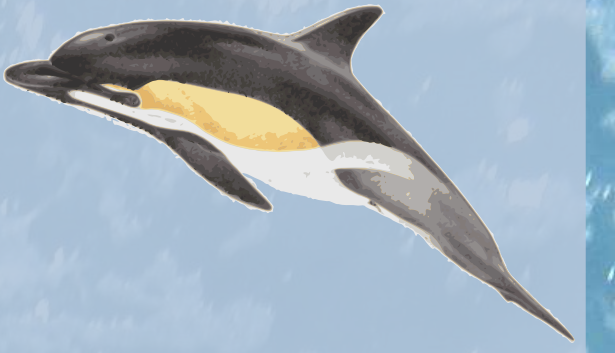




Genomic population structure of the common dolphin (*Delphinus delphis*) in the North-East Atlantic ocean



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Background

- Significant dolphin mortality events in the Bay of Biscay (BoB) since the 1990's, common dolphins (*D. delphis*) are most affected [1].
- Strandings have surged since 2016, the main cause of death being accidental capture by fishing gear [1].
- Several thousands of dolphins are affected each year; this mortality rate could threaten common dolphin populations in the North-east Atlantic Ocean [1].
- Knowledge is incomplete to understand the factors behind these accidental captures and their increase.
- Population structure provides crucial information for the determination of management units.
- Existing research did not find significant genetic population structure in the North Atlantic, using mitochondrial DNA, and nuclear microsatellite markers [2, 3].

Objective

Evaluate population structure in the North-east Atlantic Ocean, using genome-wide SNP markers.

Methods

Tissue samples:

- 46 individuals in total, 2 technical replicates
- 12 individuals from BoB oceanic zone
- 5 individuals from BoB shelf edge
- 13 individuals from BoB neritic zone
- 10 individuals from St. Pierre and Miquelon
- 8 individuals from the sister species *Stenella coeruleoalba*

Genomic analyses:

- ddRAD (HindIII, MspI), 2 × 150 bp, Illumina HiSeq MiSeq®
- Stacks ref_map.pl, *D. delphis* reference genome

Preliminary results

Based on 1000 randomly selected SNPs

Applied filters	Number of loci (variant sites) retained after filtering
Demultiplexed raw data	1 355 659
Missing data across all samples ≤ 80%, Missing data within populations ≤ 80%, MAF ≥ 5%, 1 random SNP / locus	96 994 (41 167)
1000 random loci	1000 (1000)

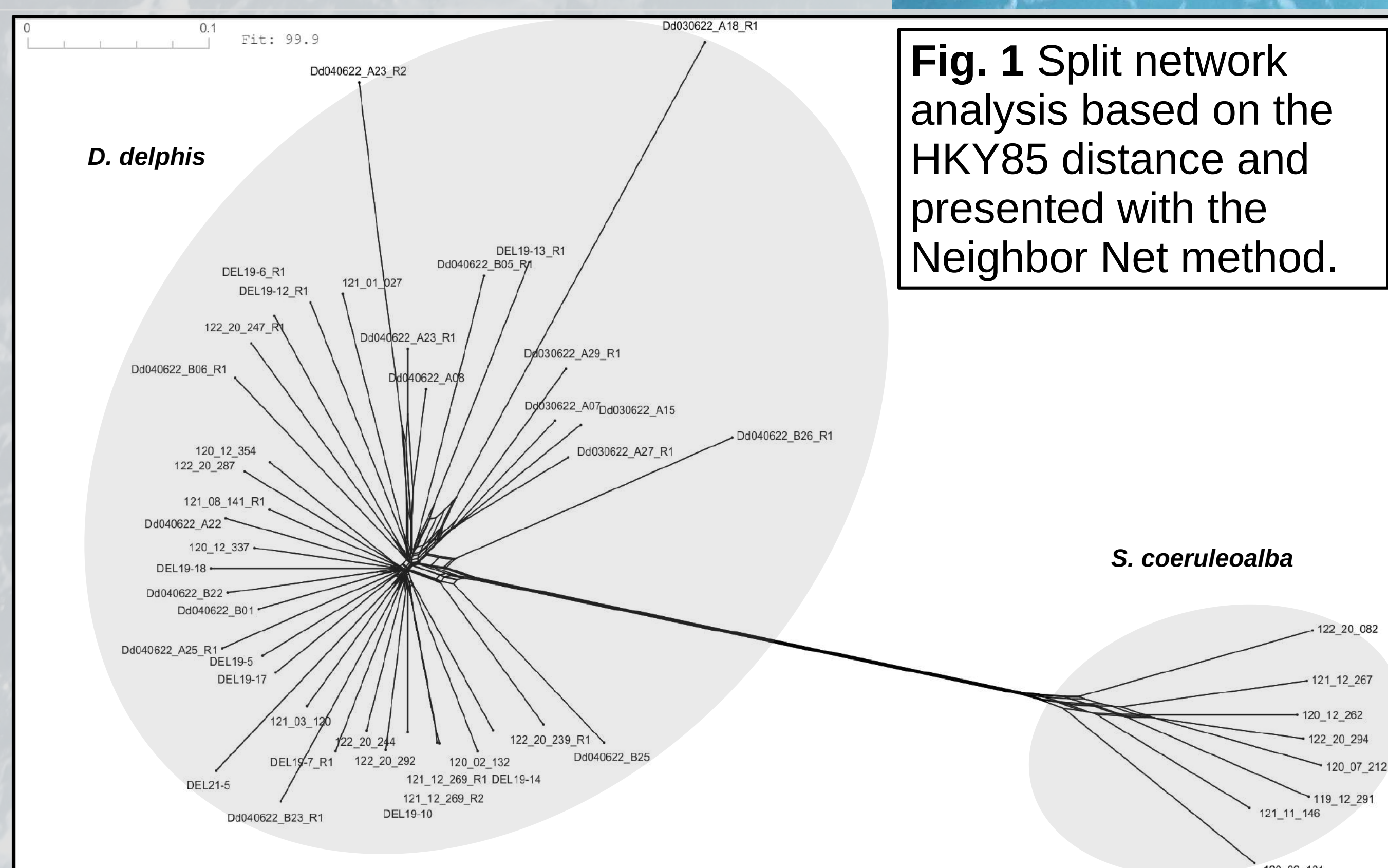


Fig. 1 Split network analysis based on the HKY85 distance and presented with the Neighbor Net method.

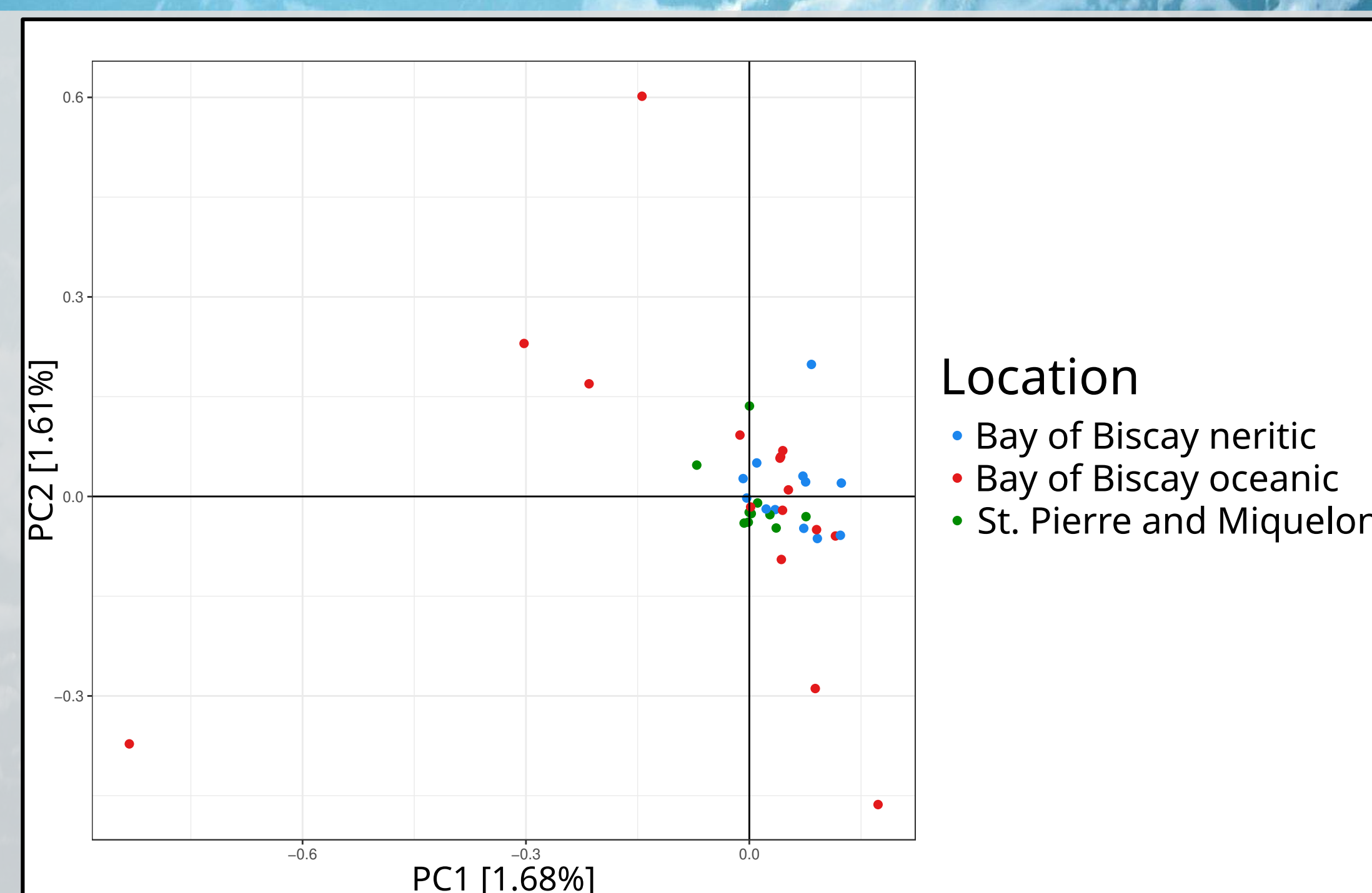


Fig. 2 Principal Component Analysis, excluding *S. coeruleoalba* individuals, and grouping BoB shelf edge individuals into the BoB oceanic group.



Fig. 3 F_{st} and Φ_{st} distance matrix, visualised in a heatmap. F_{st} values are presented in the lower, Φ_{st} values in the upper triangle.

Conclusions and perspectives

- Clear distinction between *D. delphis* and *S. coeruleoalba* based on genomic SNP markers.
- No population structure in *D. delphis* in the North Atlantic Ocean.
- No significant Isolation by Distance (data not shown).

Extending study by:

- Including more sites, more individuals
- Investigating sex-biased dispersal

References

[1] ICES, 2020. ICES Scientific Reports 2, 354.; [2] Luca et al., 2009. Mar Biol 156, 821–834.; [3] Ball et al., 2017. Behav Ecol Sociobiol 71, 123.

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