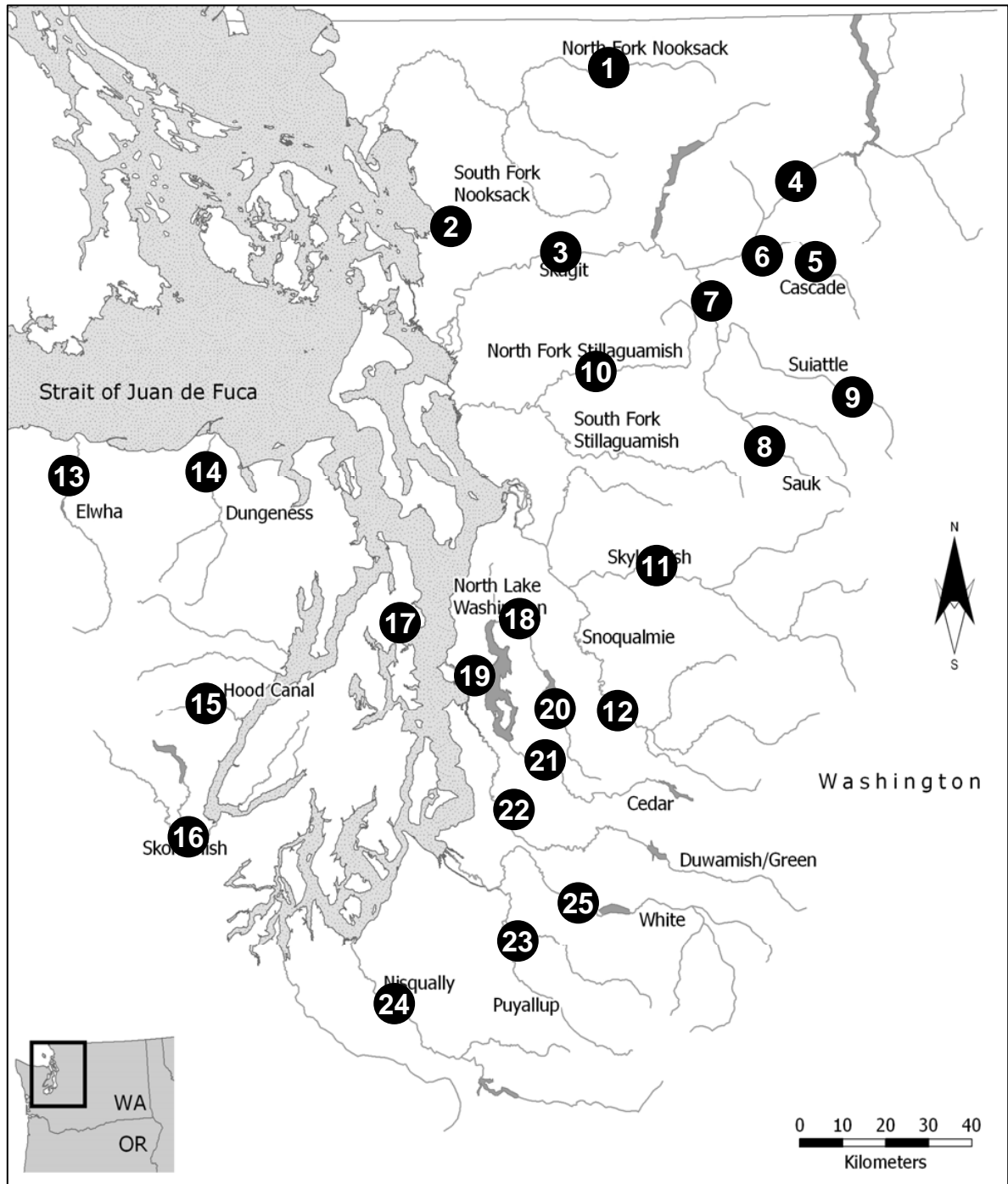
# We need to construct aggregates

1. Where the aggregates themselves are useful in fishery management

2. Where the stocks within the aggregate can be assumed to share characteristics that would result in the same or similar exploitation rates, for example

3. That can be identified genetically with minimal error

# We need to construct aggregates

1. Where the aggregates themselves are useful in fishery management

   → • Need help

2. Where the stocks within the aggregate can be assumed to share characteristics that would result in the same or similar exploitation rates

   → • Construct aggregates based on recency of common ancestry . . . that is, based on phylogeny

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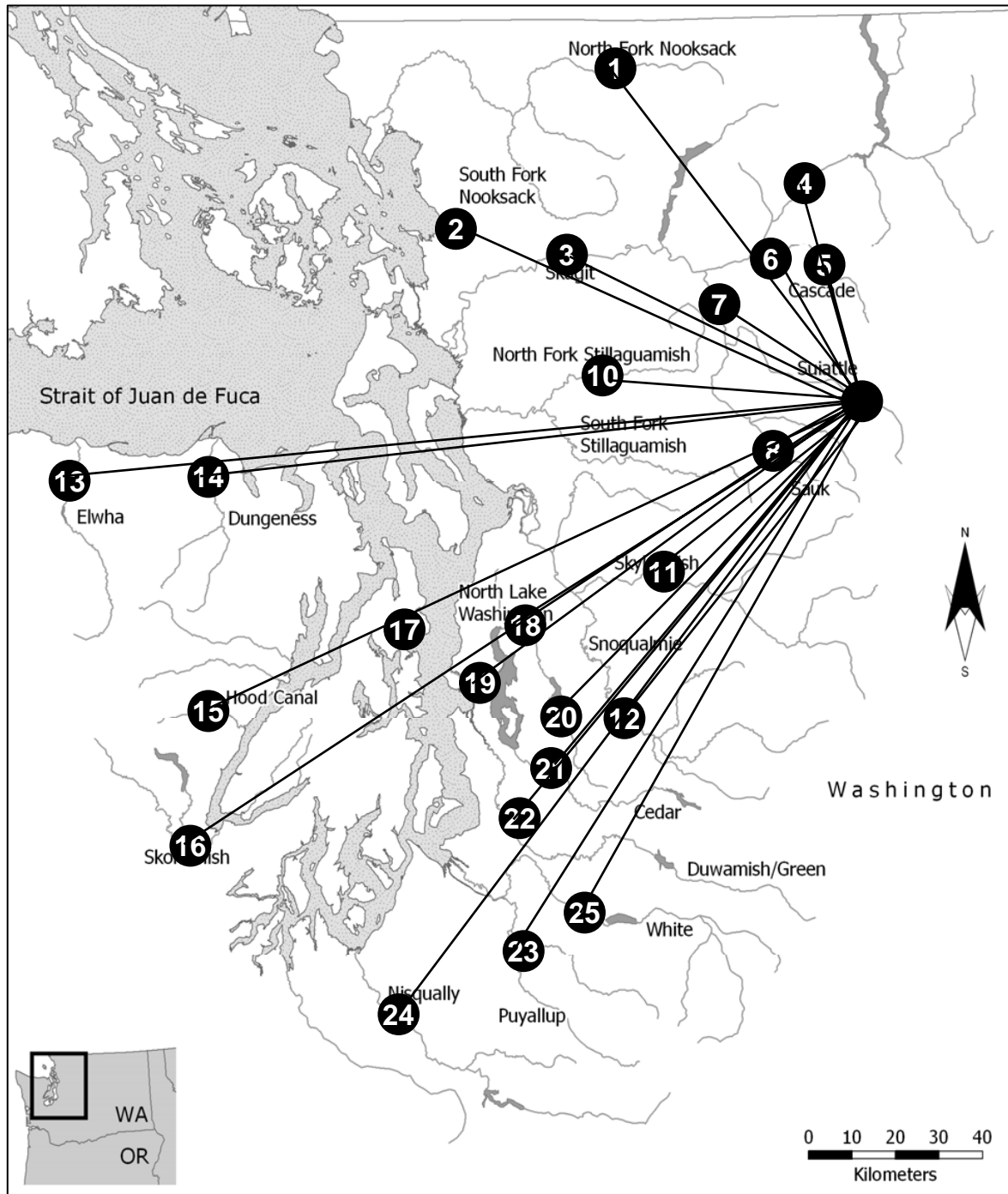   → • Construct aggregates based on genetic similarity

# Puget Sound Chinook

| | Stock Name | Timing | Origin | N | New Data[2] |
|---|---|---|---|---|---|
| 1 | North Fork Nooksack | Sp | HW | 139 | |
| 2 | Samish | F | H | 82 | |
| 3 | Lower Skagit | F | W | 108 | 1 |
| 4 | Upper Skagit[1] | Su | HW | 226 | 2 |
| 5 | Upper Cascade | Sp | W | 48 | 2 |
| 6 | Marblemount Hatchery | Sp | H | 121 | 2 |
| 7 | Lower Sauk | Su | W | 30 | |
| 8 | Upper Sauk | Sp | W | 164 | 2 |
| 9 | Suiattle | Sp | W | 152 | |
| 10 | North Fork Stillaguamish | Su | HW | 345 | |
| 11 | Skykomish | Su | HW | 309 | 2 |
| 12 | Snoqualmie | Su | W | 54 | |
| 13 | Elwha | Sp | HW | 388 | |
| 14 | Dungeness | Sp | W | 132 | |
| 15 | Hood Canal (Hamma Hamma) | F | W | 140 | |
| 16 | Skokomish | F | HW | 329 | 2 |
| 17 | Grover's Creek Hatchery | F | H | 95 | 1 |
| 18 | North Lake Washington (Bear Creek) | F | HW | 237 | 1 |
| 19 | Portage Bay (UW) Hatchery | F | H | 140 | 1 |
| 20 | Issaquah Creek | F | HW | 229 | 1 |
| 21 | Cedar River | F | HW | 221 | 1 |
| 22 | Green River (Soos Creek) Hatchery | F | H | 184 | |
| 23 | Puyallup River | F | HW | 198 | |
| 24 | Nisqually River | F | HW | 238 | 2 |
| 25 | White River (Puyallup) | Sp | HW | 242 | |

North Fork Nooksack

South Fork Nooksack

Skagit

Cascade

North Fork Stillaguamish

Suiattle

South Fork Stillaguamish

Sauk

Strait of Juan de Fuca

Elwha

Dungeness

Skykomish

North Lake Washington

Snoqualmie

Hood Canal

Cedar

Washington

Duwamish/Green

Skokomish

White

Nisqually

Puyallup

WA

OR

0 10 20 30 40
Kilometers

N

S

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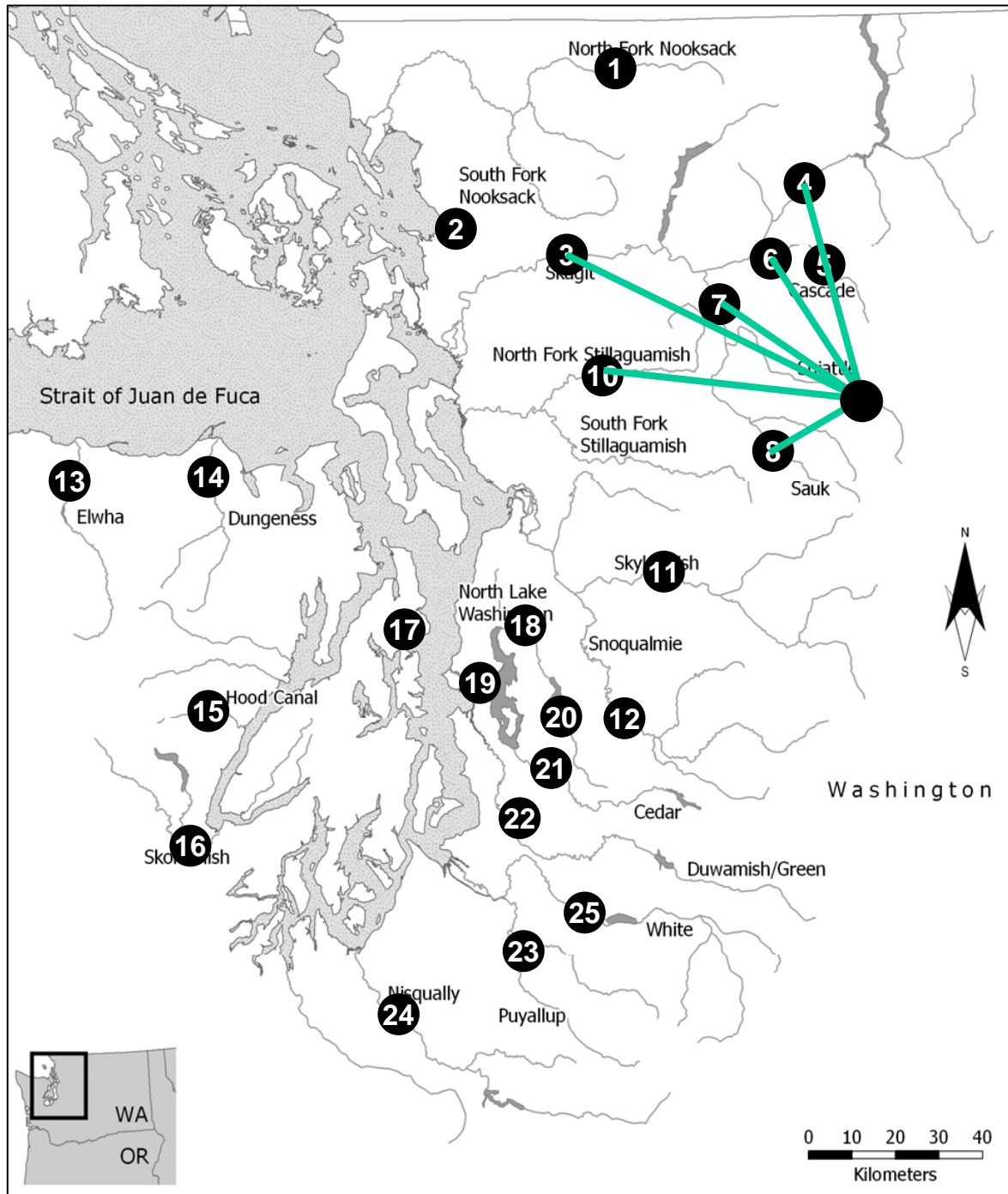   - → Construct aggregates based on genetic similarity

Suiattle; N= 152

Matrix:152 x 25
Rannala & Mountain

Means of each column

Randomized probabilities
to produce a distribution
of means for each
population

Compare actual probability
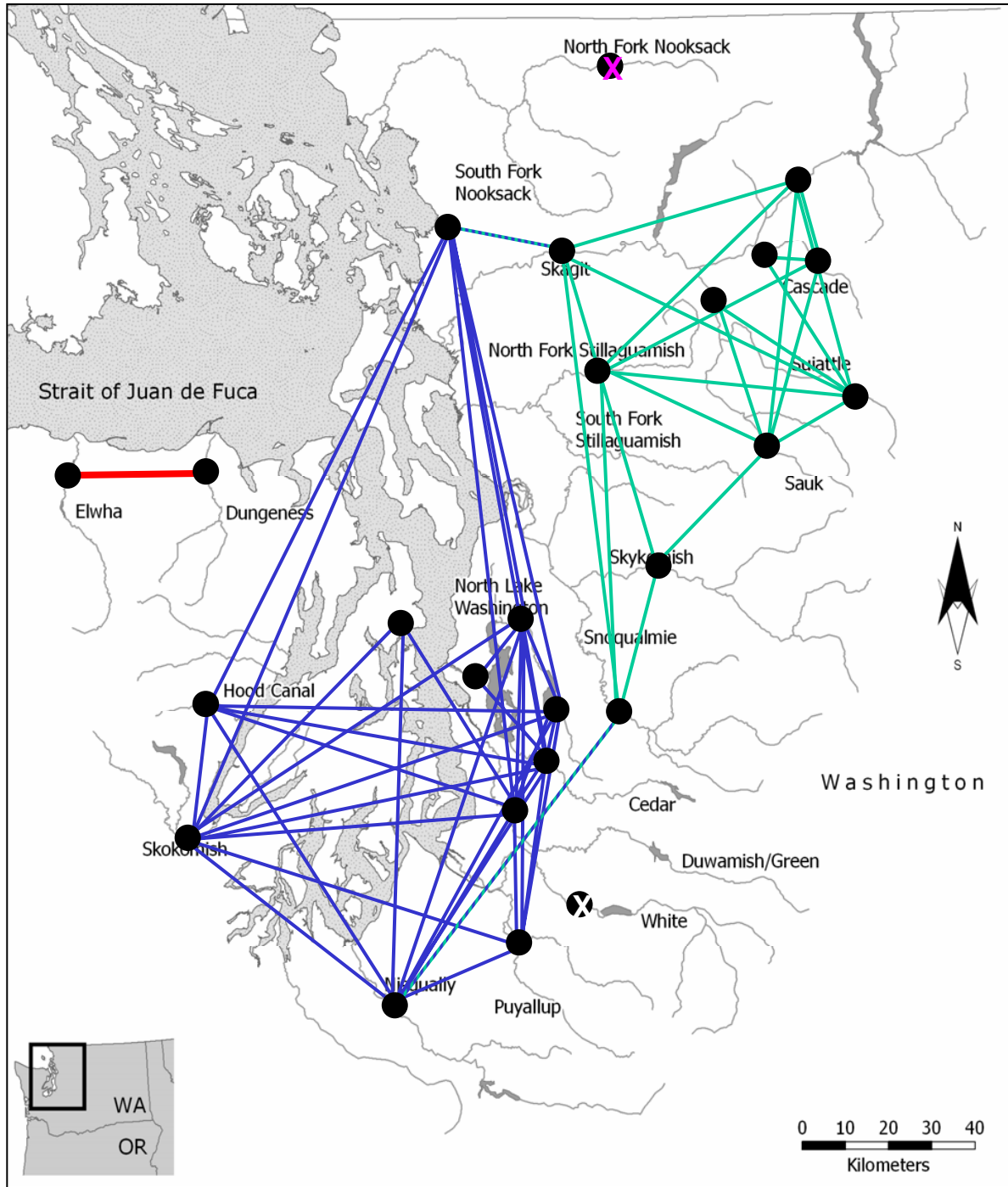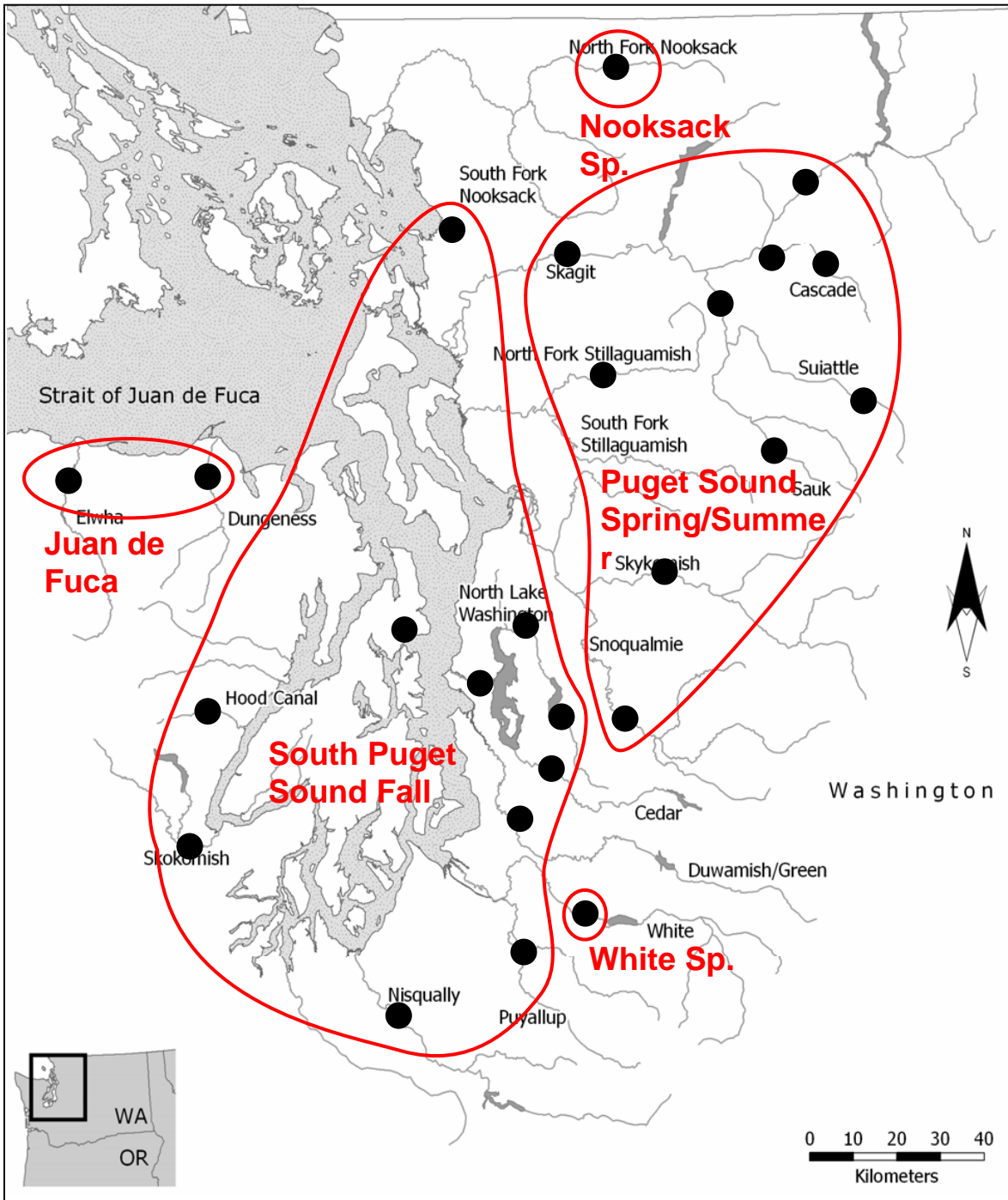to random distribution.

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Matrix:152 x 25
Rannala & Mountain

Means of each column

Randomized probabilities
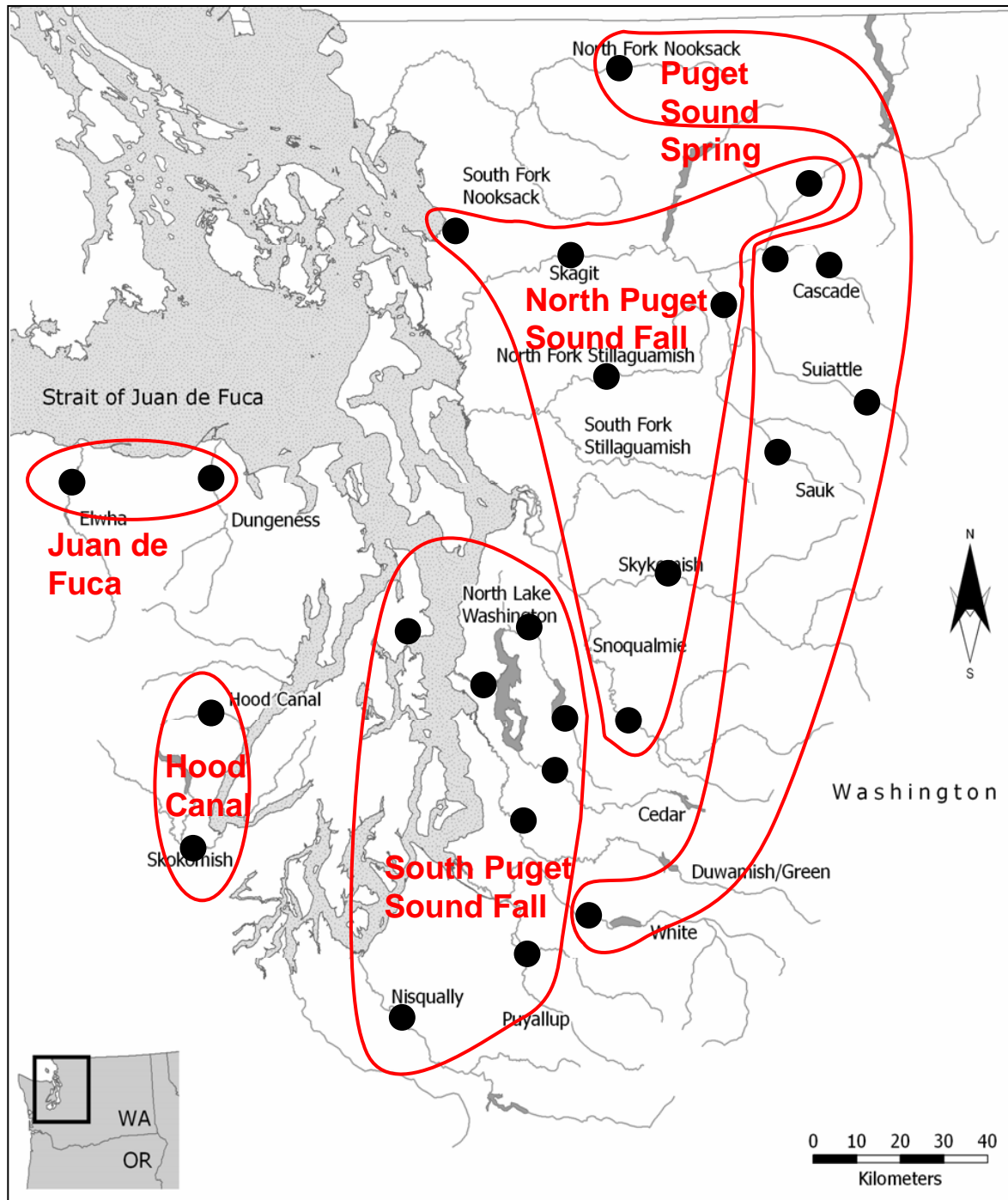to produce a distribution
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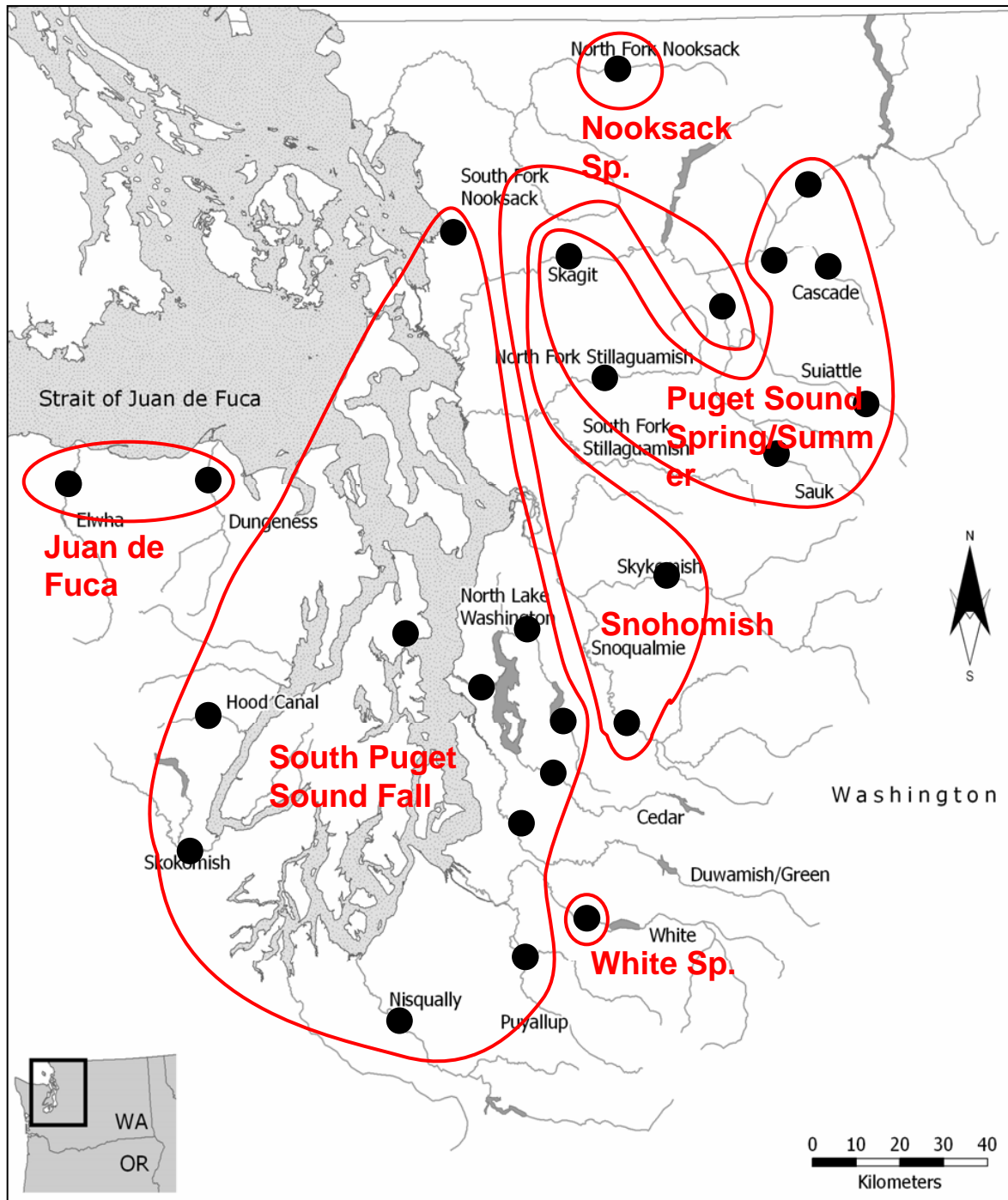
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North Fork Nooksack

South Fork
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Skagit

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Strait of Juan de Fuca

North Fork Stillaguamish

Suiattle

South Fork
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OR

0   10   20   30   40

Kilometers

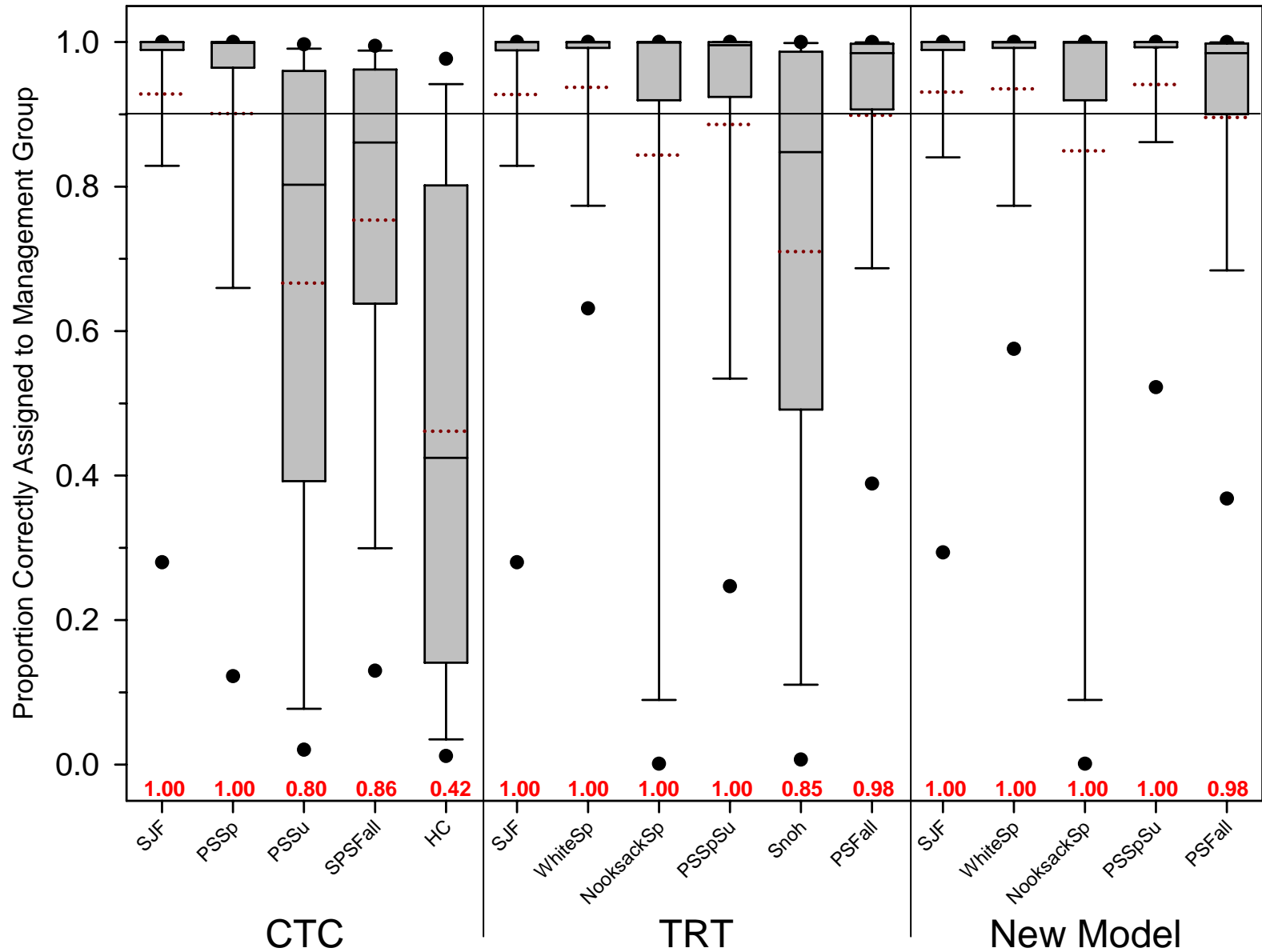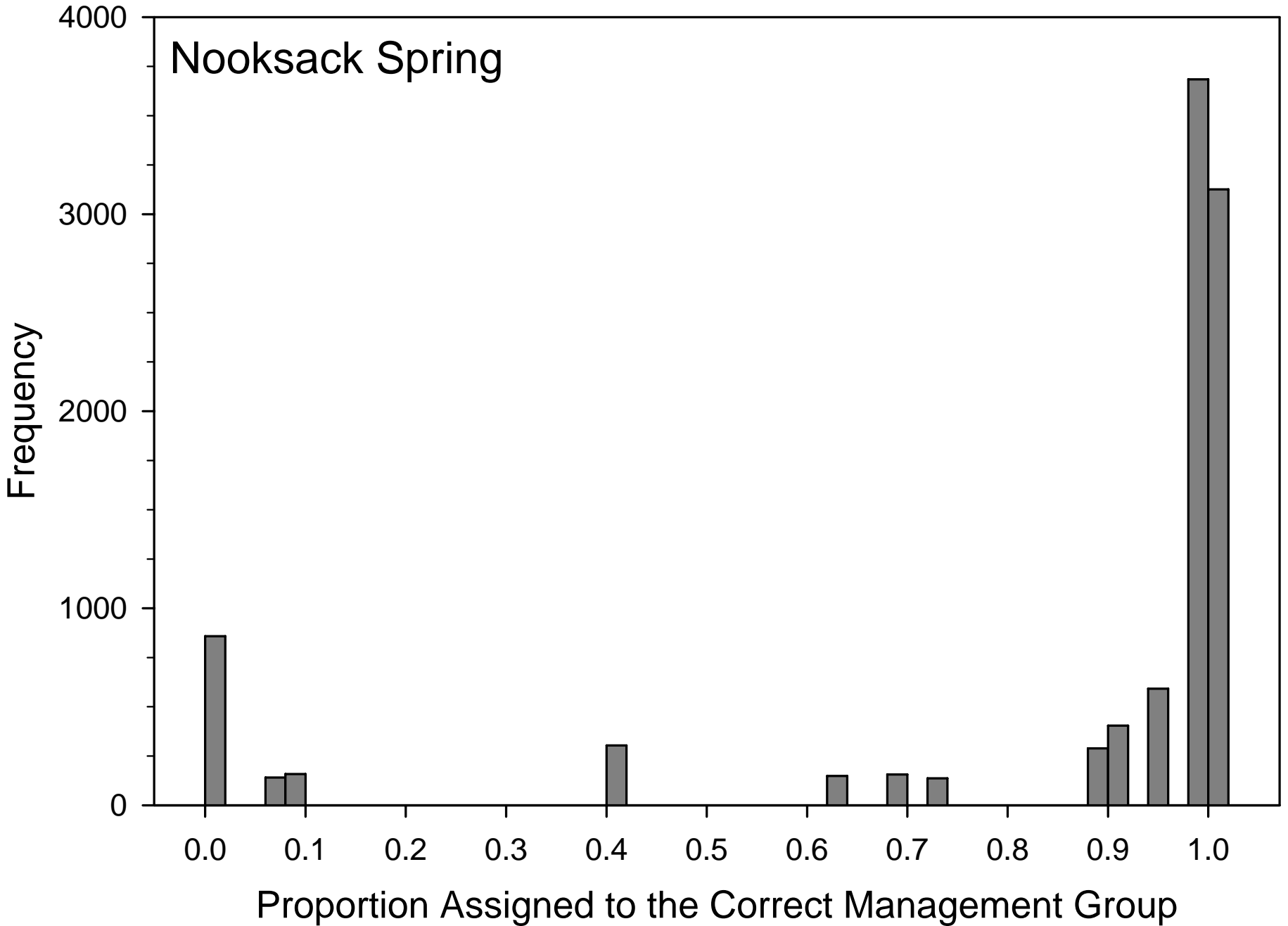# TRT

(Ruckelshaus et al., 2006)
MDS

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# 100% simulations using CV-ML method
## (Anderson, Waples, & Kalinowski, *submitted*)

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Closely related stocks with similar biology (e.g., run-timing) should have similar smolt development and outmigration timing, growth and development patterns, and ocean distributions, and should be subjected to the same or similar fishery pressures

# Neighbor-joining Tree – allele sharing matrix
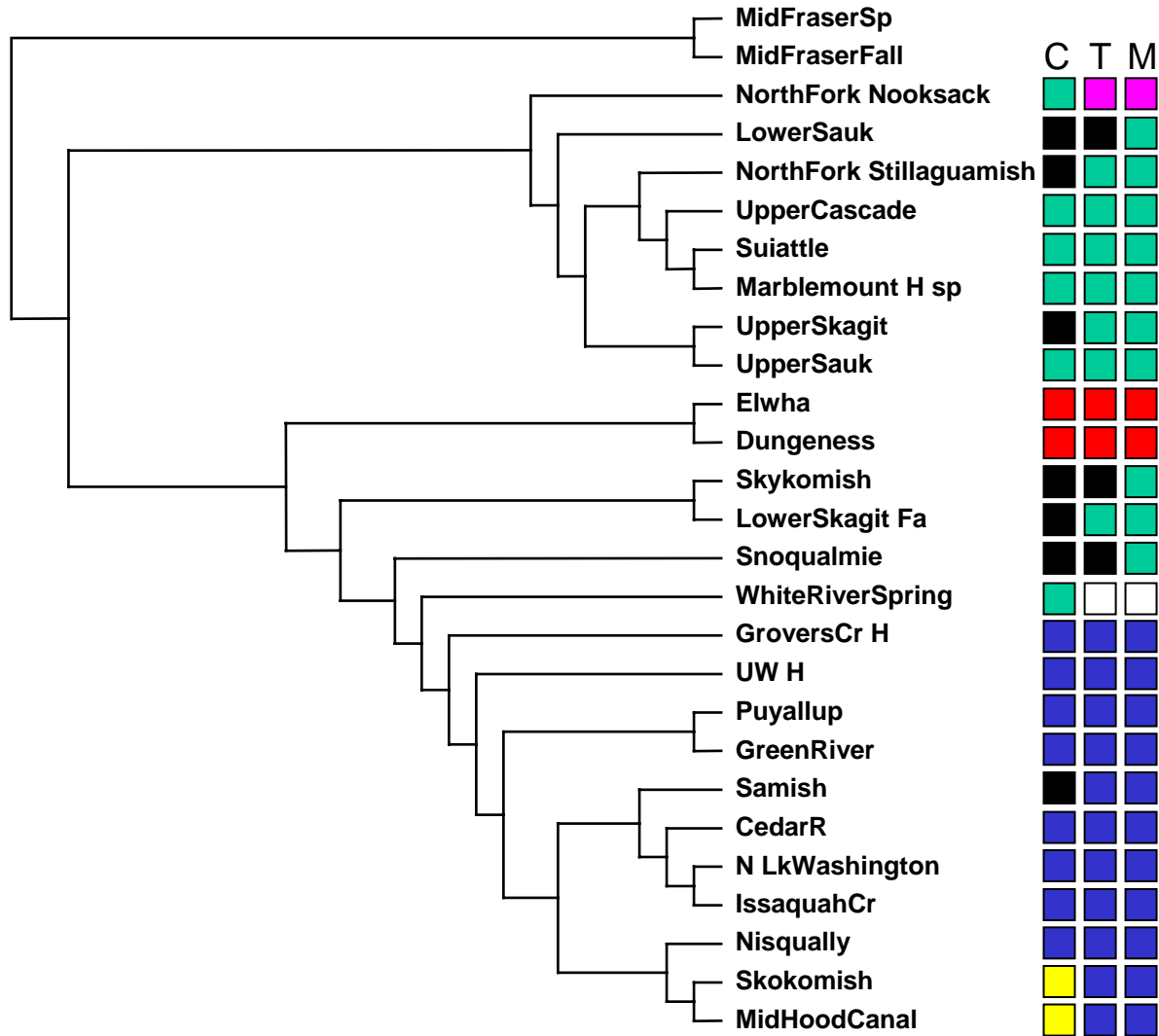
# Recommendations

Standard quantitative stock aggregations should be developed coastwide to accomplish three goals:

1. To be identified genetically with minimal error

2. To be consistent with the phylogenetic relationships of stocks

3. To maximize value to address specific fishery management needs

# Acknowledgments

- Workshop organizers, steering committee, PSC
- Stewart Grant
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- Eric Anderson (SWFSC)
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