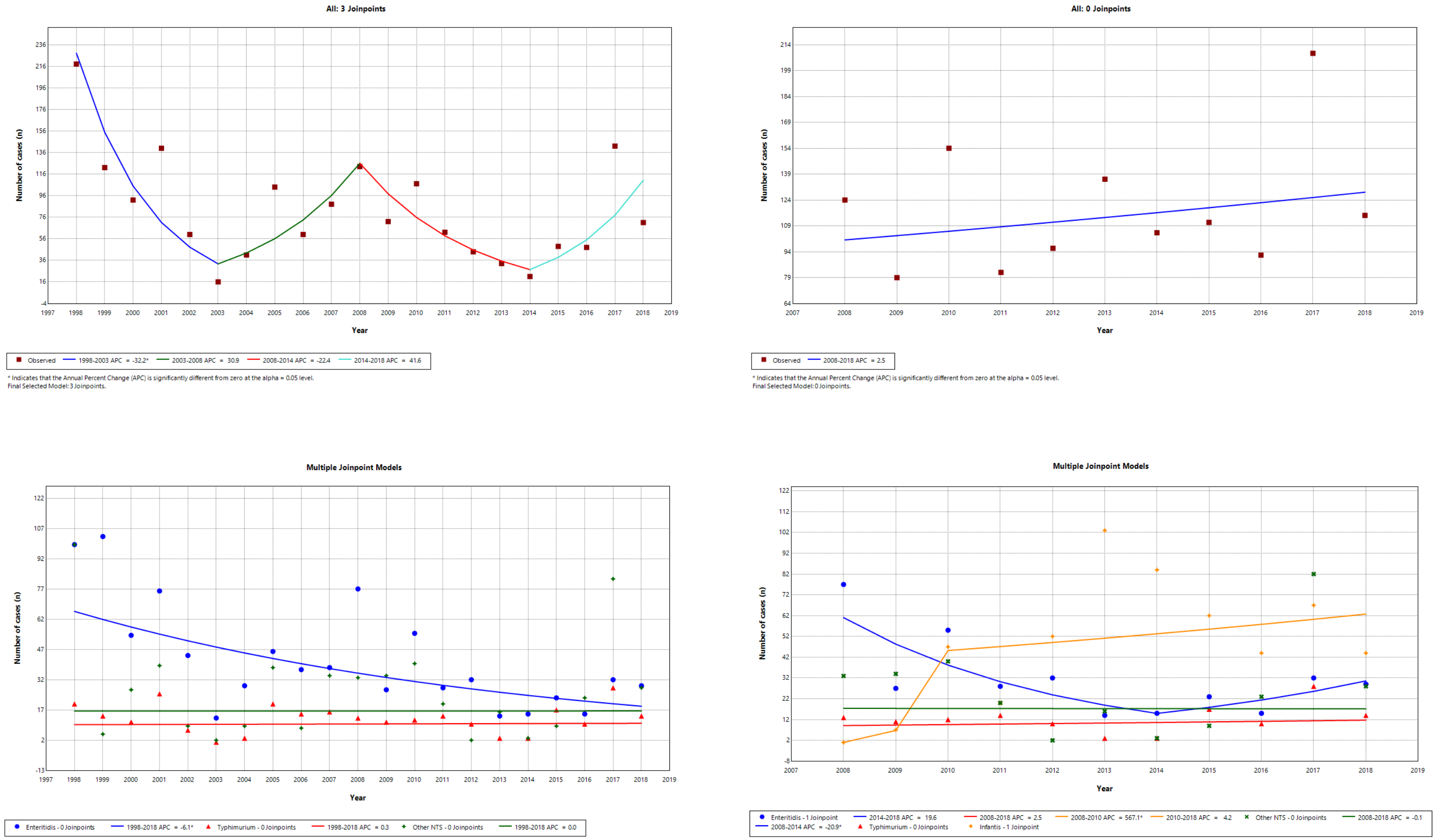
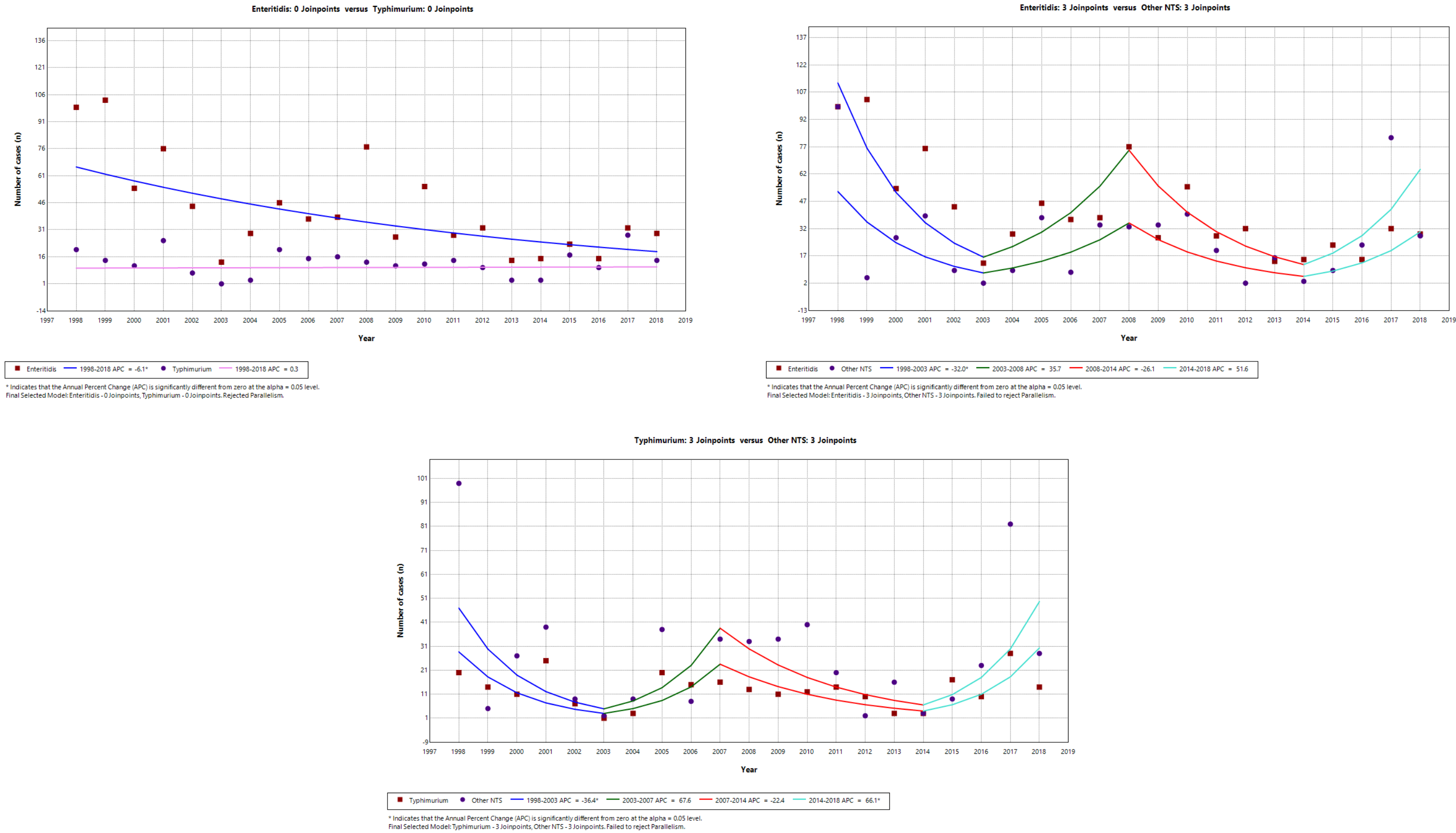


* Indicates that the Annual Percent Change (APC) is significantly different from zero at the alpha = 0.05 level.
Final Selected Model: 3 Joinpoints.

* Indicates that the Annual Percent Change (APC) is significantly different from zero at the alpha = 0.05 level.
Final Selected Model: 0 Joinpoints.

Supplementary Figure S1. Trend behavior of *Salmonella* cases by serotype for the evaluated period.



Enteritidis: 0 Joinpoints versus Typhimurium: 0 Joinpoints

* Indicates that the Annual Percent Change (APC) is significantly different from zero at the alpha = 0.05 level.
Final Selected Model: Enteritidis - 0 Joinpoints, Typhimurium - 0 Joinpoints. Rejected Parallelism.

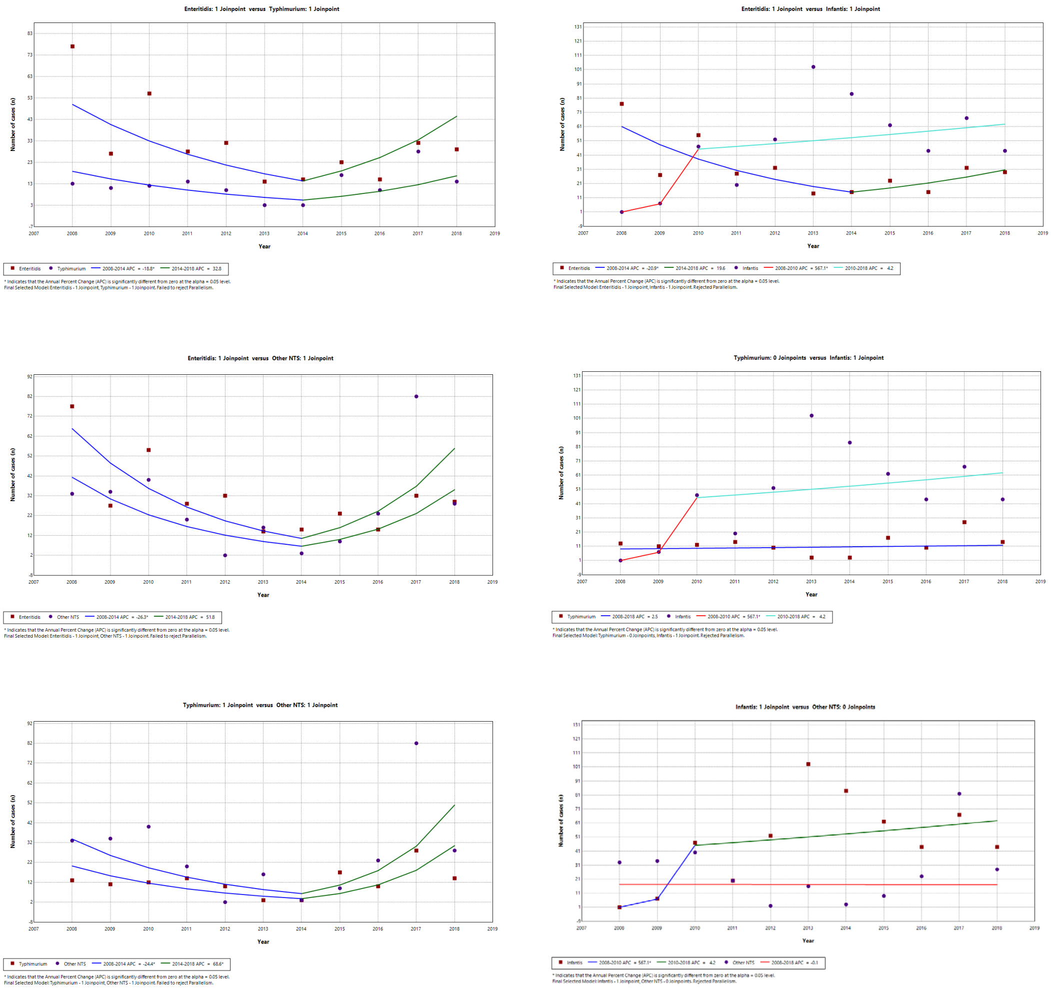
Enteritidis: 3 Joinpoints versus Other NTS: 3 Joinpoints

* Indicates that the Annual Percent Change (APC) is significantly different from zero at the alpha = 0.05 level.
Final Selected Model: Enteritidis - 3 Joinpoints, Other NTS - 3 Joinpoints. Failed to reject Parallelism.

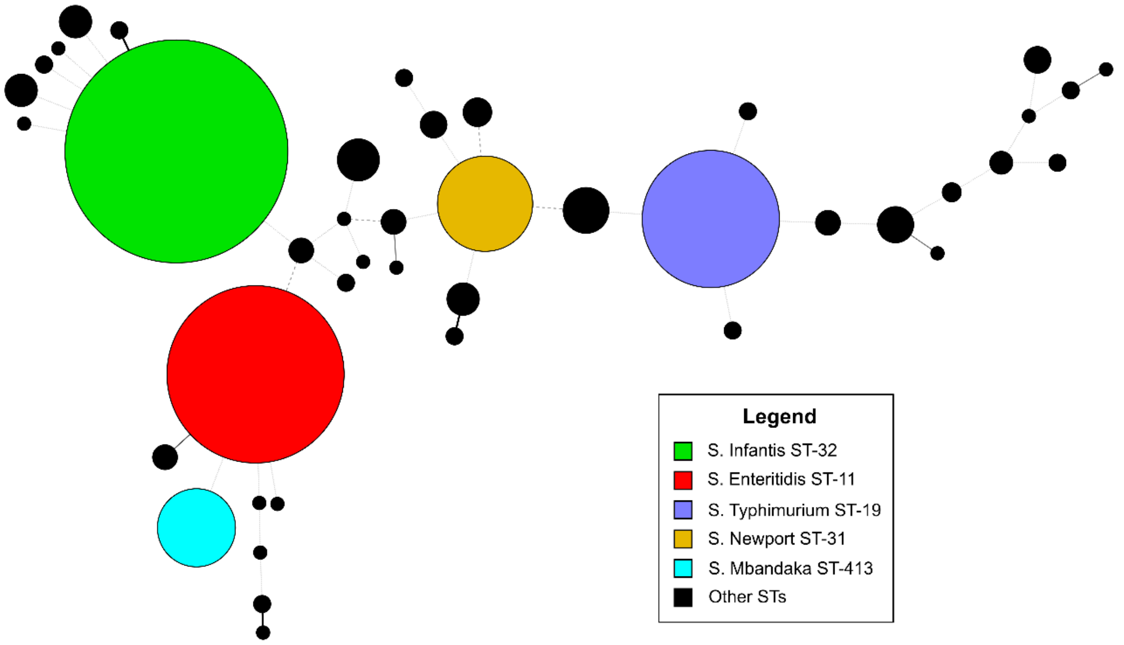
Typhimurium: 3 Joinpoints versus Other NTS: 3 Joinpoints

* Indicates that the Annual Percent Change (APC) is significantly different from zero at the alpha = 0.05 level.
Final Selected Model: Typhimurium - 3 Joinpoints, Other NTS - 3 Joinpoints. Failed to reject Parallelism.

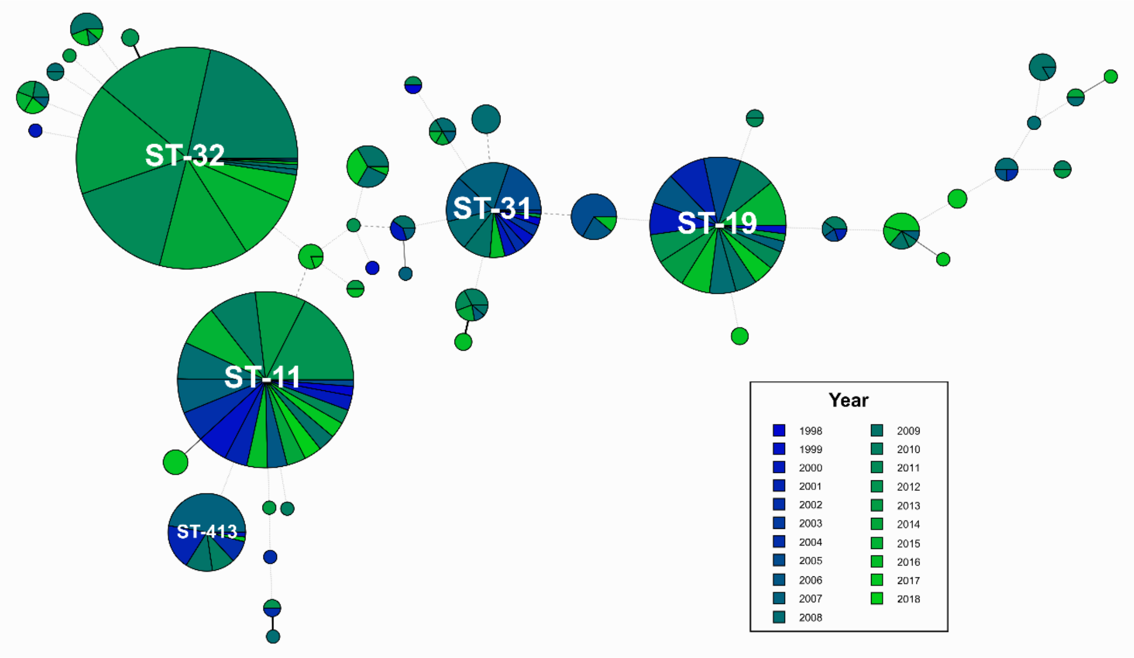
Supplementary Figure S2. Behavior of case counts by *Salmonella* serotypes between the period 1998-2018.



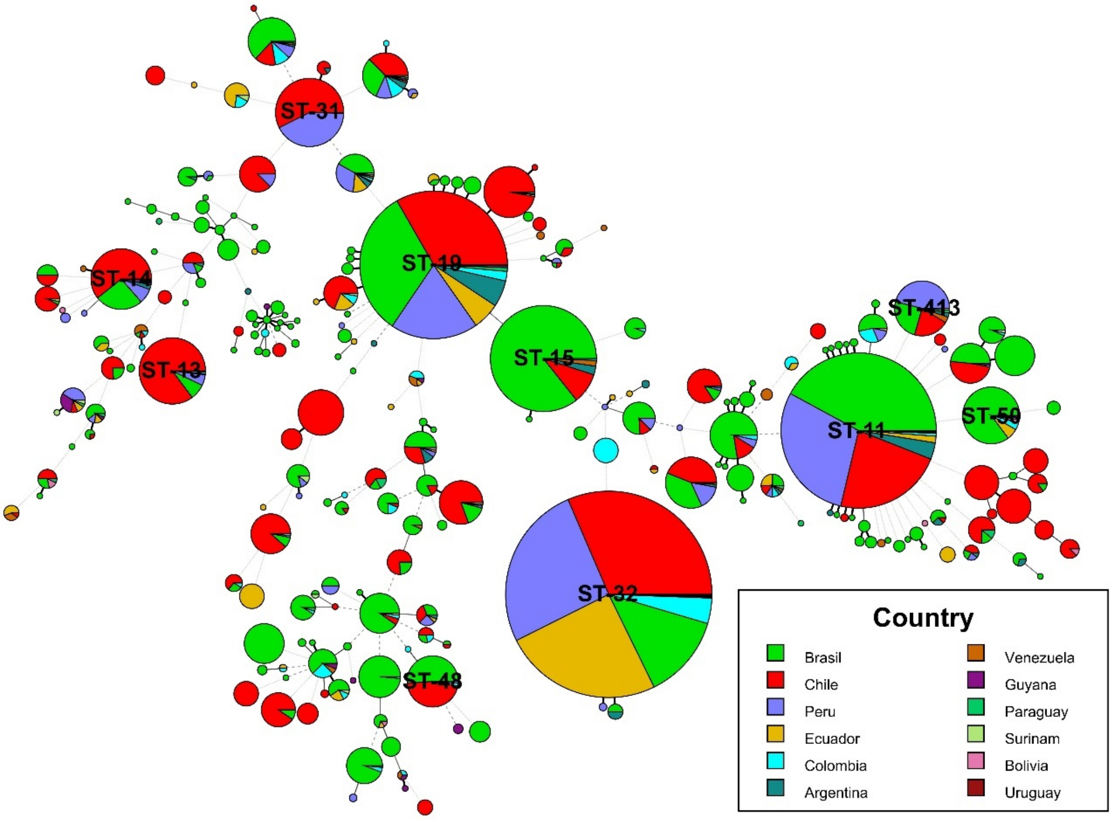
Supplementary Figure S3. Behavior of case counts by *Salmonella* serotypes between the period 2008-2018.



Supplementary Figure S4. Minimum spanning tree of NTS strains sequenced in Peru and included in this study. Each node represents a distinct ST and is sized according to the number of strains assigned to that ST. The nodes for the most frequent STs are colored according to the legend.



Supplementary Figure S5. Minimum spanning tree of NTS strains sequenced in Peru and included in this study. Each node represents a distinct ST and is sized according to the number of strains assigned to that ST. Additionally, each node indicates the frequency of strains according to the year of isolation. The most frequent STs are indicated in bold on the corresponding nodes.



Supplementary Figure S6. Minimum spanning tree of NTS strains sequenced in South America and its comparison with strains sequenced in Peru. Each node represents a different ST and is proportional to the number of strains assigned to that ST. The strains in each node are colored according to the country, while the 10 most frequent STs are indicated in bold on the corresponding nodes.