VALUES AND STATISTICS INDICATED IN MSTATSPOP:

Effective length for each population:

Eff_length1_pop_outg[0]: Effective length1 for population 0. That is, considering the outgroup, how many positions have at least one sequence per population 0 and the outgroup exist.
Useful in case considering missing positions (-u 1). In case -u 0 all lengths are equal. Useful for calculating divergence vs outgroup or versus populations.

Eff_length2_pop_outg[0]: Effective length2 for population 0. That is, considering the outgroup, how many positions have at least two sequences per population 0 and the outgroup exist.
Useful in case considering missing positions (-u 1). In case -u 0 all lengths are equal. Useful for calculating levels of variability.

Eff_length3_pop_outg[0]: Effective length3 for population 0. That is, considering the outgroup, how many positions have at least three sequences per population 0 and the outgroup exist.
Useful in case considering missing positions (-u 1). In case -u 0 all lengths are equal. Useful for calculating tests of neutrality (variances).

Eff_length1_pop[0]: Effective length1 for population 0. That is, how many positions have at least one sequence per population 0.
Useful in case considering missing positions (-u 1). In case -u 0 all lengths are equal. Useful for calculating divergence versus populations.

Eff_length2_pop[0]: Effective length2 for population 0. That is, how many positions have at least two sequences per population 0.
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In principle, if the analysis contains an outgroup, all analysis are conditioned to the presence of the outgroup variant.

STATISTICS:

Estimates of variability for each population:

S[0]: Number of segregating sites at population 0

Theta(Wat)[0]: Watterson (1975) estimation of variability.
Theta(Taj)[0]: Tajima (1983) estimation of variability.
Theta(Fu&Li)[0]: Fu and Li's (1991) estimation of variability.
Theta(Fay&Wu)[0]: Fay and Wu's (2000) estimation of variability.
Theta(Zeng)[0]: Zeng's (2006) estimation of variability.

Theta(Achaz,Wat)[0]: Watterson estimator without considering singletons (Achaz 2008)
Theta(Achaz,Taj)[0]: Tajima estimator without considering singletons (Achaz 2008)

Divergence[0]: Divergence between population 0 and the outgroup.

an_x[0]: (Σ(i=1 to n-1)1/i), that is, sumatory of (1/i) from i=1 to n-1, being n the number of samples. In case missing data (-u 1), sum of an for each position and divided by the eff_length2_pop. Used for Watterson estimator and neutrality tests.

bn_x[0]: (Σ(i=1 to n-1)1/i^2), that is, sumatory of (1/i^2) from i=1 to n-1, being n the number of samples. In case missing data (-u 1), sum of an for each position and divided by the eff_length2_pop. Used for neutrality tests.

an_xo[0]: Same but considering only those positions were the outgroup is present.
bn_xo[0]: Same but considering only those positions were the outgroup is present.

Haplotype diversity and number of haplotypes for each population:

HapW[0]: Haplotype diversity at population 0.
nHap[0]: number of haplotypes at population 0.

Neutrality tests for each population:

Tajima D[0]: Test of Tajima (1989)
Fu&Li D[0]: Test of Fu and Li D (1993)
Fu&Li F[0]: Test of Fu and Li D (1993)
Fay&Wu norm H[0]: Test of Fay and Wu (2000) normalized (Achaz 2009, Zeng 2006)
Fay&WuH[0]: Test of Fay and Wu (2000)
Ferretti L[0]: Test of Ferretti similar to Fay and Wu but using theta Watt instead Theta Taj (Ferretti et al.)
Zeng E[0]: Test of Zeng (2006)
Achaz Y[0]: Test of Achaz (2008)
Fs[0]: Test Fs (Fu 1997)
R2[0]: Test of R2 (2002)

Variants assigned to exclusive, fixed, polymorphic but fixed in rest of pops, and shared:

Ss[rest] are shared variants between populations but fixed within:
Sx[0]: Exclusive variants at population 0
Sf[0]: Fixed variants at population 0
Ss: Shared variants among populations
Sxf[0]: Exclusive variants at population 0 that are fixed at other populations.

Mismatch distribution statistics:

SDev[0]: Standard deviation of Tajima's estimator.
Skewness[0]: Third standardised moment of Tajima's estimator.
Kurtosis[0]: Fourth standardised moment of Tajima's estimator.

Differentiation statistics:

Differentiation with nucleotide sequences (even with missing data):

Fstall: 1 - mean(pi_within/nt)/mean(pi_among/nt)

Fst1all[pop1]: 1- mean(pi_within/nt[rest],pi_within_rest/nt[pop1])/mean(pi_among/nt)

Fst[pop1][pop2]: 1 - mean(pi_within/nt[pop1],pi_within/nt[pop2])/pi_among/nt[pop1][pop2] (Hudson et al. 1992)

Differentiation with haplotype data (phase is necessary):

Fsthall: 1 - mean(pih_within)/mean(pih_among)

Fsth1all[pop1]: 1- mean(pih_within[pop1]-pih_within[rest])/mean(pih_among)

Fsth[pop1][pop2]: 1 - mean(pih_within[pop1],pih_within[pop2])/pih_among[pop1][pop2]

Frequency of variants for each population:

fr[0,1]: Site frequency Spectrum per population

Frequency of each haplotype in the populations:

frH[0,hap00]: frequency of each haplotype per population

Joint frequency distribution for each variant and population (No included variants that are missing or polymorphic in the outgroup):

SNP[xx]: frequency of each SNP at each population.

Relative Site Frequency Spectrum

rSFS[pop,freq]: number of variants at frequency freq in the population pop, relative to the whole sample (excluding outgroup, only used for polarizing)