Applying biogeochemical and genetic markers to understand movement in complex systems

Britta Denise Hardesty co-author: Chris Wilcox
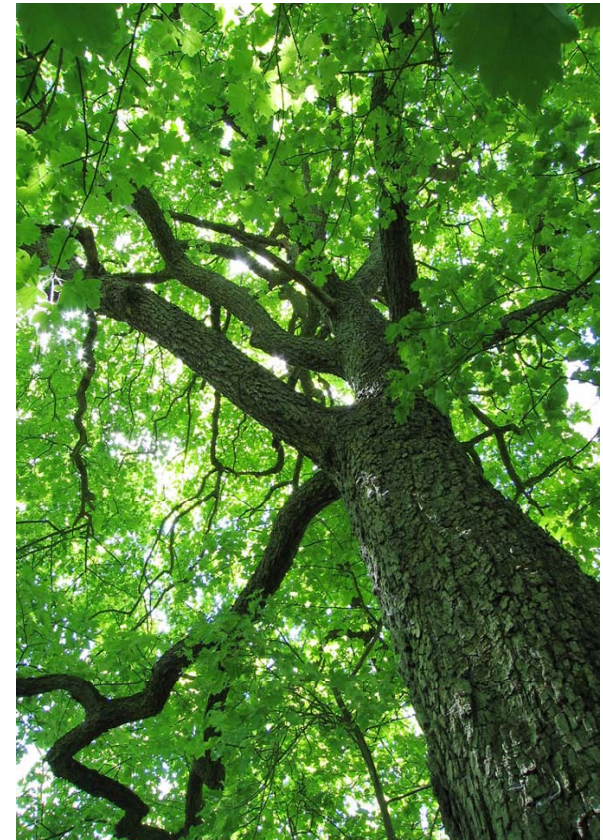
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Identifying region of origin

Ecological, evolutionary, conservation challenges

Where does [taxa x] come from?

What are movement /migratory pathways?

Where do invasives originate?

How/where to offset/mitigate?

What's the relevance?

- Understanding population/ species level consequences

- Management actions (threatened/endangered spp)

- Quantifying impact (ex. by-catch)
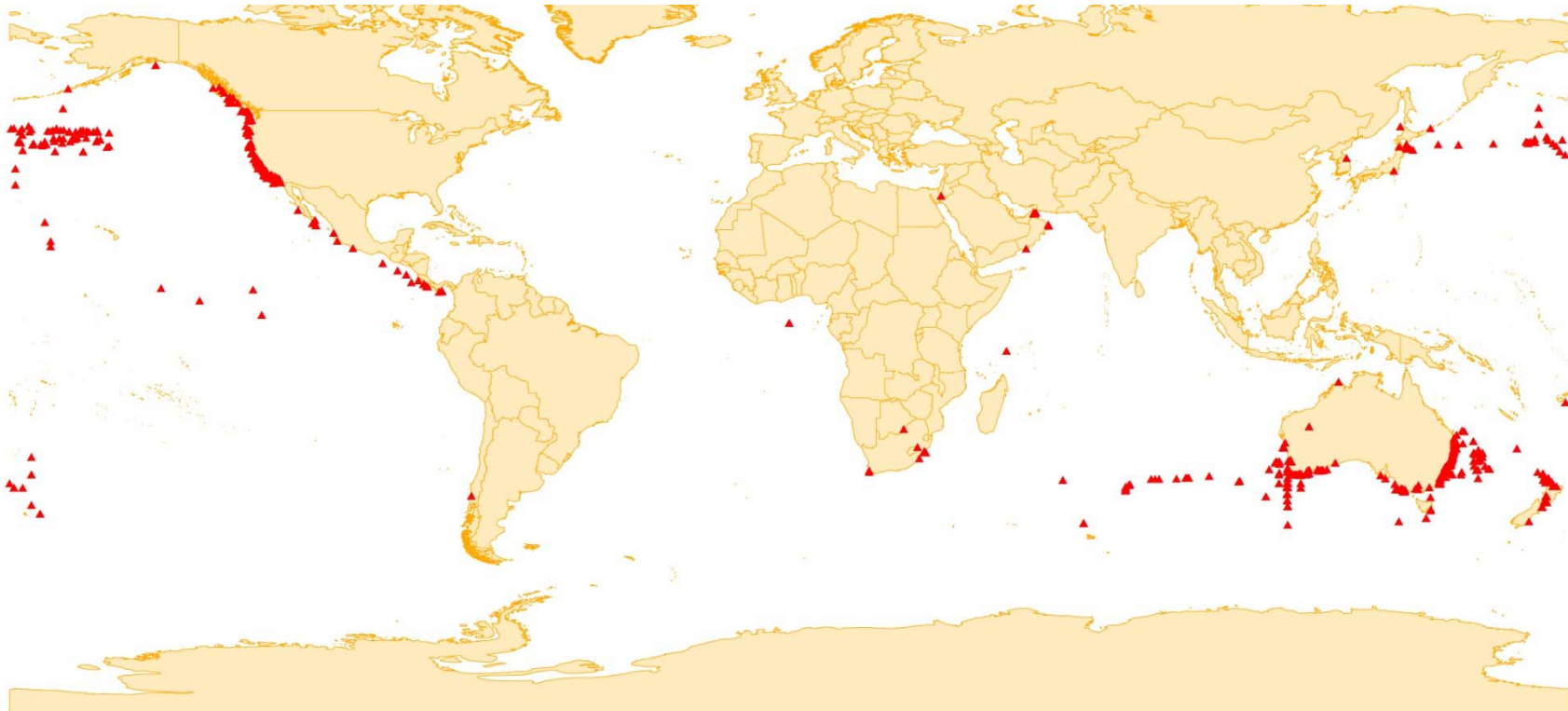
- Biosecurity issues

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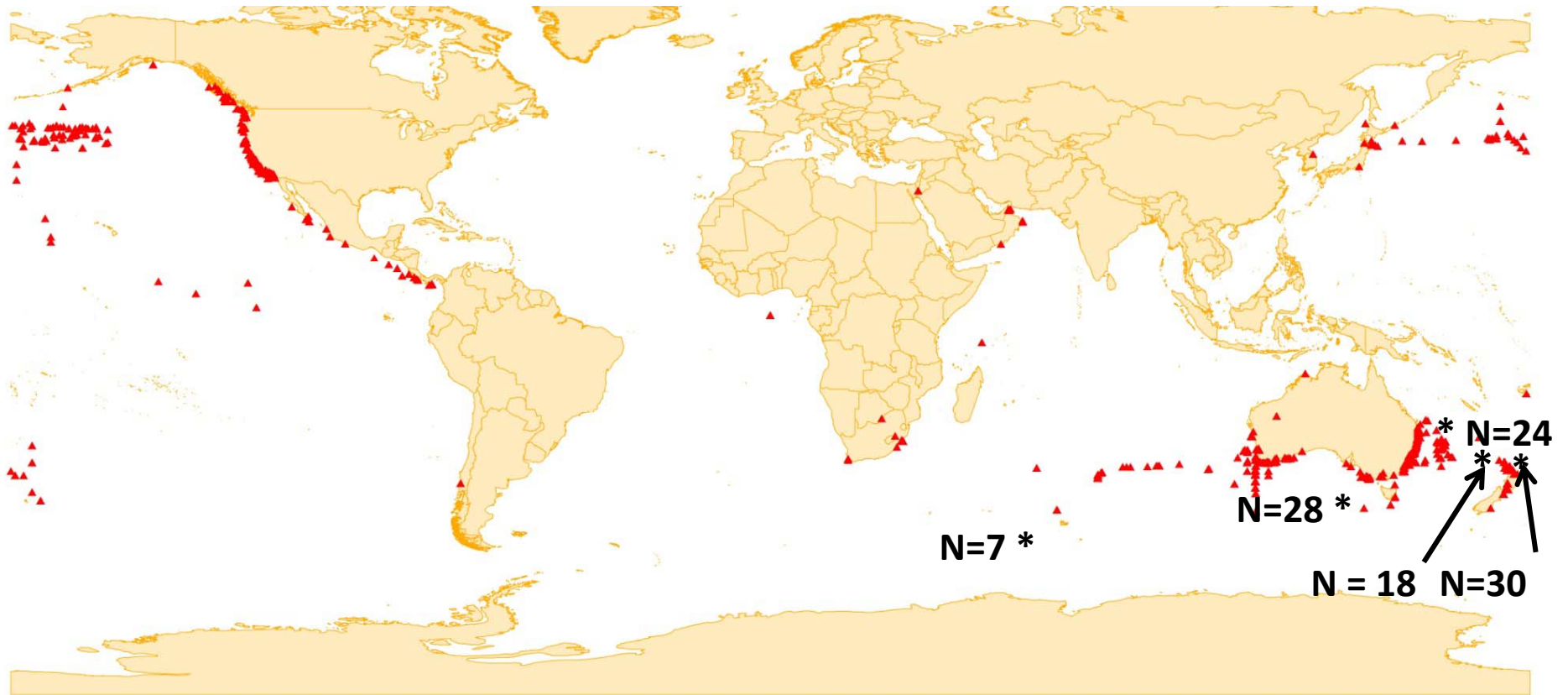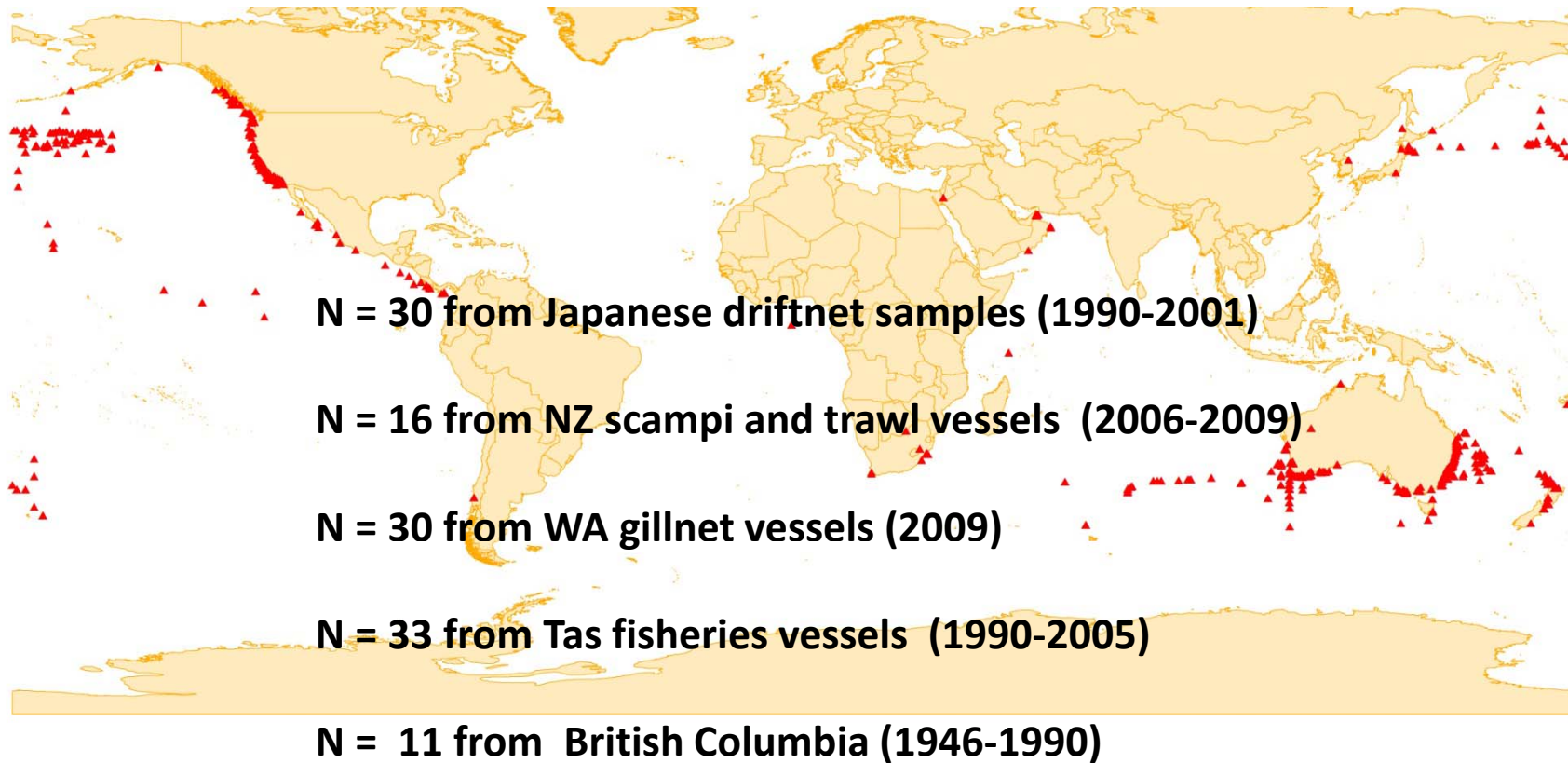# An example of our geographic assignment approach

Flesh-footed Shearwater

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Species distribution

Breeding population sampling

N=24 *

N=28 *

N=7 *

N = 18   N=30

Unknown provenance sampling

N = 30 from Japanese driftnet samples (1990-2001)

N = 16 from NZ scampi and trawl vessels (2006-2009)

N = 30 from WA gillnet vessels (2009)

N = 33 from Tas fisheries vessels (1990-2005)

N = 11 from British Columbia (1946-1990)

Markers

- 12 species-specific microsatellites (4-14 alleles)

- 18 chemical markers (isotopes/trace elements)

- Locus by locus probability distributions based on allele frequencies

- Each marker treated as independent random variable (unlinked)

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Goal – Identify geographic provenance for unknown animals

Where do by-catch birds come from?

Different data types

- Different marker types
  - Continuous data for isotopes/trace elements
    - Box-Cox transformed to normalize
    - May give some opportunities for assignment if genetic data aren't useful
  - Different range of values available for microsatellites
    - Unlinked loci
    - Each treated independently

Missing data

- Missing alleles

- Missing isotopes/element data

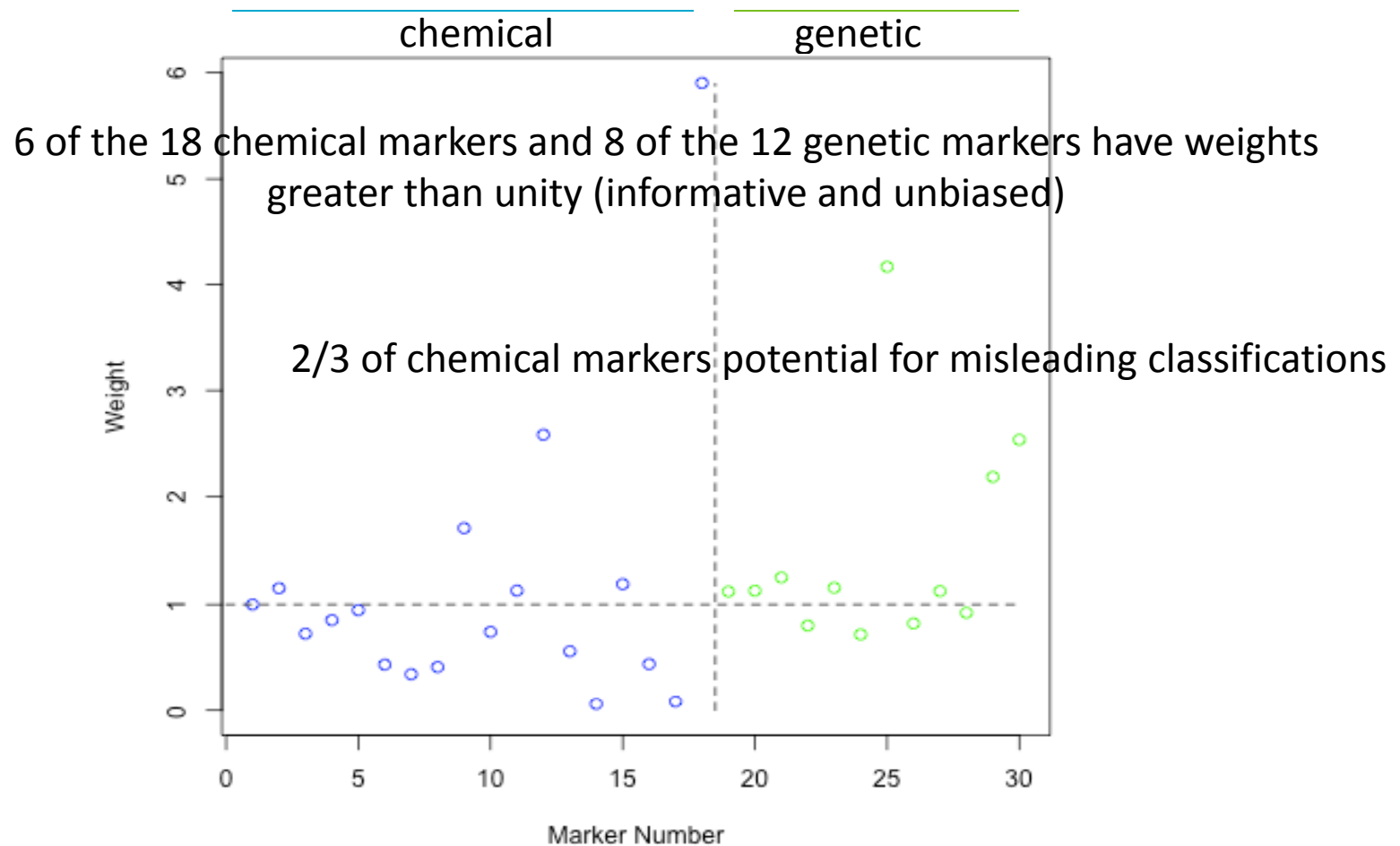- No data of one type or another for particular individuals/pops

3-step process

- Develop profiles using different markers together and use likelihood approach to assign unknown birds

- Tune model for informative markers

- Reweight informative markers for assignments and run again

Re-sampling

- Using known provenance animals

- Randomly remove 3 birds, estimated probability distribution of each marker in their absence (treating as unknowns)

- Then used distributions to assign 'unknowns' to most likely breeding site

- Then trialed 'weighting' markers based upon misclassifications from above

Relative wt by markers. First marker (Al) has a weight of 1, all others are relative to this.

6 of the 18 chemical markers and 8 of the 12 genetic markers have weights greater than unity (informative and unbiased)

2/3 of chemical markers potential for misleading classifications

Assignment findings

- Able to assign 'unknown provenance birds' with ~ 60% accuracy before weighting, even given missing data

- Average odds-ratio assignment 2.4 (best assignment on average nearly 2½ times more likely than all other possibilities together)

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Relationship between certainty of assignment and the number of available markers for assignment.
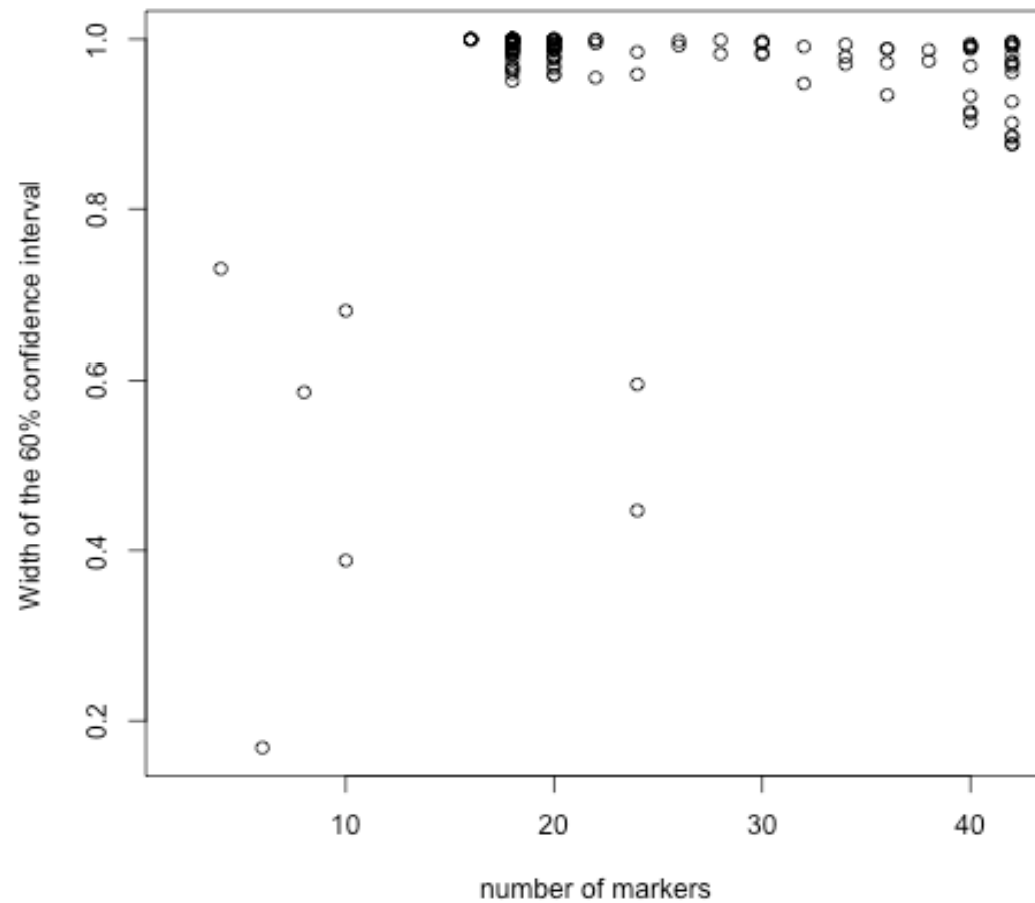
Assignment prob for unknown provenance birds, each source pop'n. Probabilities of assignment within plots are independently scaled (e.g. comparable among birds, not across plots).
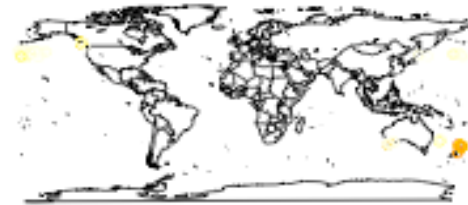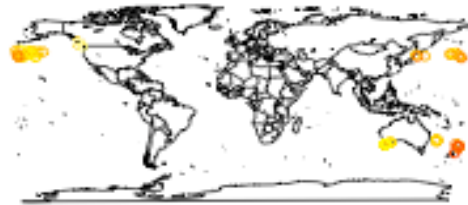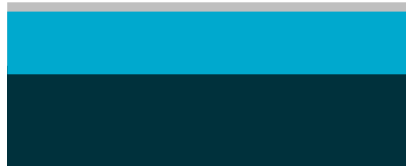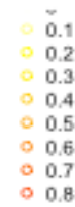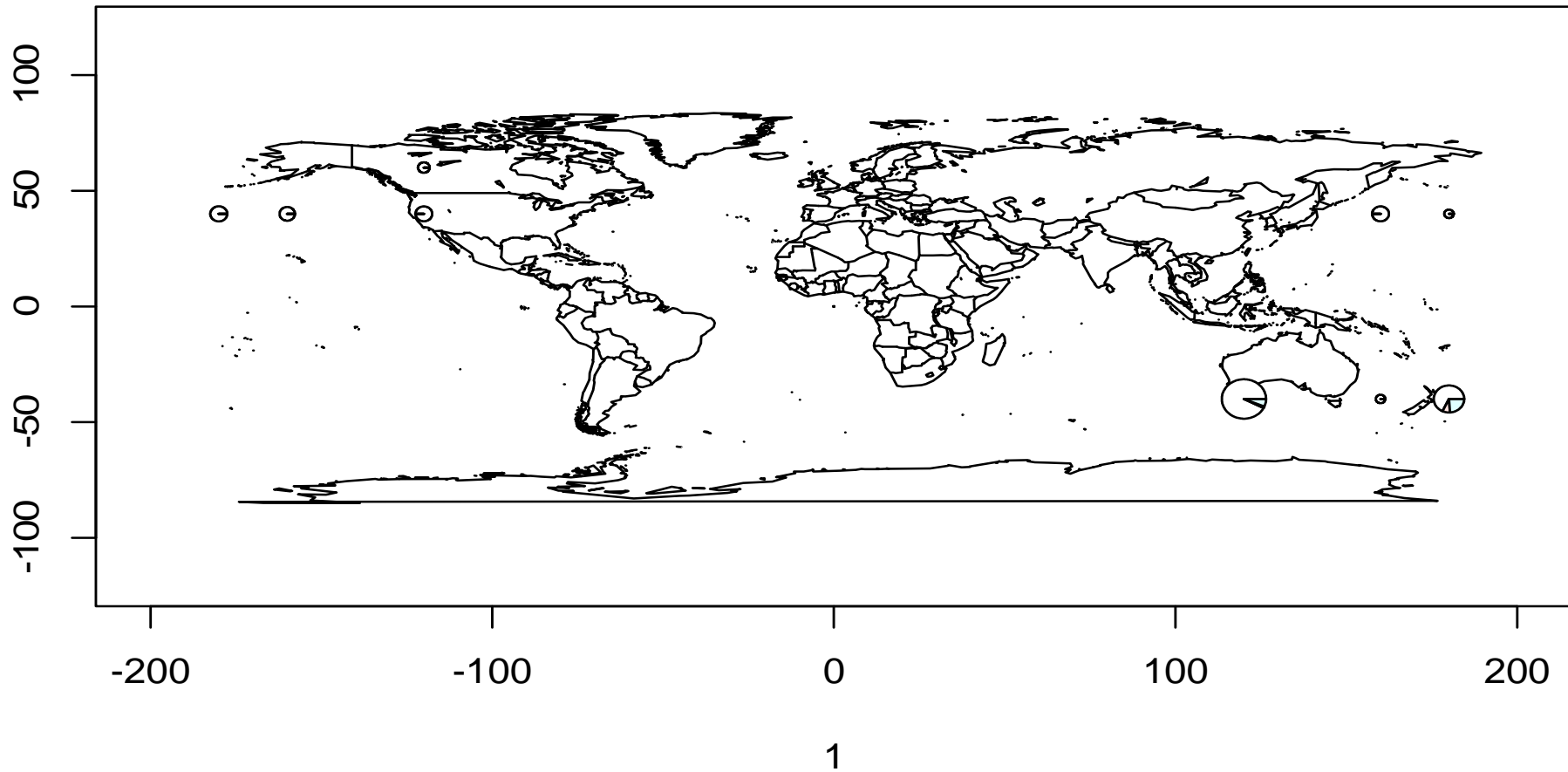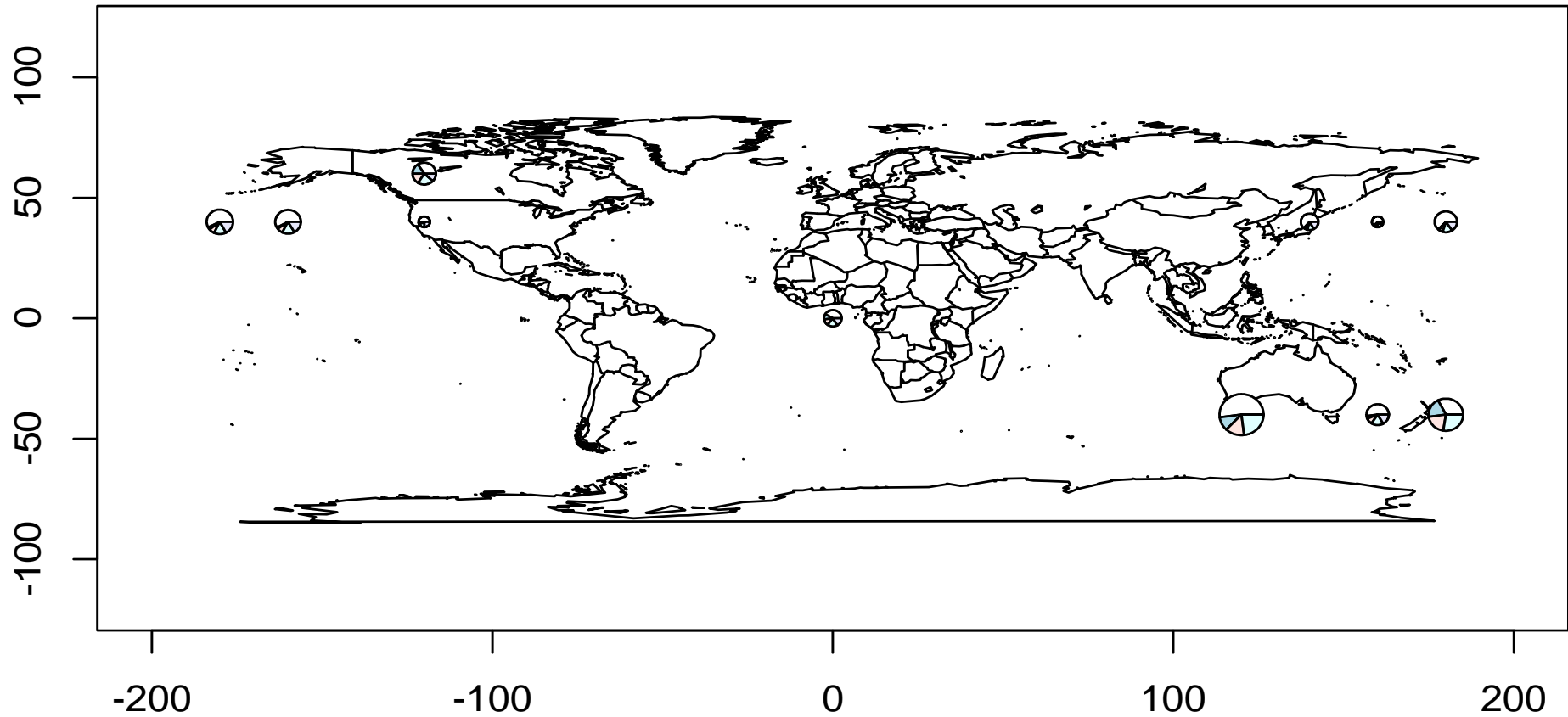
Frequencies of assignment to each possible source colony for birds reported from different areas

Mean assignment prob to each of 5 possible source populations for birds of unknown provenance recovered from a region.

Re-weighting assignments

- Improved assignments to 70%

- Birds with only genetic markers used to assign had tighter confidence intervals

- Mis-assignments were often between the two NZ pops (which may not be markedly distinct, given close geographic proximity).

Challenges

- Different timescales for samples may have different isoscapes

- Approximately 3/4 individuals had incomplete data

- Uneven sampling among sites/populations

- Unique allele at a site means bird from that provenance wouldn't be assigned there and can increase mis-assignments – could be due to low sample numbers

Summary

- In spite of challenges, useful approach
  - Using disparate data types in single assignment approach to identify geographic origin hasn't been successfully applied

- Ability to assign up to 70% of individuals to correct breeding site is pretty good, given missing data, small sample sizes etc.

- Broad applicability across systems, taxa, mobile & sessile species

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Thank you

Britta Denise Hardesty
CSIRO Ecosystem Sciences

t +61 3 6232 5276
e denise.hardesty@csiro.au

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