Nonrandom Patterns of Introgressed Regions

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2023-10-25

R Markdown

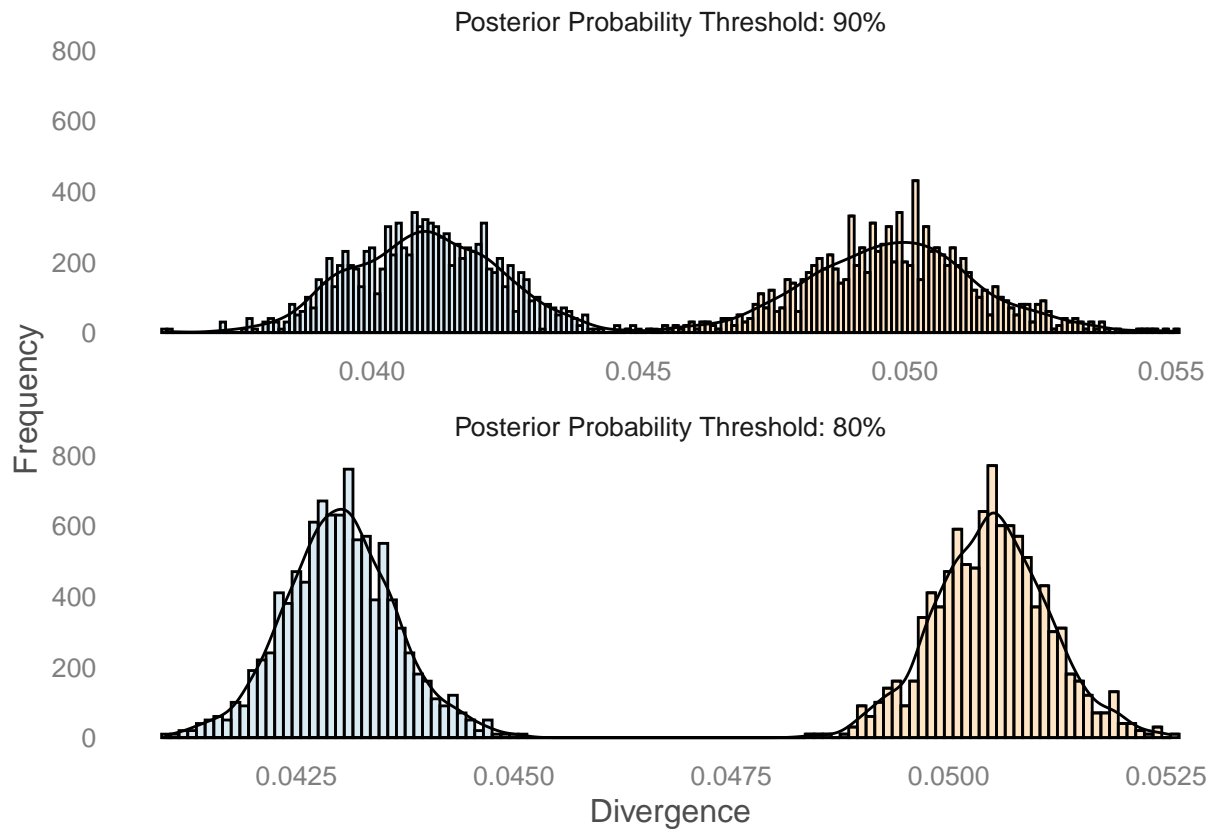### Divergence (dXY) of Introgressed Regions vs. Genome-Wide Background

Figure 1: Figure 1. Distribution of mean absolute nucleotide divergence for introgression tracts and species tree tracts by PhyloNet-HMM posterior probability threshold (90%, 80%)

Shaprio-Wilk tests and QQ Plots

Introgression Tracts: 90% posterior probability threshold

```
## Shapiro-Wilk test p-value =  0.519
```
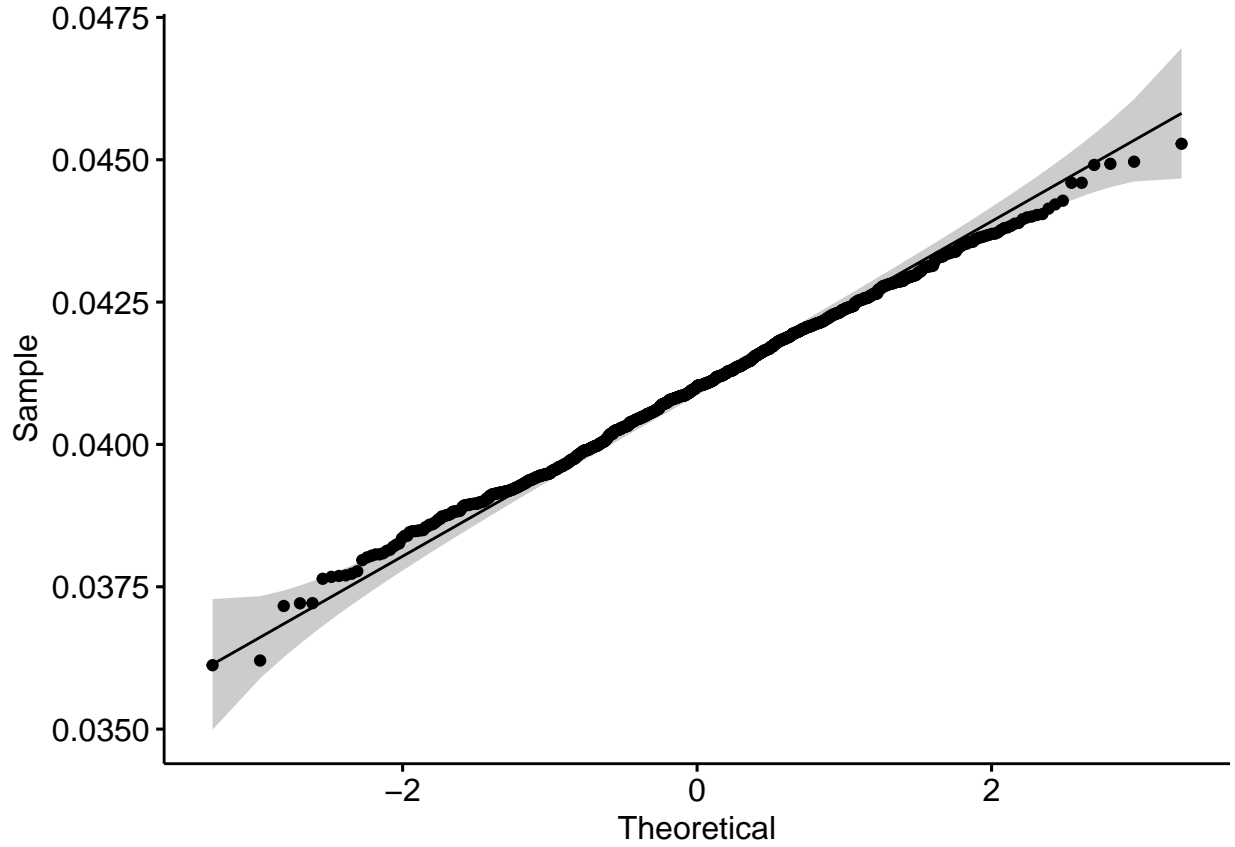
Figure 2: Figure 2. qqplot for mean dXY distribution for introgression tracts at the 90% threshold

Species Tree Tracts: 90% posterior probability threshold

```
## Shapiro-Wilk test p-value =  0.304
```

Introgression Tracts: 80% posterior probability threshold

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## Shapiro-Wilk test p-value =  0.274
```

Species Tree Tracts: 80% posterior probability threshold

```
## Shapiro-Wilk test p-value =  0.58
```

Homogeneity of variances

Tract Type	Posterior Probability	Standard Deviation	Variance
Introgression	90%	0.00138137	0.00000191
Species Tree	90%	0.00160160	0.00000257

Tract Type	Posterior Probability	Standard Deviation	Variance
Introgression	80%	0.00064030	0.00000041
Species Tree	80%	0.00065455	0.00000043

F-test to assess homogeneity of variances between Introgression Tract and Species Tree Tract

Posterior Probability	Variance Ratio	p	Confidence Interval
90%	0.744	0.000	[0.657, 0.842]
80%	0.957	0.487	[0.845, 1.083]
log(90%)	1.101	0.129	[0.972, 1.246]
log(80%)	1.319	0.000	[1.165, 1.493]

Welch Two Sample t-test

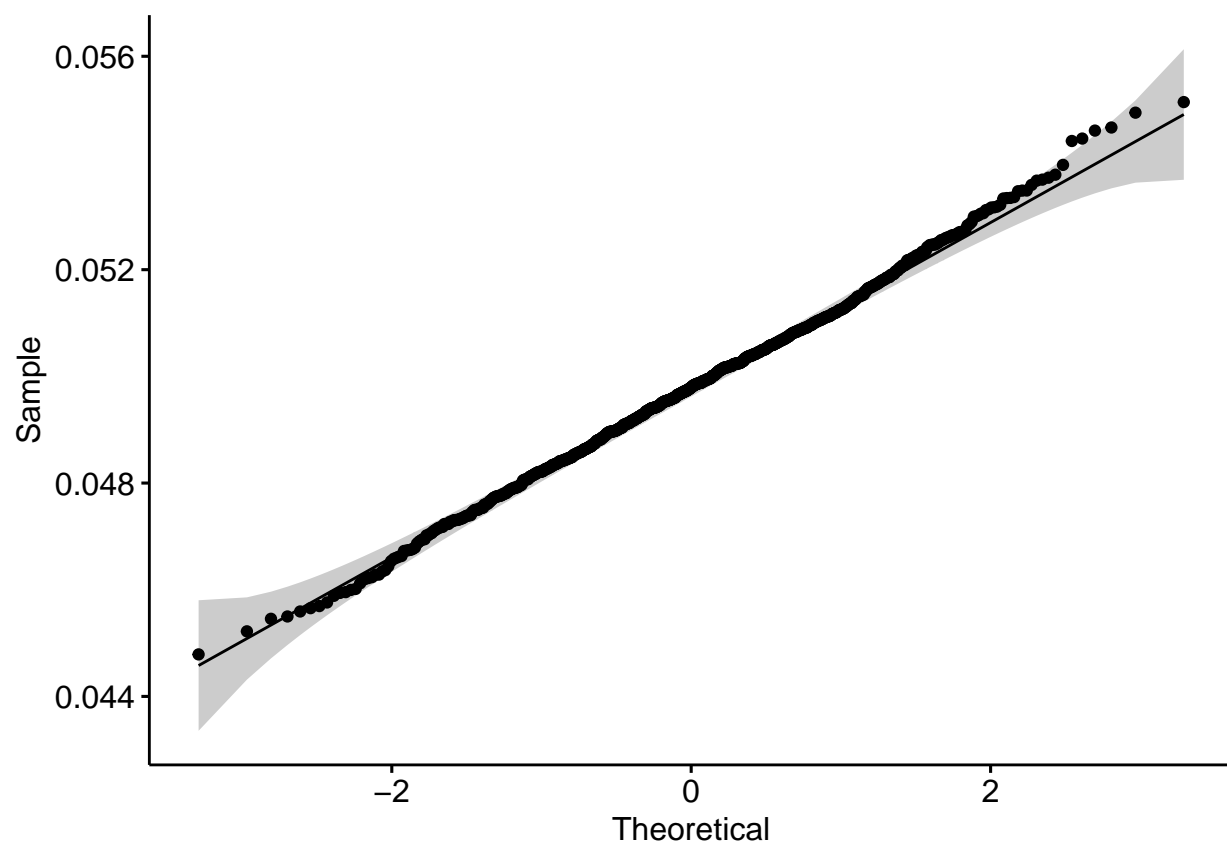| Posterior Probability	t	df	p	Confidence Interval
90%	-131.454	1955.819	0	[-0.0089, -0.0087]
80%	-258.742	1998.000	0	[-0.0075, -0.0074]

Figure for manuscript

Figure 3: Figure 3. qqplot for mean dXY distribution for species tree tracts at the 90% threshold
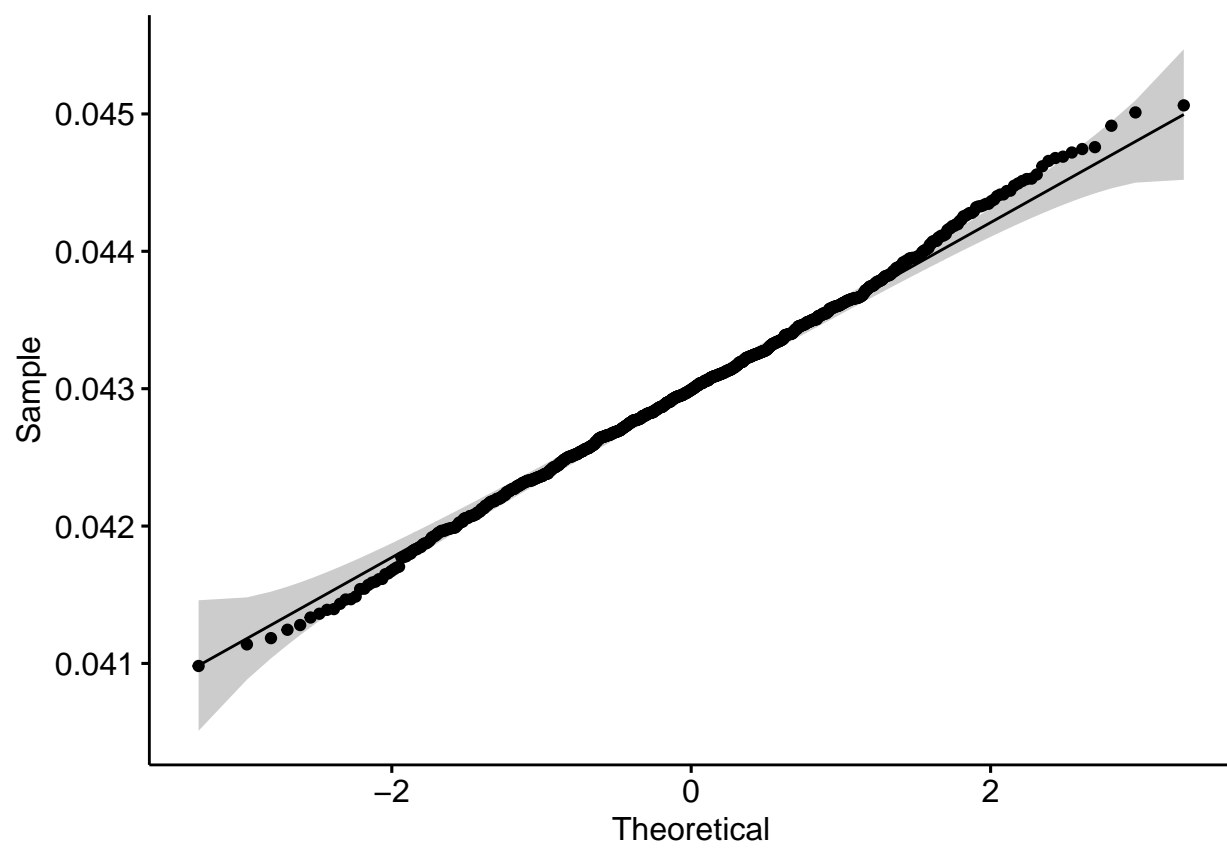
Figure 4: Figure 4. qqplot for mean dXY distribution for introgression tracts at the 80% threshold
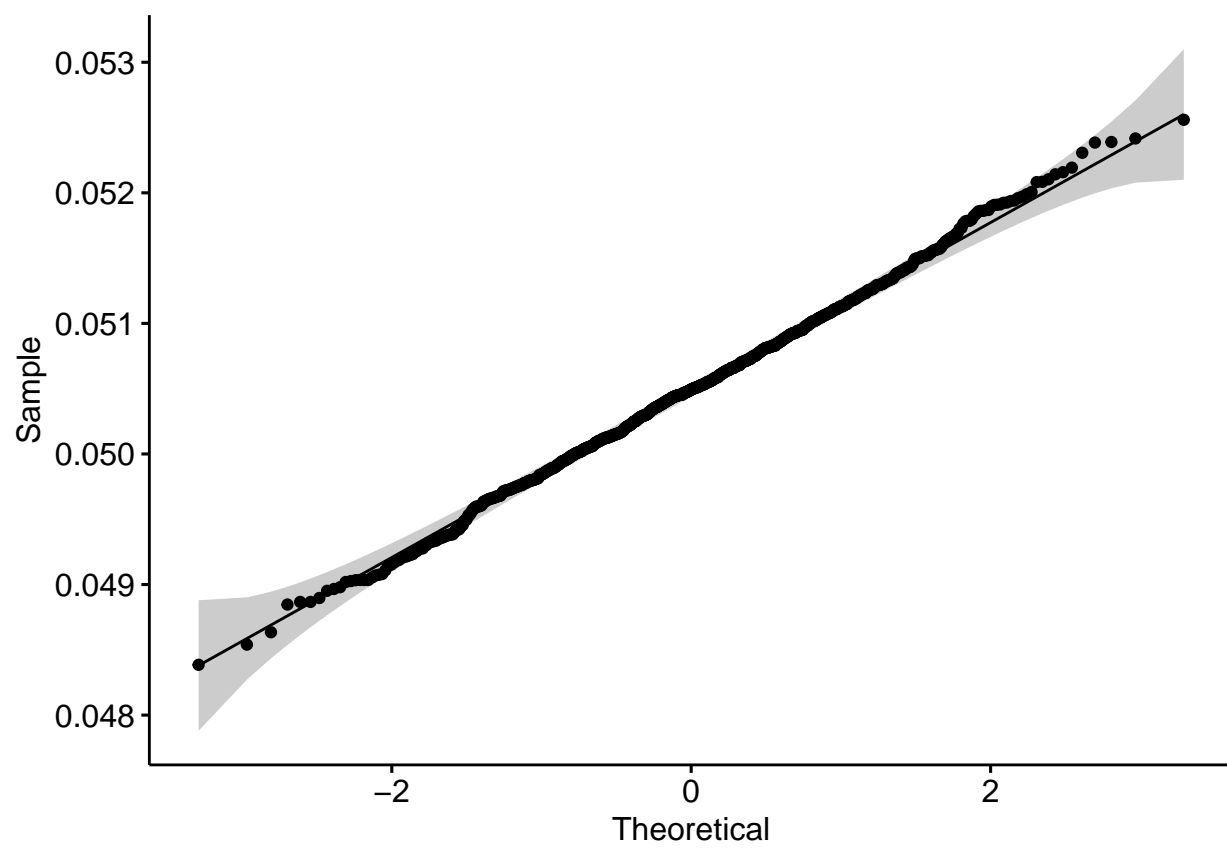
Figure 5: Figure 5. qqplot for mean dXY distribution for species tree tracts at the 80% threshold
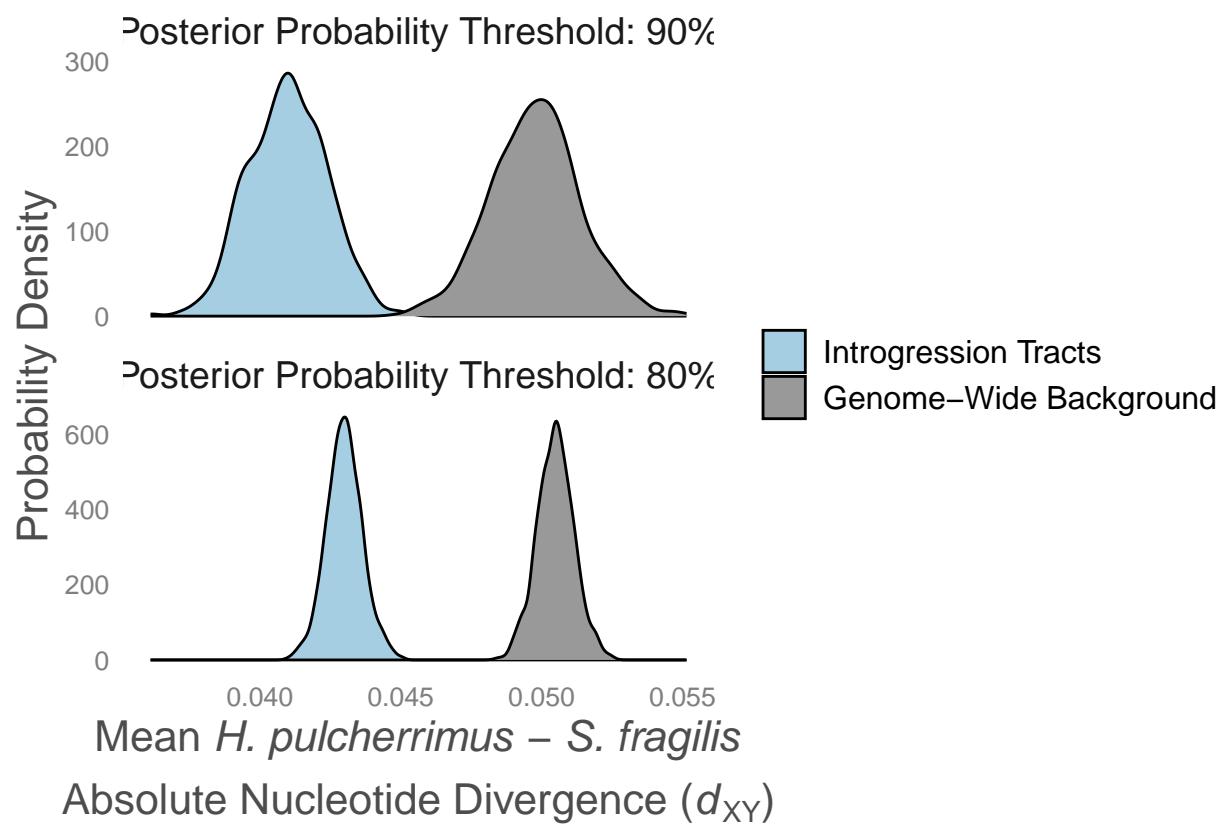
Figure 6: Figure 6. Distribution of mean absolute nucleotide divergence for introgression tracts and species tree tracts by PhyloNet-HMM posterior probability threshold (90%, 80%)