# Comparing tRNA genes found by TRNAscan1.3 vs. tRNAscan2.0 from Trytryp genomes

> As you see in the VennDiagram we have four sets of:
1. non-pseudo genes found by TSE1.3
2. pseudo genes found by TSE1.3
3. non-pseudo genes found by TSE2.0
4. pseudo genes found by TSE2.0

As we see, Both gene-finders have found same 3511 genes with the exact same coordinates. There are genes that are considered as pseudo in one version and non-pseudo in the other version.
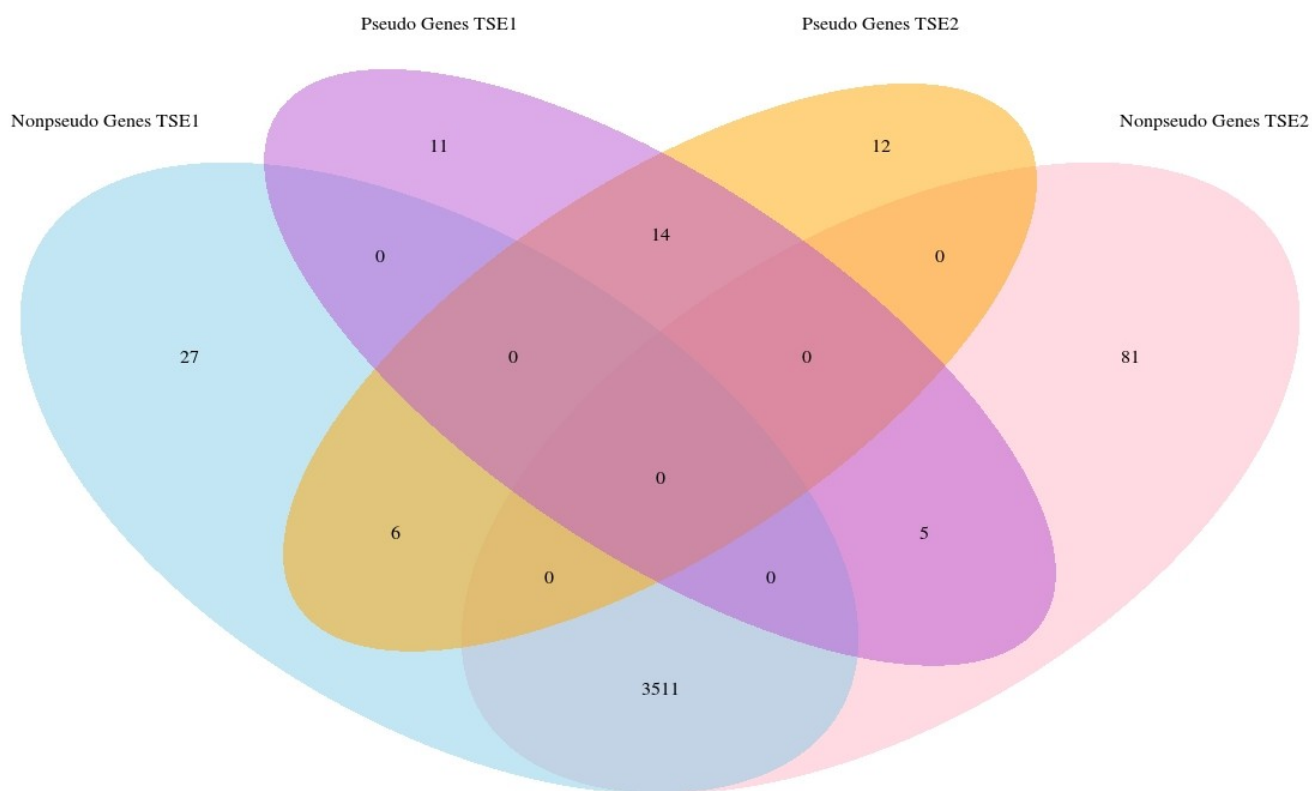
> In the fallowing plot we are comparing the scores of the genes found by both gene-finders.

1. Non-pseudo genes found by both version of TSE(red)
2. Genes found by both versions which are marked as non-pseudo in TSE1.3 and pseudo in TSE2.0(purple)
3. Genes found by both versions which are marked as non-pseudo in TSE2.0 and pseudo in TSE1.3(blue)
4. Genes found by both versions which are marked as pseudo in both versions(green)

Corelation of gene covariance scores found by tRNAscan1.3 and tRNAscan2.0
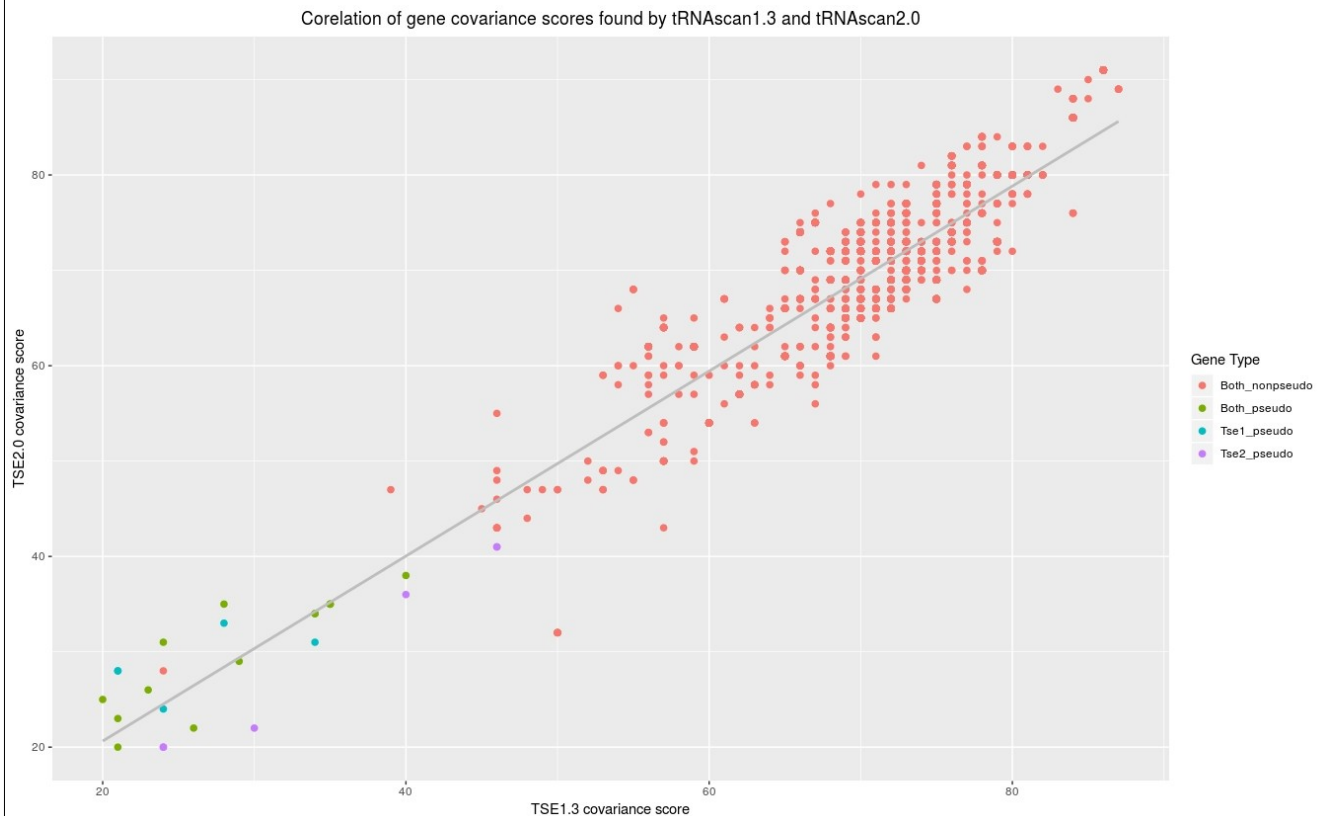
> A comparison of end-calling for TSE1.3 VS 2.0 for both pseudo and non-pseudo genes found by both versions.
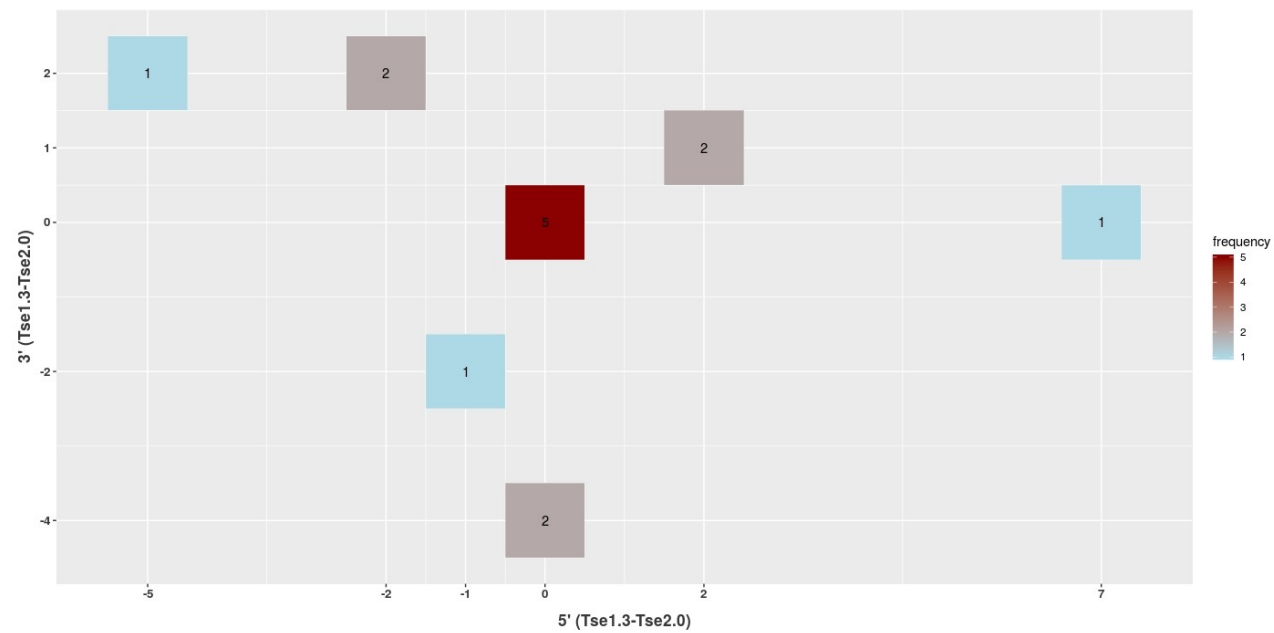

Empirical joint distribution of end displacements of 3536 TryTryp genes found by two version of tRNAscan (2.0 vs 1.3)
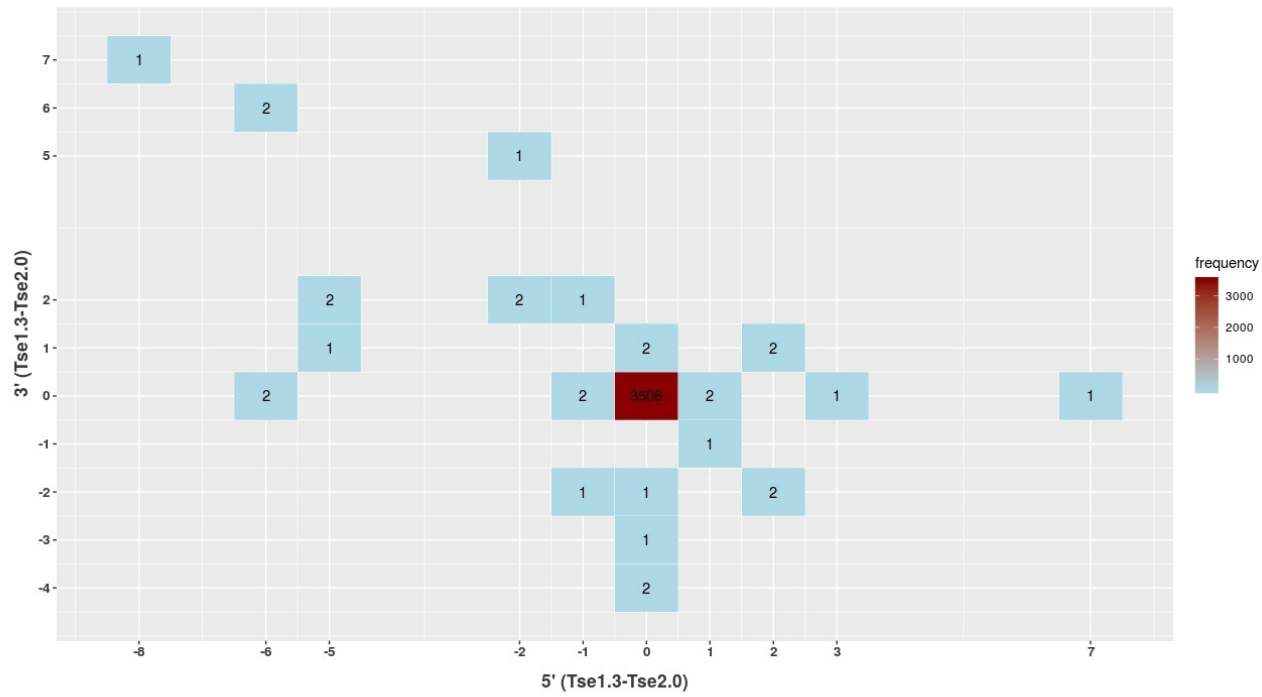
Empirical joint distribution of end displacements of 3511 TryTryp nonpseudo genes found by two version of tRNAscan (2.0 vs 1.3)
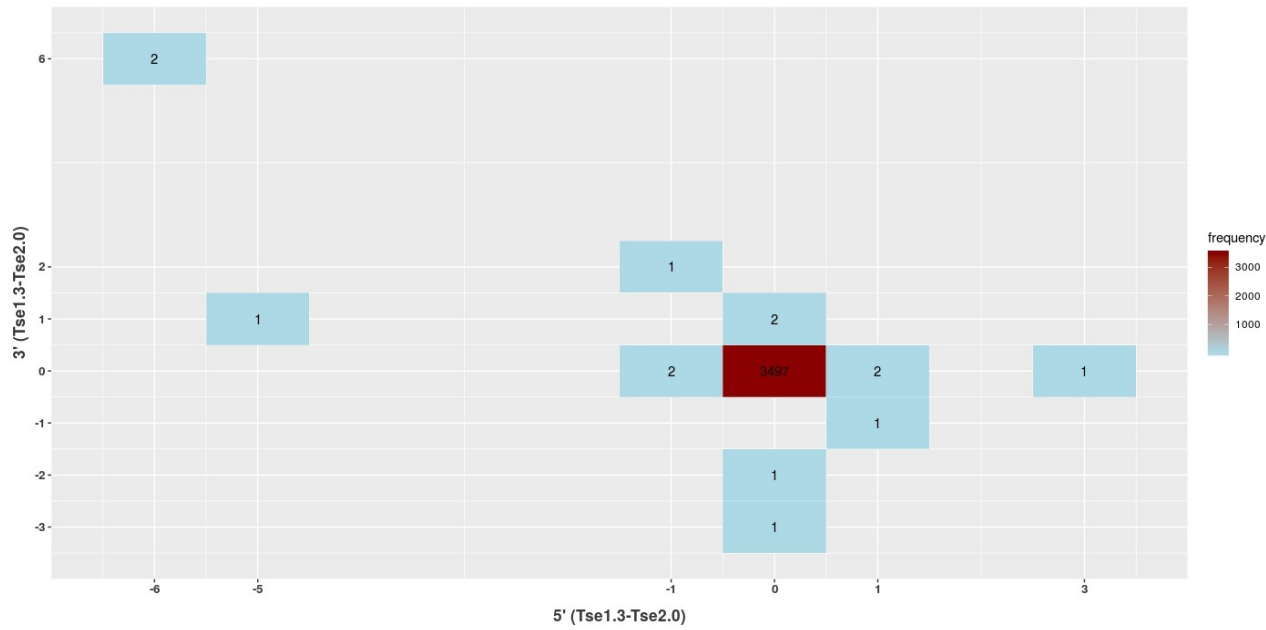
Empirical joint distribution of end displacements of 14 TryTryp pseudo genes found by two version of tRNAscan (2.0 vs 1.3)

Empirical joint distribution of end displacements of 25 TryTryp genes marked as pseudo by atleast one of the versions of tRNAscan (2.0 vs 1.3)