

Simulations for Harmon & Nuismer

August 6th, 2016

1 Symmetrical transition rates

2 Simulation parameters:

```
pSpec <- runif(n = 1000, min = 0, max = 2)
q01 <- runif(n = 1000, min = 0, max = 1)
q10 <- q01
ntaxa <- runif(n = 1000, min = 10, max = 100)
lambda <- runif(n = 1000, min = 0, max = 2)
```

```
3 ## Warning: Removed 112 rows containing missing values (geom_point).
4 ## Warning: Removed 108 rows containing missing values (geom_point).
5 ## Warning: Removed 44 rows containing missing values (geom_point).
6 ## Warning: Removed 33 rows containing missing values (geom_point).
7 ## Warning: Removed 204 rows containing missing values (geom_point).
8 ## Warning: Removed 137 rows containing missing values (geom_point).
```

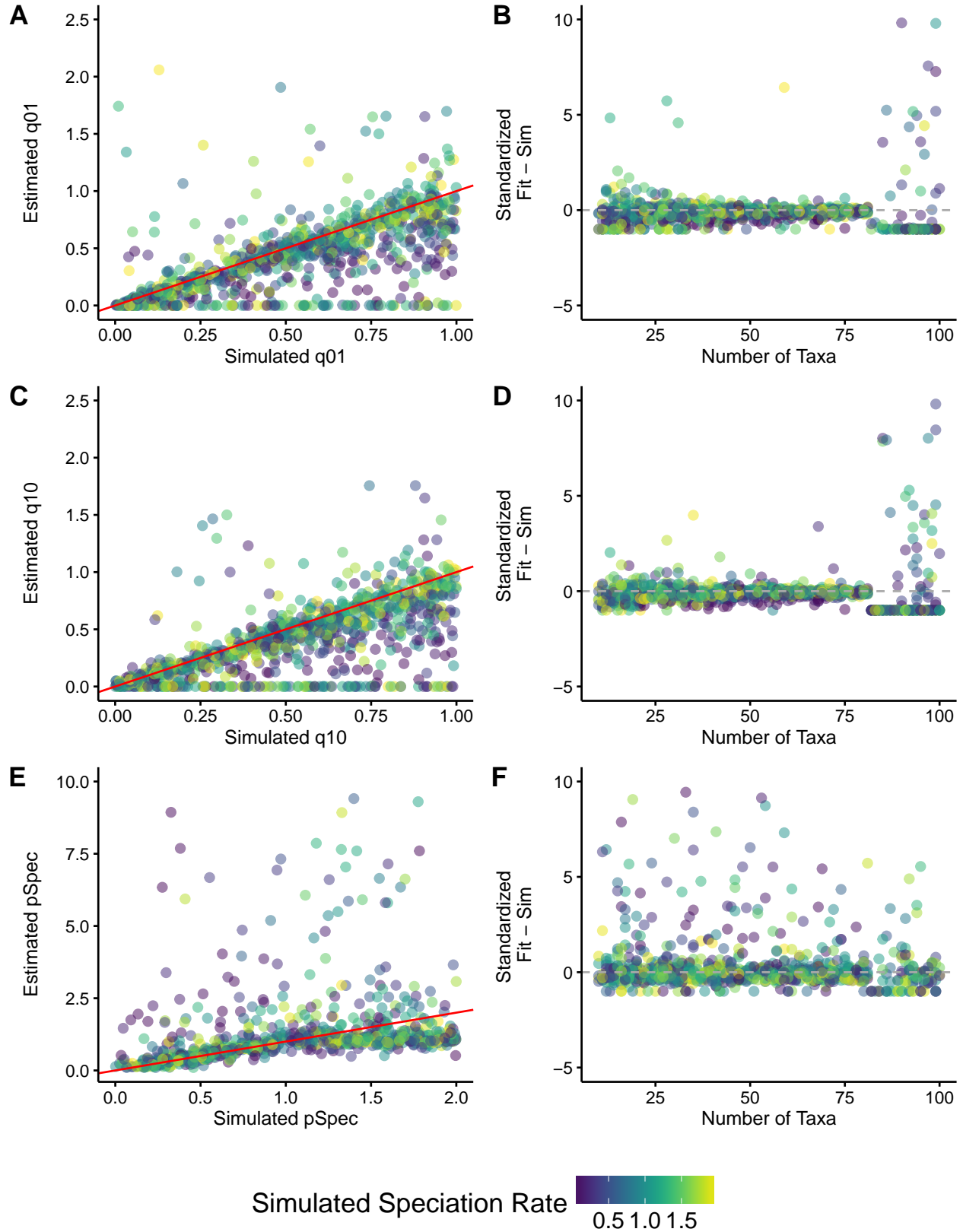


Figure 1: A - Fitted q_{01} by Simulated q_{01} ; B - Standardized (Fitted q_{01} - Simulated q_{01}) by Number of Taxa; C - Fitted q_{10} by Simulated q_{10} ; D - Standardized (Fitted q_{10} - Simulated q_{10}) by Number of Taxa; E - Fitted $pSpec$ by Simulated $pSpec$; F - Standardized (Fitted $pSpec$ - Simulated $pSpec$) by Number of Taxa

9 Asymmetrical transition rates

10 Simulation parameters:

```
pSpec <- runif(n = 1000, min = 0, max = 2)
q01 <- runif(n = 1000, min = 0, max = 1)
q10 <- q01
ntaxa <- runif(n = 1000, min = 10, max = 100)
lambda <- runif(n = 1000, min = 0, max = 2)
```

```
11 ## Warning: Removed 130 rows containing missing values (geom_point).
12 ## Warning: Removed 126 rows containing missing values (geom_point).
13 ## Warning: Removed 45 rows containing missing values (geom_point).
14 ## Warning: Removed 62 rows containing missing values (geom_point).
15 ## Warning: Removed 233 rows containing missing values (geom_point).
16 ## Warning: Removed 145 rows containing missing values (geom_point).
```

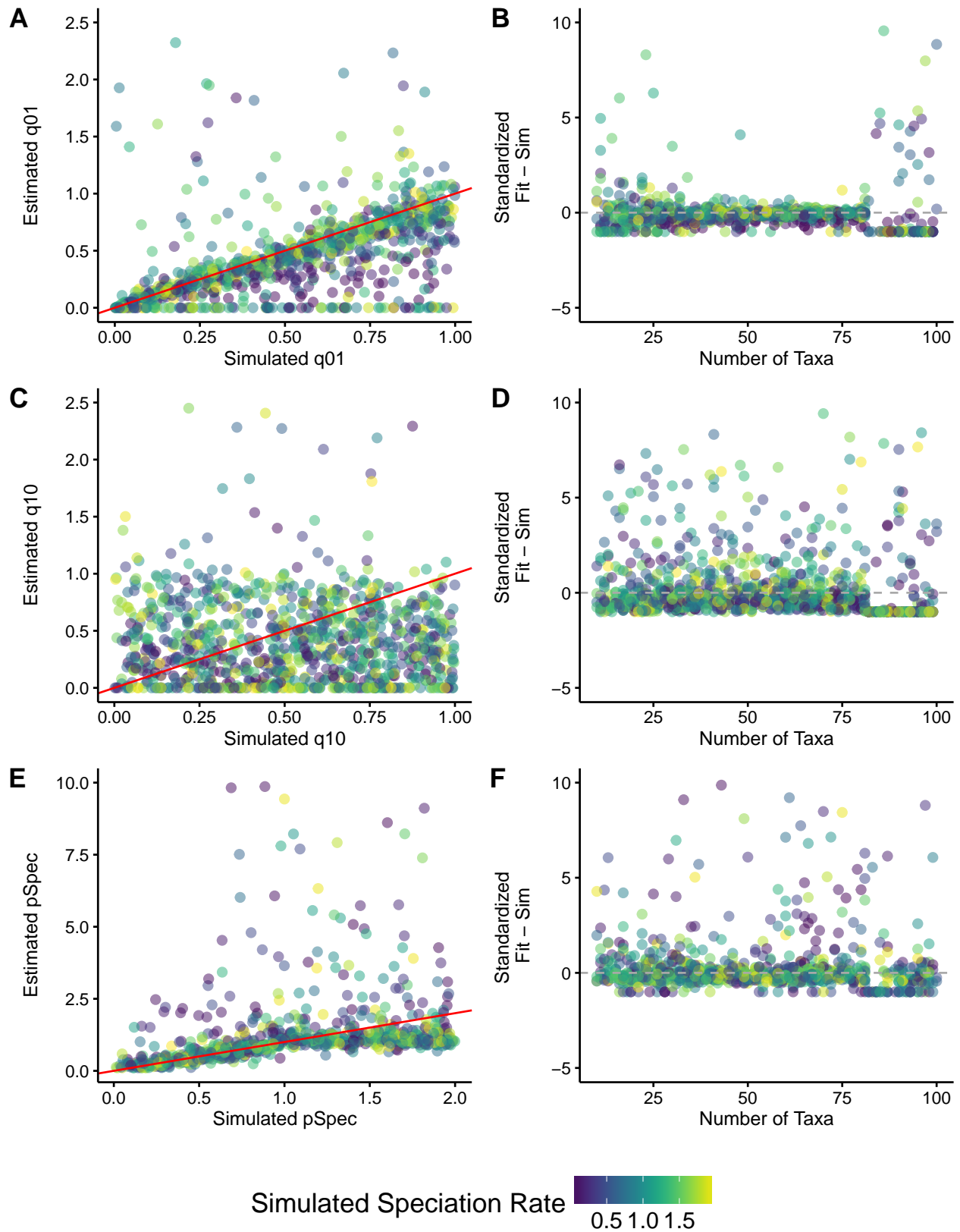


Figure 2: A - Fitted q_{01} by Simulated q_{01} ; B - Standardized (Fitted q_{01} - Simulated q_{01}) by Number of Taxa; C - Fitted q_{10} by Simulated q_{10} ; D - Standardized (Fitted q_{10} - Simulated q_{10}) by Number of Taxa; E - Fitted $pSpec$ by Simulated $pSpec$; F - Standardized (Fitted $pSpec$ - Simulated $pSpec$) by Number of Taxa