owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017 (master)

$ cd Unix\_Assignment\_1\_JMA/

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA (master)

$ ls

sample.txt UNIX\_Assignment/ Unix\_Assignment\_1\_readme\_file\_backup.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA (master)

$ cd UNIX\_Assignment

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt transpose.awk UNIX\_Assignment.pdf

snp\_position.txt UNIX\_Assignment.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMMIL" fang\_et\_al\_genotypes.txt > maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMMLR" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ grep -w "ZMMMR" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ grep -w "ZMPBA" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ grep -w "ZMPIL" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ grep -w "ZMPJA" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ awk -f transpose.awk teosinte\_genotypes.txt > transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ awk -f transpose.awk maize\_genotypes.txt > transposed\_maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ ls

fang\_et\_al\_genotypes.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

maize\_genotypes.txt transpose.awk UNIX\_Assignment.md

snp\_position.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ cut -f 1-10 transpose\_maize\_genotypes.txt | head

cut: transpose\_maize\_genotypes.txt: No such file or directory

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ ls

fang\_et\_al\_genotypes.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

maize\_genotypes.txt transpose.awk UNIX\_Assignment.md

snp\_position.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ cut -f 1-10 transposed\_maize\_genotypes.txt | head

CU0001 S1607 CU0002 CU0003 S1643 CU0004 S1644 CU0005 S1630 S1615

Zmm-IL-33-16\_f Zmm-IL-38-11 Zmm-IL-4226\_f Zmm-IL-4722\_f Zmm-IL-A188 Zmm-IL-A214N\_f Zmm -IL-A239 Zmm-IL-A272\_f Zmm-IL-A441-5\_s Zmm-IL-A554

ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL ZMMIL

G/G C/C C/C C/C C/C G/G C/C C/C C/C ?/?

A/A A/A A/A A/A A/A A/A A/A A/A A/A A/A

T/T T/T T/T T/T T/T T/T T/T T/T T/T T/T

G/G ?/? G/G G/G G/G G/G ?/? G/G G/G G/G

C/C C/C C/C C/C C/C C/C C/C C/C T/T C/C

C/C C/C C/C G/G C/C C/C C/C C/C C/C C/C

G/G G/G G/G G/G G/G G/G G/G G/G G/G G/G

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ cut -f 1-10 snp\_position.txt | head

SNP\_ID cdv\_marker\_id Chromosome Position alt\_pos mult\_positions amplicon cdv \_map\_feature.name gene candidate/random

abph1.20 5976 2 27403404 abph1 AB042260 abph1 can didate

abph1.22 5978 2 27403892 abph1 AB042260 abph1 can didate

ae1.3 6605 5 167889790 ae1 ae1 ae1 candidate

ae1.4 6606 5 167889682 ae1 ae1 ae1 candidate

ae1.5 6607 5 167889821 ae1 ae1 ae1 candidate

an1.4 5982 1 240498509 an1 an1 an1 candidate

ba1.6 3463 3 181362952 ba1 AY753892 ba1 candidate

ba1.9 3466 3 181362666 ba1 AY753892 ba1 candidate

bt2.5 5983 4 66290049 bt2 bt2 bt2 candidate

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assign ment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> transposed\_maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

maize\_genotypes.txt transpose.awk UNIX\_Assignment.md

snp\_position.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ rm transposed\_maize\_genotypes.txt transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt snp\_position.txt transpose.awk UNIX\_Assignment.pdf

maize\_genotypes.txt teosinte\_genotypes.txt UNIX\_Assignment.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "Sample\_ID" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMMIL" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMMLR" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMMMR" fang\_et\_al\_genotypes.txt >> maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMPBA" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMPIL" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ grep -w "ZMPJA" fang\_et\_al\_genotypes.txt >> teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt snp\_position.txt transpose.awk UNIX\_Assignment.pdf

maize\_genotypes.txt teosinte\_genotypes.txt UNIX\_Assignment.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ awk -f transpose.awk teosinte\_genotypes.txt > transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ awk -f transpose.awk maize\_genotypes.txt > transposed\_maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Untracked files:

(use "git add <file>..." to include in what will be committed)

maize\_genotypes.txt

teosinte\_genotypes.txt

transposed\_maize\_genotypes.txt

transposed\_teosinte\_genotypes.txt

nothing added to commit but untracked files present (use "git add" to track)

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git add

Nothing specified, nothing added.

Maybe you wanted to say 'git add .'?

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git add maize\_genotypes.txt

warning: LF will be replaced by CRLF in UNIX\_Assignment/maize\_genotypes.txt.

The file will have its original line endings in your working directory.

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k1,1V snp\_position.txt > sorted\_snp\_position.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > joined\_sorted\_transposed\_maize\_genotypes.t

join: sorted\_transposed\_maize\_genotypes.txt:955: is not sorted: lg2.11 C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C ?/? C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C ?/? ?/? C/C C/C C/C ?/? C/C ?/? C/C C/C C/C C/C ?/? T/T C/C ?/? C/C ?/? C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C ?/? C/C C/C ?/? ?/? C/C ?/? ?/? ?/? C/C C/C ?/? ?/? ?/? C/C C/C ?/? C/C C/C C/C ?/? ?/?

join: sorted\_snp\_position.txt:943: is not sorted: abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt sorted\_snp\_position.txt transpose.awk UNIX\_Assignment.md

maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

snp\_position.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > joined\_sorted\_transposed\_maize\_genotypes.t

join: sorted\_transposed\_maize\_genotypes.txt:955: is not sorted: lg2.11 C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C C/C ?/? ?/? C/C ?/? ?/? ?/? C/C C/C ?/? ?/? ?/? C/C C/C ?/? C/C C/C C/C ?/? ?/?

join: sorted\_snp\_position.txt:943: is not sorted: abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt snp\_position.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

joined\_sorted\_transposed\_maize\_genotypes.t sorted\_snp\_position.txt transpose.awk UNIX\_Assignment.md

maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -t $'\t' -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > join\_example.txt

join: sorted\_transposed\_maize\_genotypes.txt:955: is not sorted: lg2.11 C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C ?/? C/C C/C C ?/? C/T C/C C/T C/T ?/? C/T C/T C/T ?/? C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/T C/C C/C C/T C/C C/T C/T C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/T C/C ?/? C/C C/C C/C C/C C/C C/C ?/? C/C ?/? C/C C/C C/C C/C C/C ?/? ?/? C/C ?/? ?/? ?/? C/C C/C ?/? ?/? ?/? C/C C/C ?/? C/C C/C C/C ?/? ?/?

join: sorted\_snp\_position.txt:943: is not sorted: abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.pdf

join\_example.txt snp\_position.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

joined\_sorted\_transposed\_maize\_genotypes.t sorted\_snp\_position.txt transpose.awk UNIX\_Assignment.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -t $'\t' -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > joined\_sorted\_transposed\_maize\_genotypes.txt

join: sorted\_transposed\_maize\_genotypes.txt:955: is not sorted: lg2.11 C/C C/C C/C ?/? C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/C C/?/? C/C C/C C/C C/C C/C ?/? ?/? C/C ?/? ?/? ?/? C/C C/C ?/? ?/? ?/? C/C C/C ?/? C/C C/C C/C ?/? ?/?

join: sorted\_snp\_position.txt:943: is not sorted: abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -t $'\t' -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > joined\_sorted\_transposed\_maize\_genotypes.txt

bash: joined\_sorted\_transposed\_maize\_genotypes.txt: Device or resource busy

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k1,1 transposed\_maize\_genotypes.txt > sorted\_transposed\_maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

fang\_et\_al\_genotypes.txt snp\_position.txt teosinte\_genotypes.txt transposed\_maize\_genotypes.txt UNIX\_Assignment.md

maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transpose.awk transposed\_teosinte\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k1,1 snp\_position.txt > sorted\_snp\_position.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -t $'\t' -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_maize\_genotypes.txt > joined\_sorted\_transposed\_maize\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 1-10 joined\_sorted\_transposed\_maize\_genotypes.txt | head

abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate

abph1.22 5978 2 27403892 abph1 AB042260 abph1 candidate

ae1.3 6605 5 167889790 ae1 ae1 ae1 candidate

ae1.4 6606 5 167889682 ae1 ae1 ae1 candidate

ae1.5 6607 5 167889821 ae1 ae1 ae1 candidate

an1.4 5982 1 240498509 an1 an1 an1 candidate

ba1.6 3463 3 181362952 ba1 AY753892 ba1 candidate

ba1.9 3466 3 181362666 ba1 AY753892 ba1 candidate

bt2.5 5983 4 66290049 bt2 bt2 bt2 candidate

bt2.7 5985 4 66290994 bt2 bt2 bt2 candidate

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 1-15 joined\_sorted\_transposed\_maize\_genotypes.txt | head

abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

abph1.22 5978 2 27403892 abph1 AB042260 abph1 candidate 8394 10475 0 0 0

ae1.3 6605 5 167889790 ae1 ae1 ae1 candidate 8395 10477 1 1 1

ae1.4 6606 5 167889682 ae1 ae1 ae1 candidate 8396 10478 0 0 0

ae1.5 6607 5 167889821 ae1 ae1 ae1 candidate 8397 10479 0 0 0

an1.4 5982 1 240498509 an1 an1 an1 candidate 8398 10481 1 1 1

ba1.6 3463 3 181362952 ba1 AY753892 ba1 candidate 8399 10482 1 0 1

ba1.9 3466 3 181362666 ba1 AY753892 ba1 candidate 8400 10483 0 0 0

bt2.5 5983 4 66290049 bt2 bt2 bt2 candidate 8401 10486 1 1 1

bt2.7 5985 4 66290994 bt2 bt2 bt2 candidate 8402 10487 0 0 0

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 1-20 joined\_sorted\_transposed\_maize\_genotypes.txt | head

abph1.20G/G C/C6 C/C C/C03404C/C abph1 AB042260 abph1 candidate 8393 10474 1 1 1

abph1.22A/A A/A8 A/A A/A03892A/A abph1 AB042260 abph1 candidate 8394 10475 0 0 0

ae1.3 T/T5 T/T T/T88979T/T T/T ae1 ae1 ae1 candidate 8395 10477 1 1 1

ae1.4 G/G6 ?/? G/G88968G/G G/G ae1 ae1 ae1 candidate 8396 10478 0 0 0

ae1.5 C/C7 C/C C/C88982C/C C/C ae1 ae1 ae1 candidate 8397 10479 0 0 0

an1.4 C/C2 C/C C/C49850G/G C/C an1 an1 an1 candidate 8398 10481 1 1 1

ba1.6 G/G3 G/G G/G36295G/G G/G ba1 AY753892 ba1 candidate 8399 10482 1 0 1

ba1.9 G/G6 G/G ?/?36266G/G G/G ba1 AY753892 ba1 candidate 8400 10483 0 0 0

bt2.5 C/C3 C/C C/C90049C/C C/C bt2 bt2 bt2 candidate 8401 10486 1 1 1

bt2.7 G/G5 G/G G/G90994G/G A/A bt2 bt2 bt2 candidate 8402 10487 0 0 0

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 5-20 joined\_sorted\_transposed\_maize\_genotypes.txt | head

G/G C/Ch1 C/C42260C/C C/Ch1 candidate 8393 10474 1 1 1

A/A A/Ah1 A/A42260A/A A/Ah1 candidate 8394 10475 0 0 0

T/T T/T T/T T/T T/Tdidate 8395 10477 1 1 1

G/G ?/? G/G G/G G/Gdidate 8396 10478 0 0 0

C/C C/C C/C C/C C/Cdidate 8397 10479 0 0 0

C/C C/C C/C G/G C/Cdidate 8398 10481 1 1 1

G/G G/G G/G53892G/G G/G candidate 8399 10482 1 0 1

G/G G/G ?/?53892G/G G/G candidate 8400 10483 0 0 0

C/C C/C C/C C/C C/Cdidate 8401 10486 1 1 1

G/G G/G G/G G/G A/Adidate 8402 10487 0 0 0

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 10-20 joined\_sorted\_transposed\_maize\_genotypes.txt | head

candidatG/G C/C3 C/C74 C/C C/C 1

candidatA/A A/A4 A/A75 A/A A/A 0

candidatT/T T/T5 T/T77 T/T T/T 1

candidatG/G ?/?6 G/G78 G/G G/G 0

candidatC/C C/C7 C/C79 C/C C/C 0

candidatC/C C/C8 C/C81 G/G C/C 1

candidatG/G G/G9 G/G82 G/G G/G 1

candidatG/G G/G0 ?/?83 G/G G/G 0

candidatC/C C/C1 C/C86 C/C C/C 1

candidatG/G G/G2 G/G87 G/G A/A 0

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ head snp\_position.txt

SNP\_ID cdv\_marker\_id Chromosome Position alt\_pos mult\_positions amplicon cdv\_map\_feature.name gene candidate/random Genaissance\_daa\_id Sequenom\_daa\_id count\_amplicons count\_cmf count\_gene

abph1.20 5976 2 27403404 abph1 AB042260 abph1 candidate 8393 10474 1 1 1

abph1.22 5978 2 27403892 abph1 AB042260 abph1 candidate 8394 10475 0 0 0

ae1.3 6605 5 167889790 ae1 ae1 ae1 candidate 8395 10477 1 1 1

ae1.4 6606 5 167889682 ae1 ae1 ae1 candidate 8396 10478 0 0 0

ae1.5 6607 5 167889821 ae1 ae1 ae1 candidate 8397 10479 0 0 0

an1.4 5982 1 240498509 an1 an1 an1 candidate 8398 10481 1 1 1

ba1.6 3463 3 181362952 ba1 AY753892 ba1 candidate 8399 10482 1 0 1

ba1.9 3466 3 181362666 ba1 AY753892 ba1 candidate 8400 10483 0 0 0

bt2.5 5983 4 66290049 bt2 bt2 bt2 candidate 8401 10486 1 1 1

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 1,3,4,16- joined\_sorted\_transposed\_maize\_genotypes.txt > cut\_joined\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

cut\_joined\_maize.txt maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt UNIX

fang\_et\_al\_genotypes.txt snp\_position.txt teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

joined\_sorted\_transposed\_maize\_genotypes.txt sorted\_snp\_position.txt transpose.awk UNIX\_Assignment.md

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k,1 transposed\_teosinte\_genotypes.txt > sorted\_transposed\_teosinte\_genotypes.txt

sort: invalid number at field start: invalid count at start of ‘,1’

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k1,1 transposed\_teosinte\_genotypes.txt > sorted\_transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

cut\_joined\_maize.txt snp\_position.txt teosinte\_genotypes.txt UNIX\_Assignment.md

fang\_et\_al\_genotypes.txt sorted\_snp\_position.txt transpose.awk UNIX\_Assignment.pdf

joined\_sorted\_transposed\_maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt

maize\_genotypes.txt sorted\_transposed\_teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ join -t $'\t' -1 1 -2 1 sorted\_snp\_position.txt sorted\_transposed\_teosinte\_genotypes.txt > joined\_sorted\_transposed\_teosinte\_genotypes.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

cut\_joined\_maize.txt snp\_position.txt transpose.awk

fang\_et\_al\_genotypes.txt sorted\_snp\_position.txt transposed\_maize\_genotypes.txt

joined\_sorted\_transposed\_maize\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt transposed\_teosinte\_genotypes.txt

joined\_sorted\_transposed\_teosinte\_genotypes.txt sorted\_transposed\_teosinte\_genotypes.txt UNIX\_Assignment.md

maize\_genotypes.txt teosinte\_genotypes.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ cut -f 1,3,4,16- joined\_sorted\_transposed\_teosinte\_genotypes.txt > cut\_joined\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

cut\_joined\_maize.txt snp\_position.txt transposed\_maize\_genotypes.txt

cut\_joined\_teosinte.txt sorted\_snp\_position.txt transposed\_teosinte\_genotypes.txt

fang\_et\_al\_genotypes.txt sorted\_transposed\_maize\_genotypes.txt UNIX\_Assignment.md

joined\_sorted\_transposed\_maize\_genotypes.txt sorted\_transposed\_teosinte\_genotypes.txt UNIX\_Assignment.pdf

joined\_sorted\_transposed\_teosinte\_genotypes.txt teosinte\_genotypes.txt

maize\_genotypes.txt transpose.awk

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ man ls

bash: man: command not found

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

**$ for i in {1..10}; do awk '$2=='$i'' cut\_joined\_teosinte.txt > chr"$i"\_cut\_joined\_teosinte.txt; done**

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr\*

It works just need to do one at a time and put in file ? > -

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignmen t\_1\_JMA/UNIX\_Assignment (master)

$ for i in {1..10}; do awk '$2=='$i'' cut\_joined\_teosinte.txt > chr"$i"\_cut\_joined\_teosinte.txt; done

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ for i in {1..10}; do awk '$2=='$i'' cut\_joined\_maize.txt > chr"$i"\_cut\_joined\_maize.txt; done

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

chr1\_cut\_joined\_maize.txt chr4\_cut\_joined\_teosinte.txt chr9\_cut\_joined\_maize.txt sorted\_snp\_position.txt

chr1\_cut\_joined\_teosinte.txt chr5\_cut\_joined\_maize.txt chr9\_cut\_joined\_teosinte.txt sorted\_transposed\_maize\_genotypes.txt

chr10\_cut\_joined\_maize.txt chr5\_cut\_joined\_teosinte.txt cut\_joined\_maize.txt sorted\_transposed\_teosinte\_genotypes.

chr10\_cut\_joined\_teosinte.txt chr6\_cut\_joined\_maize.txt cut\_joined\_teosinte.txt teosinte\_genotypes.txt

chr2\_cut\_joined\_maize.txt chr6\_cut\_joined\_teosinte.txt fang\_et\_al\_genotypes.txt transpose.awk

chr2\_cut\_joined\_teosinte.txt chr7\_cut\_joined\_maize.txt joined\_sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt

chr3\_cut\_joined\_maize.txt chr7\_cut\_joined\_teosinte.txt joined\_sorted\_transposed\_teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

chr3\_cut\_joined\_teosinte.txt chr8\_cut\_joined\_maize.txt maize\_genotypes.txt UNIX\_Assignment.md

chr4\_cut\_joined\_maize.txt chr8\_cut\_joined\_teosinte.txt snp\_position.txt UNIX\_Assignment.pdf

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3,1n chr1

chr1\_cut\_joined\_maize.txt chr1\_cut\_joined\_teosinte.txt chr10\_cut\_joined\_maize.txt chr10\_cut\_joined\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ for i in {1..10}; do awk '$2=='$i'' cut\_joined\_teosinte.txt > chr"$i"\_teosinte.txt; done

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ for i in {1..10}; do awk '$2=='$i'' cut\_joined\_maize.txt > chr"$i"\_maize.txt; done

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

chr1\_maize.txt chr4\_teosinte.txt chr9\_maize.txt sorted\_snp\_position.txt

chr1\_teosinte.txt chr5\_maize.txt chr9\_teosinte.txt sorted\_transposed\_maize\_genotypes.txt

chr10\_maize.txt chr5\_teosinte.txt cut\_joined\_maize.txt sorted\_transposed\_teosinte\_genotypes.txt

chr10\_teosinte.txt chr6\_maize.txt cut\_joined\_teosinte.txt teosinte\_genotypes.txt

chr2\_maize.txt chr6\_teosinte.txt fang\_et\_al\_genotypes.txt transpose.awk

chr2\_teosinte.txt chr7\_maize.txt joined\_sorted\_transposed\_maize\_genotypes.txt transposed\_maize\_genotypes.txt

chr3\_maize.txt chr7\_teosinte.txt joined\_sorted\_transposed\_teosinte\_genotypes.txt transposed\_teosinte\_genotypes.txt

chr3\_teosinte.txt chr8\_maize.txt maize\_genotypes.txt UNIX\_Assignment.md

chr4\_maize.txt chr8\_teosinte.txt snp\_position.txt UNIX\_Assignment.pdf

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Changes not staged for commit:

(use "git add/rm <file>..." to update what will be committed)

(use "git checkout -- <file>..." to discard changes in working directory)

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr10\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr1\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr2\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr3\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr4\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr5\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr6\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr7\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr8\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr9\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr10\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr1\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr2\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr3\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr4\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr5\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr6\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr7\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr8\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr9\_increasingposition\_maize.txt

no changes added to commit (use "git add" and/or "git commit -a")

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git add Chro\*

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Changes to be committed:

(use "git reset HEAD <file>..." to unstage)

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr10\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr1\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr2\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr3\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr4\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr5\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr6\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr7\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr8\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr9\_decreasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr10\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr1\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr2\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr3\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr4\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr5\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr6\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr7\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr8\_increasingposition\_maize.txt

deleted: Chromosomes of maize sorted by increasing position values/chr9\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git commit -m "\_(chromo)"

[master d120917] \_(chromo)

20 files changed, 1900 deletions(-)

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr10\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr1\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr2\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr3\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr4\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr5\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr6\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr7\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr8\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by decreasing position values, question marke changed to dash/chr9\_decreasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr10\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr1\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr2\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr3\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr4\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr5\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr6\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr7\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr8\_increasingposition\_maize.txt

delete mode 100644 UNIX\_Assignment/Chromosomes of maize sorted by increasing position values/chr9\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git push -u origin master

Counting objects: 3, done.

Delta compression using up to 4 threads.

Compressing objects: 100% (3/3), done.

Writing objects: 100% (3/3), 284 bytes | 284.00 KiB/s, done.

Total 3 (delta 2), reused 0 (delta 0)

remote: Resolving deltas: 100% (2/2), completed with 2 local objects.

To https://github.com/jmanast/Unix\_Assignment\_1\_JMA

dc060fc..d120917 master -> master

Branch master set up to track remote branch master from origin.

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr1\_teosinte.txt | sort -k3 -nr > chr1\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr2\_teosinte.txt | sort -k3 -nr > chr2\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr3\_teosinte.txt | sort -k3 -nr > chr3\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr4\_teosinte.txt | sort -k3 -nr > chr4\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr5\_teosinte.txt | sort -k3 -nr > chr5\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr6\_teosinte.txt | sort -k3 -nr > chr6\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr7\_teosinte.txt | sort -k3 -nr > chr7\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr8\_teosinte.txt | sort -k3 -nr > chr8\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr9\_teosinte.txt | sort -k3 -nr > chr9\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr10\_teosinte.txt | sort -k3 -nr > chr10\_decreasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr1\_maize.txt | sort -k3 -nr > chr1\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr2\_maize.txt | sort -k3 -nr > chr2\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr3\_maize.txt | sort -k3 -nr > chr3\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr4\_maize.txt | sort -k3 -nr > chr4\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr5\_maize.txt | sort -k3 -nr > chr5\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr6\_maize.txt | sort -k3 -nr > chr6\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr7\_maize.txt | sort -k3 -nr > chr7\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr8\_maize.txt | sort -k3 -nr > chr8\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr9\_maize.txt | sort -k3 -nr > chr9\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr9\_maize.txt | sort -k3 -nr > chr10\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sed 's/?/-/g' chr10\_maize.txt | sort -k3 -nr > chr10\_decreasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr1\_teosinte.txt > chr1\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr2\_teosinte.txt > chr2\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr3\_teosinte.txt > chr3\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr4\_teosinte.txt > chr4\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr5\_teosinte.txt > chr5\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr6\_teosinte.txt > chr6\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr7\_teosinte.txt > chr7\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr8\_teosinte.txt > chr8\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr9\_teosinte.txt > chr9\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr10\_teosinte.txt > chr10\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr1\_maize.txt > chr1\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr2\_maize.txt > chr2\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr3\_maize.txt > chr3\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr4\_maize.txt > chr4\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr5\_maize.txt > chr5\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr6\_maize.txt > chr6\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr7\_maize.txt > chr7\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr8\_maize.txt > chr8\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr9\_maize.txt > chr9\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ sort -k3 -n chr10\_maize.txt > chr10\_increasingposition\_maize.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Untracked files:

(use "git add <file>..." to include in what will be committed)

Maize chromosomes sorted by decreasing position value, question mark changed to dash/

Maize chromosomes sorted by increasing position value/

Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/

Teosinte chromosomes sorted by increasing position values/

nothing added to commit but untracked files present (use "git add" to track)

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git add Maize\*

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr10\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr1\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr2\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr3\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr4\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr5\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr6\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr7\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr8\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr9\_increasingposition\_maize.txt.

The file will have its original line endings in your working directory.

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Changes to be committed:

(use "git reset HEAD <file>..." to unstage)

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr10\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr1\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr2\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr3\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr4\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr5\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr6\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr7\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr8\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr9\_increasingposition\_maize.txt

Untracked files:

(use "git add <file>..." to include in what will be committed)

Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/

Teosinte chromosomes sorted by increasing position values/

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git add Teo\*

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr10\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr1\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr2\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr3\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr4\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr5\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr6\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr7\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr8\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

warning: LF will be replaced by CRLF in UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr9\_increasingposition\_teosinte.txt.

The file will have its original line endings in your working directory.

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git staus

git: 'staus' is not a git command. See 'git --help'.

The most similar command is

status

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git status

On branch master

Your branch is up-to-date with 'origin/master'.

Changes to be committed:

(use "git reset HEAD <file>..." to unstage)

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr10\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr1\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr2\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr3\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr4\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr5\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr6\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr7\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr8\_increasingposition\_maize.txt

new file: Maize chromosomes sorted by increasing position value/chr9\_increasingposition\_maize.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr10\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr1\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr2\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr3\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr4\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr5\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr6\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr7\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr8\_increasingposition\_teosinte.txt

new file: Teosinte chromosomes sorted by increasing position values/chr9\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git commit -m "final product!(yes)"

bash: !: event not found

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git commit -m "final product (\*.txt)"

[master 0637d75] final product (\*.txt)

40 files changed, 3800 insertions(+)

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr10\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr1\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr2\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr3\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr4\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr5\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr6\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr7\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr8\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Maize chromosomes sorted by increasing position value/chr9\_increasingposition\_maize.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr10\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr1\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr2\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr3\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr4\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr5\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr6\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr7\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr8\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by decreasing position value, question mark changed to dash/chr9\_decreasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr10\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr1\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr2\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr3\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr4\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr5\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr6\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr7\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr8\_increasingposition\_teosinte.txt

create mode 100644 UNIX\_Assignment/Teosinte chromosomes sorted by increasing position values/chr9\_increasingposition\_teosinte.txt

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ git push -u origin master

Counting objects: 47, done.

Delta compression using up to 4 threads.

Compressing objects: 100% (47/47), done.

Writing objects: 100% (47/47), 2.29 MiB | 901.00 KiB/s, done.

Total 47 (delta 40), reused 0 (delta 0)

remote: Resolving deltas: 100% (40/40), completed with 2 local objects.

To https://github.com/jmanast/Unix\_Assignment\_1\_JMA

d120917..0637d75 master -> master

Branch master set up to track remote branch master from origin.

owner@DESKTOP-SIR8KL0 MINGW64 ~/Desktop/BCB\_546X/BCB546X-Fall2017/Unix\_Assignment\_1\_JMA/UNIX\_Assignment (master)

$ ls

chr1\_maize.txt cut\_joined\_maize.txt

chr1\_teosinte.txt cut\_joined\_teosinte.txt

chr10\_maize.txt fang\_et\_al\_genotypes.txt

chr10\_teosinte.txt joined\_sorted\_transposed\_maize\_genotypes.txt

chr2\_maize.txt joined\_sorted\_transposed\_teosinte\_genotypes.txt

chr2\_teosinte.txt 'Maize chromosomes sorted by decreasing position value, question mark changed to dash'/

chr3\_maize.txt 'Maize chromosomes sorted by increasing position value'/

chr3\_teosinte.txt maize\_genotypes.txt

chr4\_maize.txt snp\_position.txt

chr4\_teosinte.txt sorted\_snp\_position.txt

chr5\_maize.txt sorted\_transposed\_maize\_genotypes.txt

chr5\_teosinte.txt sorted\_transposed\_teosinte\_genotypes.txt

chr6\_maize.txt 'Teosinte chromosomes sorted by decreasing position value, question mark changed to dash'/

chr6\_teosinte.txt 'Teosinte chromosomes sorted by increasing position values'/

chr7\_maize.txt teosinte\_genotypes.txt

chr7\_teosinte.txt transpose.awk

chr8\_maize.txt transposed\_maize\_genotypes.txt

chr8\_teosinte.txt transposed\_teosinte\_genotypes.txt