**The whole genome focused array SNP typing (WG-FAST) pipeline**

**Citation:**

**Contact:** Please address queries, concerns, improvements to jasonsahl at gmail dot com

**What does WG-FAST do?**

WG-FAST was designed as a tool to phylogenetically genotype unknown samples, even those with extremely low read coverage, in the context of a well-studied dataset.

**What does WG-FAST not do?**

WG-FAST is not intended to identify new SNPs in a dataset. If too many samples are processed with WG-FAST, a phylogenetic discovery bias can most certainly exist.

**Installation**

-The code is housed here: https://github.com/jasonsahl/wgfast.git

-Install the code with:

>git clone <https://github.com/jasonsahl/wgfast.git>

-The following line must be edited to reflect your installation directory:

WGFAST\_PATH**=**"/Users/jsahl/wgfast"

**Dependencies**

1. GATK – tested version is 2.72. This version requires Java 1.7. Should be back compatible with older versions. Download Jar file and place in WGFAST\_PATH/bin. Can be obtained from: <https://www.broadinstitute.org/gatk/download>
2. Samtools – tested version is 0.1.19. Must be in PATH as “samtools”. Can be obtained from: <http://samtools.sourceforge.net/>
3. BWA-MEM – tested version is 0.7.5a. Must be in PATH as “bwa”. Can be obtained from: <http://bio-bwa.sourceforge.net/>
4. Picard tools – tested version is 1.79. Included in “binary” directory and does not need to be independently installed
5. RAxML – tested version is 8.0.17. Must be in PATH as “raxmlHPC-SSE3”. Can be obtained from: <https://github.com/stamatak/standard-RAxML>. The PTHREADS version does not support the ASC substitution models.
6. DendroPy – tested version is 3.12.0, must be installed in PYTHONPATH. Can be obtained from: <https://github.com/jeetsukumaran/DendroPy>. Dendropy is included with WG-FAST with the following included information:

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1. BioPython – must be in PYTHONPATH. Can be obtained from: <https://github.com/biopython/biopython>

**Required input files**

1. Directory of sequence reads. The reads must be named according to Illumina HiSeq or MiSeq conventions. Reads must be in the Illumina 1.9+ FastQ format. If you have old Illumina FastQ encodings, they must be converted before running WG-FAST.
2. SNP matrix. The easiest way to generate this is by using NASP (<https://github.com/TGenNorth/NASP>). If other SNP matrix formats are used, they must conform to having the first column including (contig::coordinate) and the column following the SNP calls must be (#SNPCall).
3. Phylogeny. A script is included with WG-FAST that can generate an appropriate phylogeny from a NASP matrix.
4. Reference genome in FASTA format. This should be the same FASTA that was used to call SNPs with NASP.

**Output printed to screen**