curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/pan\_troglodytes/pep/Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 10.6M 100 10.6M 0 0 3202k 0 0:00:03 0:00:03 --:--:-- 3202k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa > chimp\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "cntnap2" -A 1 chimp\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 chimp\_unwrap.fa

>ENSPTRP00000064715.1 pep chromosome:Pan\_tro\_3.0:7:150621934:152928814:1 gene:ENSPTRG00000048103.1 transcript:ENSPTRT00000097270.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding gene\_symbol:**CNTNAP2** description:contactin associated protein 2 [Source:VGNC Symbol;Acc:VGNC:57683]

MQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCDEPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSDHYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNWKPYHQDGNIWAFPGNVNSDGVVRHELQHPIIARYVRIVPLDWNEEGRIGLRVEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVIALKFKTSESEGVILHGEGQQGDYITLELKKAKLVLSLNLGSNQLGPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFRTNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNGINITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPGRLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVGVHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDGDEASAVRTNSPLQVKTGKKYFFGGFLNQMNNSSHSVLQPSFQGCMQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCEHGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQTSNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVGYNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLLNTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPKYYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKLSVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFKTLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVRSPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRLELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFISGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKDVGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQEEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLGGTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSYHLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLSRVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPMSSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVIAVVIFTILCTLVFLIRYMFRHKGTYHTNEAKGAESAESADAAIMNNDPNFTETIDESKKEWLI

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 chimp\_unwrap.fa > chimp\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ ls

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa chimp\_unwrap\_gene.fa

chimp\_unwrap.fa chimpanzee\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ rm chimpanzee\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/cebus\_capucinus/pep/Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Gorilla\_gorilla.gorGor4.pep.all.fa.gz > gorilla\_unwrap.fa

awk: fatal: cannot open file `Gorilla\_gorilla.gorGor4.pep.all.fa.gz' for reading (No such file or directory)

**tab1020@js-157-183**:**~/finalproj**$ ls

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa chimp\_unwrap.fa gorilla\_unwrap\_gene.fa

**Gorilla\_gorilla.gorGor4.pep.all.fa.gz.gz** chimp\_unwrap\_gene.fa monkey\_unwrap.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa gorilla\_unwrap.fa monkey\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Gorilla\_gorilla.gorGor4.pep.all.fa.gz.gz

**tab1020@js-157-183**:**~/finalproj**$ ls

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa chimp\_unwrap.fa gorilla\_unwrap\_gene.fa

**Gorilla\_gorilla.gorGor4.pep.all.fa.gz** chimp\_unwrap\_gene.fa monkey\_unwrap.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa gorilla\_unwrap.fa monkey\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Gorilla\_gorilla.gorGor4.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ ls

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa chimp\_unwrap.fa gorilla\_unwrap\_gene.fa

Gorilla\_gorilla.gorGor4.pep.all.fa chimp\_unwrap\_gene.fa monkey\_unwrap.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa gorilla\_unwrap.fa monkey\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Gorilla\_gorilla.gorGor4.pep.all.fa > gorilla\_unwrap1.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 gorilla\_unwrap1.fa > gorilla\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ cat gorilla\_unwrap\_gene.fa

>ENSGGOP00000038200.1 pep chromosome:gorGor4:7:145694640:148024464:1 gene:ENSGGOG00000037296.1 transcript:ENSGGOT00000047655.1 gene\_biotype:protein\_coding transcript\_biotype:protein\_coding gene\_symbol:CNTNAP2 description:contactin associated protein 2 [Source:HGNC Symbol;Acc:HGNC:13830]

MQAAPRAGCGAALLLWILSSCLCRAWTAPSTSQKCDEPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSDHYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNWKPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNGEGRIGLRSEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVIALKFKTSESEGVILHGEGQQGDYITLELKKAKLVLSLNLGSNQLGPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFRTNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNGINITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPGRLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVGVHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDGDEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQGCMQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCEHGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQTSNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVGYNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLLNTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPKYYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKLSVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFKTLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVRSPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRLELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFISGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKDVGAFFEEGMWLRYNFQAPATNARDSSSRADNAPDQQNSHPDLAQEEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLGGTREPYNIDIDQRNMANGQPHSVNITRHEKTIFLKLDHYPSVSYHLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLSRVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPMSSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVIAVVIFTILCTLVFLIRYMFRHKGTYHTNEAKGAESAESADAAIMNNDPNFTETIDESKKEWLI

**tab1020@js-157-183**:**~/finalproj**$ ls

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa chimp\_unwrap.fa gorilla\_unwrap1.fa monkey\_unwrap\_gene.fa

Gorilla\_gorilla.gorGor4.pep.all.fa chimp\_unwrap\_gene.fa gorilla\_unwrap\_gene.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa gorilla\_unwrap.fa monkey\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ rm gorilla\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ ls

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa chimp\_unwrap.fa gorilla\_unwrap\_gene.fa

Gorilla\_gorilla.gorGor4.pep.all.fa chimp\_unwrap\_gene.fa monkey\_unwrap.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa gorilla\_unwrap1.fa monkey\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/homo\_sapiens/pep/Homo\_sapiens.GRCh38.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 13.5M 100 13.5M 0 0 4248k 0 0:00:03 0:00:03 --:--:-- 4248k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Homo\_sapiens.GRCh38.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Homo\_sapiens.GRCh38.pep.all.fa > human\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 human\_unwrap.fa > human\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/pongo\_abelii/pep/Pongo\_abelii.PPYG2.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 7275k 100 7275k 0 0 2717k 0 0:00:02 0:00:02 --:--:-- 2716k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Pongo\_abelii.PPYG2.pep.all.fa.gz > orangutan\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 orangutan\_unwrap.fa > orangutan\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/nomascus\_leucogenys/pep/Nomascus\_leucogenys.Nleu\_3.0.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 9252k 100 9252k 0 0 3043k 0 0:00:03 0:00:03 --:--:-- 3043k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Nomascus\_leucogenys.Nleu\_3.0.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Nomascus\_leucogenys.Nleu\_3.0.pep.all.fa > gibbon\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 gibbon\_unwrap.fa > gibbon\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/amazona\_collaria/pep/Amazona\_collaria.ASM394721v1.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 7157k 100 7157k 0 0 2641k 0 0:00:02 0:00:02 --:--:-- 2641k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Amazona\_collaria.ASM394721v1.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Amazona\_collaria.ASM394721v1.pep.all.fa > parrot\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 parrot\_unwrap.fa > parrot\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/carlito\_syrichta/pep/Carlito\_syrichta.Tarsius\_syrichta-2.0.1.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 7838k 100 7838k 0 0 2698k 0 0:00:02 0:00:02 --:--:-- 2699k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Carlito\_syrichta.Tarsius\_syrichta-2.0.1.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Carlito\_syrichta.Tarsius\_syrichta-2.0.1.pep.all.fa > tarsier\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 tarsier\_unwrap.fa > tarsier\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/cavia\_aperea/pep/Cavia\_aperea.CavAp1.0.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 5442k 100 5442k 0 0 1992k 0 0:00:02 0:00:02 --:--:-- 1991k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d "Cavia\_aperea.CavAp1.0.pep.all.fa.gz"

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Cavia\_aperea.CavAp1.0.pep.all.fa > guineapig\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 guineapig\_unwrap.fa > guineapig\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ curl -LO ftp://ftp.ensembl.org/pub/release-100/fasta/mus\_musculus/pep/Mus\_musculus.GRCm38.pep.all.fa.gz

% Total % Received % Xferd Average Speed Time Time Time Current

Dload Upload Total Spent Left Speed

100 11.1M 100 11.1M 0 0 3918k 0 0:00:02 0:00:02 --:--:-- 3918k

**tab1020@js-157-183**:**~/finalproj**$ gzip -d Mus\_musculus.GRCm38.pep.all.fa.gz

**tab1020@js-157-183**:**~/finalproj**$ awk '{if(NR==1) {print $0} else {if($0 ~ /^>/) {print "\n"$0} else {printf $0}}}' Mus\_musculus.GRCm38.pep.all.fa > mouse\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 mouse\_unwrap.fa > mouse\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ ls

Amazona\_collaria.ASM394721v1.pep.all.fa chimp\_unwrap.fa monkey\_unwrap.fa

Carlito\_syrichta.Tarsius\_syrichta-2.0.1.pep.all.fa chimp\_unwrap\_gene.fa monkey\_unwrap\_gene.fa

Cavia\_aperea.CavAp1.0.pep.all.fa gibbon\_unwrap.fa mouse\_unwrap.fa

Cebus\_capucinus.Cebus\_imitator-1.0.pep.all.fa gibbon\_unwrap\_gene.fa mouse\_unwrap\_gene.fa

Gorilla\_gorilla.gorGor4.pep.all.fa gorilla\_unwrap1.fa orangutan\_unwrap.fa

Homo\_sapiens.GRCh38.pep.all.fa gorilla\_unwrap\_gene.fa orangutan\_unwrap\_gene.fa

Mus\_musculus.GRCm38.pep.all.fa guineapig\_gene.fa parrot\_unwrap.fa

Nomascus\_leucogenys.Nleu\_3.0.pep.all.fa guineapig\_unwrap.fa parrot\_unwrap\_gene.fa

Pan\_troglodytes.Pan\_tro\_3.0.pep.all.fa human\_unwrap.fa tarsier\_unwrap.fa

Pongo\_abelii.PPYG2.pep.all.fa human\_unwrap\_gene.fa tarsier\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">chimp\_" ++i; next}{print}' chimp\_unwrap\_gene.fa > header\_chimp.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">gibbon\_" ++i; next}{print}' gibbon\_unwrap\_gene.fa > header\_gibbon.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">gorilla\_" ++i; next}{print}' gorilla\_unwrap\_gene.fa > header\_gorilla.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">guineapig\_" ++i; next}{print}' guineapig\_gene.fa > header\_guineapig.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">human\_" ++i' next}{print}' human\_unwrap\_gene.fa > header\_human.fa

> ^C

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">human\_" ++i; next}{print}' human\_unwrap\_gene.fa > header\_human.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">monkey\_" ++i; next}{print}' monkey\_unwrap\_gene.fa > header\_monkey.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">mouse\_" ++i; next}{print}' mouse\_unwrap\_gene.fa > header\_mouse.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">orangutan\_" ++i; next}{print}' orangutan\_unwrap\_gene.fa > header\_orangutan.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">parrot\_" ++i; next}{print}' parrot\_unwrap\_gene.fa > header\_parrot.fa

**tab1020@js-157-183**:**~/finalproj**$ awk '/^>/{print ">tarsier\_" ++i; next}{print}' tarsier\_unwrap\_gene.fa > header\_tarsier.fa

**tab1020@js-157-183**:**~/finalproj**$ header\_chimp.fa, header\_gibbon.fa, header\_gorilla.fa, header\_guineapig.fa, header\_human.fa, header\_monkey.fa, header\_mouse.fa, header\_orangutan.fa, header\_parrot.fa, header\_tarsier.fa > CNTNAP2\_all.fa

header\_chimp.fa,: command not found

**tab1020@js-157-183**:**~/finalproj**$ cat header\_chimp.fa header\_gibbon.fa header\_gorilla.fa header\_guineapig.fa header\_human.fa header\_monkey.fa header\_mouse.fa header\_orangutan.fa header\_parrot.fa header\_tarsier.fa > CNTNAP2\_all.fa

**tab1020@js-157-183**:**~/finalproj**$ mafft --auto CNTNAP2\_all.fa > CNTNAP2\_mafft.fa

Command 'mafft' not found, but can be installed with:

apt install mafft

**tab1020@js-157-183**:**~/finalproj**$ apt install mafft

E: Could not open lock file /var/lib/dpkg/lock-frontend - open (13: Permission denied)

E: Unable to acquire the dpkg frontend lock (/var/lib/dpkg/lock-frontend), are you root?

**tab1020@js-157-183**:**~/finalproj**$ sudo apt install mafft

Reading package lists... Done

Building dependency tree

Reading state information... Done

The following additional packages will be installed:

blast2 fonts-lato javascript-common libjs-jquery libruby2.5 lynx lynx-common ncbi-blast+ ncbi-blast+-legacy ncbi-data rake

ruby ruby-did-you-mean ruby-minitest ruby-net-telnet ruby-power-assert ruby-test-unit ruby2.5 rubygems-integration unzip zip

Suggested packages:

apache2 | lighttpd | httpd ri ruby-dev bundler

The following NEW packages will be installed:

blast2 fonts-lato javascript-common libjs-jquery libruby2.5 lynx lynx-common mafft ncbi-blast+ ncbi-blast+-legacy ncbi-data

rake ruby ruby-did-you-mean ruby-minitest ruby-net-telnet ruby-power-assert ruby-test-unit ruby2.5 rubygems-integration unzip

zip

0 upgraded, 22 newly installed, 0 to remove and 0 not upgraded.

Need to get 22.1 MB of archives.

After this operation, 111 MB of additional disk space will be used.

Do you want to continue? [Y/n] Y

Get:1 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 fonts-lato all 2.0-2 [2698 kB]

Get:2 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 ncbi-data all 6.1.20170106-2 [3645 kB]

Get:3 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 ncbi-blast+ amd64 2.6.0-1 [9446 kB]

Get:4 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 ncbi-blast+-legacy all 2.6.0-1 [4754 B]

Get:5 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 blast2 all 1:2.6.0-1 [4246 B]

Get:6 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 javascript-common all 11 [6066 B]

Get:7 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 libjs-jquery all 3.2.1-1 [152 kB]

Get:8 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 rubygems-integration all 1.11 [4994 B]

Get:9 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 ruby2.5 amd64 2.5.1-1ubuntu1.6 [48.6 kB]

Get:10 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby amd64 1:2.5.1 [5712 B]

Get:11 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 rake all 12.3.1-1ubuntu0.1 [44.9 kB]

Get:12 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby-did-you-mean all 1.2.0-2 [9700 B]

Get:13 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby-minitest all 5.10.3-1 [38.6 kB]

Get:14 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby-net-telnet all 0.1.1-2 [12.6 kB]

Get:15 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby-power-assert all 0.3.0-1 [7952 B]

Get:16 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ruby-test-unit all 3.2.5-1 [61.1 kB]

Get:17 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 libruby2.5 amd64 2.5.1-1ubuntu1.6 [3069 kB]

Get:18 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 lynx-common all 2.8.9dev16-3 [940 kB]

Get:19 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 mafft amd64 7.310-1 [912 kB]

Get:20 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 unzip amd64 6.0-21ubuntu1 [167 kB]

Get:21 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 zip amd64 3.0-11build1 [167 kB]

Get:22 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 lynx amd64 2.8.9dev16-3 [628 kB]

Fetched 22.1 MB in 8s (2883 kB/s)

Selecting previously unselected package fonts-lato.

(Reading database ... 177482 files and directories currently installed.)

Preparing to unpack .../00-fonts-lato\_2.0-2\_all.deb ...

Unpacking fonts-lato (2.0-2) ...

Selecting previously unselected package ncbi-data.

Preparing to unpack .../01-ncbi-data\_6.1.20170106-2\_all.deb ...

Unpacking ncbi-data (6.1.20170106-2) ...

Selecting previously unselected package ncbi-blast+.

Preparing to unpack .../02-ncbi-blast+\_2.6.0-1\_amd64.deb ...

Unpacking ncbi-blast+ (2.6.0-1) ...

Selecting previously unselected package ncbi-blast+-legacy.

Preparing to unpack .../03-ncbi-blast+-legacy\_2.6.0-1\_all.deb ...

Unpacking ncbi-blast+-legacy (2.6.0-1) ...

Selecting previously unselected package blast2.

Preparing to unpack .../04-blast2\_1%3a2.6.0-1\_all.deb ...

Unpacking blast2 (1:2.6.0-1) ...

Selecting previously unselected package javascript-common.

Preparing to unpack .../05-javascript-common\_11\_all.deb ...

Unpacking javascript-common (11) ...

Selecting previously unselected package libjs-jquery.

Preparing to unpack .../06-libjs-jquery\_3.2.1-1\_all.deb ...

Unpacking libjs-jquery (3.2.1-1) ...

Selecting previously unselected package rubygems-integration.

Preparing to unpack .../07-rubygems-integration\_1.11\_all.deb ...

Unpacking rubygems-integration (1.11) ...

Selecting previously unselected package ruby2.5.

Preparing to unpack .../08-ruby2.5\_2.5.1-1ubuntu1.6\_amd64.deb ...

Unpacking ruby2.5 (2.5.1-1ubuntu1.6) ...

Selecting previously unselected package ruby.

Preparing to unpack .../09-ruby\_1%3a2.5.1\_amd64.deb ...

Unpacking ruby (1:2.5.1) ...

Selecting previously unselected package rake.

Preparing to unpack .../10-rake\_12.3.1-1ubuntu0.1\_all.deb ...

Unpacking rake (12.3.1-1ubuntu0.1) ...

Selecting previously unselected package ruby-did-you-mean.

Preparing to unpack .../11-ruby-did-you-mean\_1.2.0-2\_all.deb ...

Unpacking ruby-did-you-mean (1.2.0-2) ...

Selecting previously unselected package ruby-minitest.

Preparing to unpack .../12-ruby-minitest\_5.10.3-1\_all.deb ...

Unpacking ruby-minitest (5.10.3-1) ...

Selecting previously unselected package ruby-net-telnet.

Preparing to unpack .../13-ruby-net-telnet\_0.1.1-2\_all.deb ...

Unpacking ruby-net-telnet (0.1.1-2) ...

Selecting previously unselected package ruby-power-assert.

Preparing to unpack .../14-ruby-power-assert\_0.3.0-1\_all.deb ...

Unpacking ruby-power-assert (0.3.0-1) ...

Selecting previously unselected package ruby-test-unit.

Preparing to unpack .../15-ruby-test-unit\_3.2.5-1\_all.deb ...

Unpacking ruby-test-unit (3.2.5-1) ...

Selecting previously unselected package libruby2.5:amd64.

Preparing to unpack .../16-libruby2.5\_2.5.1-1ubuntu1.6\_amd64.deb ...

Unpacking libruby2.5:amd64 (2.5.1-1ubuntu1.6) ...

Selecting previously unselected package lynx-common.

Preparing to unpack .../17-lynx-common\_2.8.9dev16-3\_all.deb ...

Unpacking lynx-common (2.8.9dev16-3) ...

Selecting previously unselected package mafft.

Preparing to unpack .../18-mafft\_7.310-1\_amd64.deb ...

Unpacking mafft (7.310-1) ...

Selecting previously unselected package unzip.

Preparing to unpack .../19-unzip\_6.0-21ubuntu1\_amd64.deb ...

Unpacking unzip (6.0-21ubuntu1) ...

Selecting previously unselected package zip.

Preparing to unpack .../20-zip\_3.0-11build1\_amd64.deb ...

Unpacking zip (3.0-11build1) ...

Selecting previously unselected package lynx.

Preparing to unpack .../21-lynx\_2.8.9dev16-3\_amd64.deb ...

Unpacking lynx (2.8.9dev16-3) ...

Setting up libjs-jquery (3.2.1-1) ...

Setting up mafft (7.310-1) ...

Setting up unzip (6.0-21ubuntu1) ...

Setting up zip (3.0-11build1) ...

Setting up fonts-lato (2.0-2) ...

Setting up ruby-did-you-mean (1.2.0-2) ...

Setting up ncbi-data (6.1.20170106-2) ...

Setting up ruby-net-telnet (0.1.1-2) ...

Setting up rubygems-integration (1.11) ...

Setting up javascript-common (11) ...

Setting up ruby-minitest (5.10.3-1) ...

Setting up lynx-common (2.8.9dev16-3) ...

Setting up ruby-power-assert (0.3.0-1) ...

Setting up lynx (2.8.9dev16-3) ...

update-alternatives: using /usr/bin/lynx to provide /usr/bin/www-browser (www-browser) in auto mode

Setting up ncbi-blast+ (2.6.0-1) ...

Setting up ncbi-blast+-legacy (2.6.0-1) ...

Setting up blast2 (1:2.6.0-1) ...

Setting up rake (12.3.1-1ubuntu0.1) ...

Setting up ruby2.5 (2.5.1-1ubuntu1.6) ...

Setting up ruby (1:2.5.1) ...

Setting up ruby-test-unit (3.2.5-1) ...

Setting up libruby2.5:amd64 (2.5.1-1ubuntu1.6) ...

Processing triggers for mime-support (3.60ubuntu1) ...

Processing triggers for libc-bin (2.27-3ubuntu1) ...

Processing triggers for man-db (2.8.3-2ubuntu0.1) ...

Processing triggers for hicolor-icon-theme (0.17-2) ...

Processing triggers for fontconfig (2.12.6-0ubuntu2) ...

**tab1020@js-157-183**:**~/finalproj**$ mafft --auto CNTNAP2\_all.fa > CNTNAP2\_mafft.fa

All-to-all alignment.

tbfast-pair (aa) Version 7.310 alg=L, model=BLOSUM62, 2.00, -0.10, +0.10, noshift, amax=0.0

0 thread(s)

Loading 'hat3.seed' ...

done.

Writing hat3 for iterative refinement

Gap Penalty = -1.53, +0.00, +0.00

treein = 0

compacttree = 0

Constructing a UPGMA tree ...

0 / 11

done.

Progressive alignment ...

STEP 10 /10 c

done.

tbfast (aa) Version 7.310 alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0

0 thread(s)

minimumweight = 0.000010

autosubalignment = 0.000000

nthread = 0

randomseed = 0

blosum 62 / kimura 200

poffset = 0

niter = 16

sueff\_global = 0.100000

Loading 'hat3' ... done.

0 / 11

Segment 1/ 1 1-1355

STEP 002-009-1 identical.

Converged.

done

dvtditr (aa) Version 7.310 alg=A, model=BLOSUM62, 1.53, -0.00, -0.00, noshift, amax=0.0

0 thread(s)

Strategy:

L-INS-i (Probably most accurate, very slow)

Iterative refinement method (<16) with LOCAL pairwise alignment information

If unsure which option to use, try 'mafft --auto input > output'.

For more information, see 'mafft --help', 'mafft --man' and the mafft page.

The default gap scoring scheme has been changed in version 7.110 (2013 Oct).

It tends to insert more gaps into gap-rich regions than previous versions.

To disable this change, add the --leavegappyregion option.

**tab1020@js-157-183**:**~/finalproj**$ iqtree -s CNTNAP2\_mafft.fa -m LG -bb 1000 -pre speech

Command 'iqtree' not found, but can be installed with:

apt install iqtree

Please ask your administrator.

**tab1020@js-157-183**:**~/finalproj**$ apt install iqtree

E: Could not open lock file /var/lib/dpkg/lock-frontend - open (13: Permission denied)

E: Unable to acquire the dpkg frontend lock (/var/lib/dpkg/lock-frontend), are you root?

**tab1020@js-157-183**:**~/finalproj**$ sudo apt install iqtree

Reading package lists... Done

Building dependency tree

Reading state information... Done

The following additional packages will be installed:

ibverbs-providers libfabric1 libhwloc-plugins libhwloc5 libibverbs1 libnl-3-200 libnl-route-3-200 libopenmpi2

libpsm-infinipath1 librdmacm1 ocl-icd-libopencl1 openmpi-bin openmpi-common

Suggested packages:

libhwloc-contrib-plugins opencl-icd

The following NEW packages will be installed:

ibverbs-providers iqtree libfabric1 libhwloc-plugins libhwloc5 libibverbs1 libnl-3-200 libnl-route-3-200 libopenmpi2

libpsm-infinipath1 librdmacm1 ocl-icd-libopencl1 openmpi-bin openmpi-common

0 upgraded, 14 newly installed, 0 to remove and 0 not upgraded.

Need to get 6057 kB of archives.

After this operation, 28.0 MB of additional disk space will be used.

Do you want to continue? [Y/n] y

Get:1 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 libnl-3-200 amd64 3.2.29-0ubuntu3 [52.8 kB]

Get:2 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 libnl-route-3-200 amd64 3.2.29-0ubuntu3 [146 kB]

Get:3 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 libibverbs1 amd64 17.1-1ubuntu0.2 [44.4 kB]

Get:4 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 ibverbs-providers amd64 17.1-1ubuntu0.2 [160 kB]

Get:5 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 libpsm-infinipath1 amd64 3.3+20.604758e7-5 [174 kB]

Get:6 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic-updates/main amd64 librdmacm1 amd64 17.1-1ubuntu0.2 [56.1 kB]

Get:7 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 libfabric1 amd64 1.5.3-1 [302 kB]

Get:8 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 libhwloc5 amd64 1.11.9-1 [105 kB]

Get:9 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/main amd64 ocl-icd-libopencl1 amd64 2.2.11-1ubuntu1 [30.3 kB]

Get:10 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 libhwloc-plugins amd64 1.11.9-1 [12.5 kB]

Get:11 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 libopenmpi2 amd64 2.1.1-8 [2056 kB]

Get:12 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 iqtree amd64 1.6.1+dfsg-1 [2689 kB]

Get:13 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 openmpi-common all 2.1.1-8 [140 kB]

Get:14 http://zone-r1.clouds.archive.ubuntu.com/ubuntu bionic/universe amd64 openmpi-bin amd64 2.1.1-8 [88.2 kB]

Fetched 6057 kB in 1s (5876 kB/s)

Selecting previously unselected package libnl-3-200:amd64.

(Reading database ... 179214 files and directories currently installed.)

Preparing to unpack .../00-libnl-3-200\_3.2.29-0ubuntu3\_amd64.deb ...

Unpacking libnl-3-200:amd64 (3.2.29-0ubuntu3) ...

Selecting previously unselected package libnl-route-3-200:amd64.

Preparing to unpack .../01-libnl-route-3-200\_3.2.29-0ubuntu3\_amd64.deb ...

Unpacking libnl-route-3-200:amd64 (3.2.29-0ubuntu3) ...

Selecting previously unselected package libibverbs1:amd64.

Preparing to unpack .../02-libibverbs1\_17.1-1ubuntu0.2\_amd64.deb ...

Unpacking libibverbs1:amd64 (17.1-1ubuntu0.2) ...

Selecting previously unselected package ibverbs-providers:amd64.

Preparing to unpack .../03-ibverbs-providers\_17.1-1ubuntu0.2\_amd64.deb ...

Unpacking ibverbs-providers:amd64 (17.1-1ubuntu0.2) ...

Selecting previously unselected package libpsm-infinipath1.

Preparing to unpack .../04-libpsm-infinipath1\_3.3+20.604758e7-5\_amd64.deb ...

Unpacking libpsm-infinipath1 (3.3+20.604758e7-5) ...

Selecting previously unselected package librdmacm1:amd64.

Preparing to unpack .../05-librdmacm1\_17.1-1ubuntu0.2\_amd64.deb ...

Unpacking librdmacm1:amd64 (17.1-1ubuntu0.2) ...

Selecting previously unselected package libfabric1.

Preparing to unpack .../06-libfabric1\_1.5.3-1\_amd64.deb ...

Unpacking libfabric1 (1.5.3-1) ...

Selecting previously unselected package libhwloc5:amd64.

Preparing to unpack .../07-libhwloc5\_1.11.9-1\_amd64.deb ...

Unpacking libhwloc5:amd64 (1.11.9-1) ...

Selecting previously unselected package ocl-icd-libopencl1:amd64.

Preparing to unpack .../08-ocl-icd-libopencl1\_2.2.11-1ubuntu1\_amd64.deb ...

Unpacking ocl-icd-libopencl1:amd64 (2.2.11-1ubuntu1) ...

Selecting previously unselected package libhwloc-plugins.

Preparing to unpack .../09-libhwloc-plugins\_1.11.9-1\_amd64.deb ...

Unpacking libhwloc-plugins (1.11.9-1) ...

Selecting previously unselected package libopenmpi2:amd64.

Preparing to unpack .../10-libopenmpi2\_2.1.1-8\_amd64.deb ...

Unpacking libopenmpi2:amd64 (2.1.1-8) ...

Selecting previously unselected package iqtree.

Preparing to unpack .../11-iqtree\_1.6.1+dfsg-1\_amd64.deb ...

Unpacking iqtree (1.6.1+dfsg-1) ...

Selecting previously unselected package openmpi-common.

Preparing to unpack .../12-openmpi-common\_2.1.1-8\_all.deb ...

Unpacking openmpi-common (2.1.1-8) ...

Selecting previously unselected package openmpi-bin.

Preparing to unpack .../13-openmpi-bin\_2.1.1-8\_amd64.deb ...

Unpacking openmpi-bin (2.1.1-8) ...

Setting up libhwloc5:amd64 (1.11.9-1) ...

Setting up libpsm-infinipath1 (3.3+20.604758e7-5) ...

update-alternatives: using /usr/lib/libpsm1/libpsm\_infinipath.so.1.16 to provide /usr/lib/x86\_64-linux-gnu/libpsm\_infinipath.so.1 (libpsm\_infinipath.so.1) in auto mode

Setting up openmpi-common (2.1.1-8) ...

Setting up ocl-icd-libopencl1:amd64 (2.2.11-1ubuntu1) ...

Setting up libnl-3-200:amd64 (3.2.29-0ubuntu3) ...

Setting up libnl-route-3-200:amd64 (3.2.29-0ubuntu3) ...

Setting up libhwloc-plugins (1.11.9-1) ...

Setting up libibverbs1:amd64 (17.1-1ubuntu0.2) ...

Setting up librdmacm1:amd64 (17.1-1ubuntu0.2) ...

Setting up ibverbs-providers:amd64 (17.1-1ubuntu0.2) ...

Setting up libfabric1 (1.5.3-1) ...

Setting up libopenmpi2:amd64 (2.1.1-8) ...

Setting up iqtree (1.6.1+dfsg-1) ...

Setting up openmpi-bin (2.1.1-8) ...

update-alternatives: using /usr/bin/mpirun.openmpi to provide /usr/bin/mpirun (mpirun) in auto mode

Processing triggers for man-db (2.8.3-2ubuntu0.1) ...

Processing triggers for libc-bin (2.27-3ubuntu1) ...

**tab1020@js-157-183**:**~/finalproj**$ iqtree -s CNTNAP2\_mafft.fa -m LG -bb 1000 -pre speech

IQ-TREE multicore version 1.6.1 for Linux 64-bit built Feb 16 2018

Developed by Bui Quang Minh, Nguyen Lam Tung, Olga Chernomor,

Heiko Schmidt, Dominik Schrempf, Michael Woodhams.

Host: js-157-183.jetstream-cloud.org (AVX2, FMA3, 118 GB RAM)

Command: iqtree -s CNTNAP2\_mafft.fa -m LG -bb 1000 -pre speech

Seed: 816253 (Using SPRNG - Scalable Parallel Random Number Generator)

Time: Wed May 13 16:12:48 2020

Kernel: AVX+FMA - 1 threads (44 CPU cores detected)

HINT: Use -nt option to specify number of threads because your CPU has 44 cores!

HINT: -nt AUTO will automatically determine the best number of threads to use.

Reading alignment file CNTNAP2\_mafft.fa ... Fasta format detected

Alignment most likely contains protein sequences

Alignment has 11 sequences with 1354 columns, 314 distinct patterns

5 parsimony-informative, 215 singleton sites, 1134 constant sites

Gap/Ambiguity Composition p-value

1 chimp\_1 1.70% passed 100.00%

2 gorilla\_1 1.70% passed 100.00%

3 human\_1 91.21% failed 4.31%

4 human\_2 1.70% passed 100.00%

5 human\_3 71.20% passed 96.65%

6 human\_4 92.02% passed 74.56%

7 human\_5 75.85% passed 79.49%

8 human\_6 75.85% passed 79.49%

9 human\_7 92.02% passed 74.56%

10 monkey\_1 7.24% passed 100.00%

11 parrot\_1 0.74% passed 99.62%

WARNING: 6 sequences contain more than 50% gaps/ambiguity

\*\*\*\* TOTAL 46.48% 1 sequences failed composition chi2 test (p-value<5%; df=19)

NOTE: human\_7 is identical to human\_4 but kept for subsequent analysis

NOTE: human\_6 is identical to human\_5 but kept for subsequent analysis

Create initial parsimony tree by phylogenetic likelihood library (PLL)... 0.001 seconds

Generating 1000 samples for ultrafast bootstrap (seed: 816253)...

NOTE: 1 MB RAM (0 GB) is required!

Estimate model parameters (epsilon = 0.100)

1. Initial log-likelihood: -5315.044

Optimal log-likelihood: -5292.446

Parameters optimization took 1 rounds (0.012 sec)

Computing ML distances based on estimated model parameters... 0.004 sec

WARNING: Some pairwise ML distances are too long (saturated)

Computing BIONJ tree...

0.000 seconds

Log-likelihood of BIONJ tree: -5301.120

--------------------------------------------------------------------

| INITIALIZING CANDIDATE TREE SET |

--------------------------------------------------------------------

Generating 98 parsimony trees... 0.044 second

Computing log-likelihood of 98 initial trees ... 0.491 seconds

Current best score: -5292.432

Do NNI search on 20 best initial trees

Estimate model parameters (epsilon = 0.100)

BETTER TREE FOUND at iteration 1: -5292.432

BETTER TREE FOUND at iteration 2: -5292.432

BETTER TREE FOUND at iteration 5: -5292.432

Iteration 10 / LogL: -5292.432 / Time: 0h:0m:0s

BETTER TREE FOUND at iteration 17: -5292.432

Iteration 20 / LogL: -5292.432 / Time: 0h:0m:1s

Finish initializing candidate tree set (20)

Current best tree score: -5292.432 / CPU time: 1.067

Number of iterations: 20

--------------------------------------------------------------------

| OPTIMIZING CANDIDATE TREE SET |

--------------------------------------------------------------------

BETTER TREE FOUND at iteration 24: -5292.432

Iteration 30 / LogL: -5292.433 / Time: 0h:0m:1s (0h:0m:4s left)

BETTER TREE FOUND at iteration 40: -5292.432

Iteration 40 / LogL: -5292.432 / Time: 0h:0m:1s (0h:0m:4s left)

Iteration 50 / LogL: -5292.432 / Time: 0h:0m:2s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5302.517

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 60 / LogL: -5297.414 / Time: 0h:0m:2s (0h:0m:3s left)

BETTER TREE FOUND at iteration 63: -5292.432

BETTER TREE FOUND at iteration 70: -5292.432

Iteration 70 / LogL: -5292.432 / Time: 0h:0m:2s (0h:0m:3s left)

Iteration 80 / LogL: -5292.432 / Time: 0h:0m:3s (0h:0m:3s left)

BETTER TREE FOUND at iteration 83: -5292.432

BETTER TREE FOUND at iteration 84: -5292.432

Iteration 90 / LogL: -5297.413 / Time: 0h:0m:3s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

BETTER TREE FOUND at iteration 98: -5292.432

Iteration 100 / LogL: -5292.432 / Time: 0h:0m:3s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5304.878

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.467

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 110 / LogL: -5292.432 / Time: 0h:0m:4s (0h:0m:3s left)

Iteration 120 / LogL: -5292.432 / Time: 0h:0m:4s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 130 / LogL: -5292.432 / Time: 0h:0m:4s (0h:0m:2s left)

Iteration 140 / LogL: -5292.432 / Time: 0h:0m:5s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 150 / LogL: -5292.432 / Time: 0h:0m:5s (0h:0m:1s left)

Log-likelihood cutoff on original alignment: -5305.030

Iteration 160 / LogL: -5292.433 / Time: 0h:0m:5s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

BETTER TREE FOUND at iteration 165: -5292.432

BETTER TREE FOUND at iteration 168: -5292.432

Iteration 170 / LogL: -5297.413 / Time: 0h:0m:6s (0h:0m:3s left)

Iteration 180 / LogL: -5292.432 / Time: 0h:0m:6s (0h:0m:3s left)

BETTER TREE FOUND at iteration 182: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 190 / LogL: -5292.432 / Time: 0h:0m:6s (0h:0m:3s left)

Iteration 200 / LogL: -5292.432 / Time: 0h:0m:7s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5305.921

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.813

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 210 / LogL: -5297.413 / Time: 0h:0m:7s (0h:0m:3s left)

Iteration 220 / LogL: -5292.432 / Time: 0h:0m:8s (0h:0m:2s left)

Iteration 230 / LogL: -5292.432 / Time: 0h:0m:8s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 240 / LogL: -5292.432 / Time: 0h:0m:8s (0h:0m:2s left)

Iteration 250 / LogL: -5297.414 / Time: 0h:0m:9s (0h:0m:1s left)

Log-likelihood cutoff on original alignment: -5306.477

UPDATE BEST LOG-LIKELIHOOD: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 260 / LogL: -5292.433 / Time: 0h:0m:9s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 270 / LogL: -5292.432 / Time: 0h:0m:9s (0h:0m:1s left)

BETTER TREE FOUND at iteration 273: -5292.432

BETTER TREE FOUND at iteration 276: -5292.432

Iteration 280 / LogL: -5292.432 / Time: 0h:0m:10s (0h:0m:3s left)

BETTER TREE FOUND at iteration 284: -5292.432

BETTER TREE FOUND at iteration 288: -5292.432

Iteration 290 / LogL: -5292.432 / Time: 0h:0m:10s (0h:0m:3s left)

BETTER TREE FOUND at iteration 294: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 300 / LogL: -5292.432 / Time: 0h:0m:10s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5306.477

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.817

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 310 / LogL: -5297.413 / Time: 0h:0m:11s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

BETTER TREE FOUND at iteration 319: -5292.432

Iteration 320 / LogL: -5292.432 / Time: 0h:0m:11s (0h:0m:3s left)

Iteration 330 / LogL: -5292.432 / Time: 0h:0m:11s (0h:0m:3s left)

BETTER TREE FOUND at iteration 339: -5292.432

Iteration 340 / LogL: -5292.432 / Time: 0h:0m:12s (0h:0m:3s left)

BETTER TREE FOUND at iteration 346: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 350 / LogL: -5292.432 / Time: 0h:0m:12s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5307.275

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 360 / LogL: -5292.432 / Time: 0h:0m:13s (0h:0m:3s left)

Iteration 370 / LogL: -5292.432 / Time: 0h:0m:13s (0h:0m:2s left)

BETTER TREE FOUND at iteration 371: -5292.432

Iteration 380 / LogL: -5292.432 / Time: 0h:0m:13s (0h:0m:3s left)

BETTER TREE FOUND at iteration 388: -5292.432

Iteration 390 / LogL: -5292.432 / Time: 0h:0m:14s (0h:0m:3s left)

BETTER TREE FOUND at iteration 397: -5292.432

Iteration 400 / LogL: -5292.432 / Time: 0h:0m:14s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5306.477

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.798

NOTE: UFBoot does not converge, continue at least 100 more iterations

BETTER TREE FOUND at iteration 408: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 410 / LogL: -5292.432 / Time: 0h:0m:14s (0h:0m:3s left)

Iteration 420 / LogL: -5297.414 / Time: 0h:0m:15s (0h:0m:3s left)

Iteration 430 / LogL: -5292.432 / Time: 0h:0m:15s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 440 / LogL: -5292.432 / Time: 0h:0m:15s (0h:0m:2s left)

Iteration 450 / LogL: -5292.432 / Time: 0h:0m:16s (0h:0m:2s left)

Log-likelihood cutoff on original alignment: -5306.882

Iteration 460 / LogL: -5292.432 / Time: 0h:0m:16s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 470 / LogL: -5292.432 / Time: 0h:0m:16s (0h:0m:1s left)

BETTER TREE FOUND at iteration 472: -5292.432

BETTER TREE FOUND at iteration 474: -5292.432

Iteration 480 / LogL: -5297.412 / Time: 0h:0m:17s (0h:0m:3s left)

Iteration 490 / LogL: -5292.432 / Time: 0h:0m:17s (0h:0m:3s left)

Iteration 500 / LogL: -5292.432 / Time: 0h:0m:17s (0h:0m:2s left)

Log-likelihood cutoff on original alignment: -5306.882

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.784

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 510 / LogL: -5292.432 / Time: 0h:0m:18s (0h:0m:3s left)

Iteration 520 / LogL: -5292.432 / Time: 0h:0m:18s (0h:0m:2s left)

Iteration 530 / LogL: -5292.432 / Time: 0h:0m:18s (0h:0m:2s left)

Iteration 540 / LogL: -5292.432 / Time: 0h:0m:19s (0h:0m:2s left)

Iteration 550 / LogL: -5292.432 / Time: 0h:0m:19s (0h:0m:1s left)

Log-likelihood cutoff on original alignment: -5306.882

Iteration 560 / LogL: -5292.432 / Time: 0h:0m:19s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 570 / LogL: -5297.412 / Time: 0h:0m:20s (0h:0m:1s left)

Iteration 580 / LogL: -5292.432 / Time: 0h:0m:20s (0h:0m:0s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 590 / LogL: -5292.432 / Time: 0h:0m:20s (0h:0m:0s left)

Iteration 600 / LogL: -5292.433 / Time: 0h:0m:21s (0h:0m:0s left)

Log-likelihood cutoff on original alignment: -5306.882

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.690

NOTE: UFBoot does not converge, continue at least 100 more iterations

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 610 / LogL: -5292.432 / Time: 0h:0m:21s (0h:0m:3s left)

Iteration 620 / LogL: -5292.432 / Time: 0h:0m:22s (0h:0m:2s left)

Iteration 630 / LogL: -5292.432 / Time: 0h:0m:22s (0h:0m:2s left)

Iteration 640 / LogL: -5297.414 / Time: 0h:0m:22s (0h:0m:2s left)

Iteration 650 / LogL: -5292.432 / Time: 0h:0m:23s (0h:0m:1s left)

Log-likelihood cutoff on original alignment: -5308.030

UPDATE BEST LOG-LIKELIHOOD: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 660 / LogL: -5292.432 / Time: 0h:0m:23s (0h:0m:1s left)

BETTER TREE FOUND at iteration 670: -5292.432

Iteration 670 / LogL: -5292.432 / Time: 0h:0m:23s (0h:0m:3s left)

Iteration 680 / LogL: -5292.432 / Time: 0h:0m:24s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 690 / LogL: -5292.432 / Time: 0h:0m:24s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 700 / LogL: -5297.412 / Time: 0h:0m:24s (0h:0m:2s left)

Log-likelihood cutoff on original alignment: -5308.030

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.755

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 710 / LogL: -5292.432 / Time: 0h:0m:25s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 720 / LogL: -5292.432 / Time: 0h:0m:25s (0h:0m:2s left)

Iteration 730 / LogL: -5292.432 / Time: 0h:0m:25s (0h:0m:2s left)

Iteration 740 / LogL: -5292.432 / Time: 0h:0m:26s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 750 / LogL: -5292.432 / Time: 0h:0m:26s (0h:0m:1s left)

Log-likelihood cutoff on original alignment: -5308.030

Iteration 760 / LogL: -5292.432 / Time: 0h:0m:26s (0h:0m:1s left)

Iteration 770 / LogL: -5292.432 / Time: 0h:0m:27s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 780 / LogL: -5292.432 / Time: 0h:0m:27s (0h:0m:0s left)

Iteration 790 / LogL: -5292.432 / Time: 0h:0m:27s (0h:0m:0s left)

Iteration 800 / LogL: -5292.432 / Time: 0h:0m:28s (0h:0m:0s left)

Log-likelihood cutoff on original alignment: -5308.030

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.686

NOTE: UFBoot does not converge, continue at least 100 more iterations

Iteration 810 / LogL: -5292.432 / Time: 0h:0m:28s (0h:0m:3s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 820 / LogL: -5292.432 / Time: 0h:0m:28s (0h:0m:2s left)

BETTER TREE FOUND at iteration 821: -5292.432

Iteration 830 / LogL: -5292.432 / Time: 0h:0m:29s (0h:0m:3s left)

BETTER TREE FOUND at iteration 835: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 840 / LogL: -5292.432 / Time: 0h:0m:29s (0h:0m:3s left)

BETTER TREE FOUND at iteration 849: -5292.432

Iteration 850 / LogL: -5292.432 / Time: 0h:0m:30s (0h:0m:3s left)

Log-likelihood cutoff on original alignment: -5308.030

BETTER TREE FOUND at iteration 851: -5292.432

Iteration 860 / LogL: -5292.433 / Time: 0h:0m:30s (0h:0m:3s left)

Iteration 870 / LogL: -5292.432 / Time: 0h:0m:30s (0h:0m:2s left)

BETTER TREE FOUND at iteration 875: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 880 / LogL: -5292.432 / Time: 0h:0m:31s (0h:0m:3s left)

BETTER TREE FOUND at iteration 883: -5292.432

Iteration 890 / LogL: -5292.432 / Time: 0h:0m:31s (0h:0m:3s left)

Iteration 900 / LogL: -5292.432 / Time: 0h:0m:31s (0h:0m:2s left)

Log-likelihood cutoff on original alignment: -5308.030

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.859

NOTE: UFBoot does not converge, continue at least 100 more iterations

BETTER TREE FOUND at iteration 901: -5292.432

BETTER TREE FOUND at iteration 908: -5292.432

BETTER TREE FOUND at iteration 909: -5292.432

Iteration 910 / LogL: -5292.432 / Time: 0h:0m:32s (0h:0m:3s left)

BETTER TREE FOUND at iteration 915: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 920 / LogL: -5292.432 / Time: 0h:0m:32s (0h:0m:3s left)

Iteration 930 / LogL: -5292.432 / Time: 0h:0m:33s (0h:0m:3s left)

Iteration 940 / LogL: -5292.432 / Time: 0h:0m:33s (0h:0m:2s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 950 / LogL: -5292.432 / Time: 0h:0m:33s (0h:0m:2s left)

Log-likelihood cutoff on original alignment: -5308.597

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 960 / LogL: -5292.432 / Time: 0h:0m:33s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 970 / LogL: -5292.432 / Time: 0h:0m:34s (0h:0m:1s left)

Iteration 980 / LogL: -5292.432 / Time: 0h:0m:34s (0h:0m:1s left)

UPDATE BEST LOG-LIKELIHOOD: -5292.432

Iteration 990 / LogL: -5292.432 / Time: 0h:0m:35s (0h:0m:0s left)

Iteration 1000 / LogL: -5292.432 / Time: 0h:0m:35s (0h:0m:0s left)

Log-likelihood cutoff on original alignment: -5308.597

NOTE: Bootstrap correlation coefficient of split occurrence frequencies: 0.885

NOTE: UFBoot does not converge, continue at least 100 more iterations

TREE SEARCH COMPLETED AFTER 1001 ITERATIONS / Time: 0h:0m:35s

--------------------------------------------------------------------

| FINALIZING TREE SEARCH |

--------------------------------------------------------------------

Performs final model parameters optimization

Estimate model parameters (epsilon = 0.010)

1. Initial log-likelihood: -5292.432

Optimal log-likelihood: -5292.432

Parameters optimization took 1 rounds (0.004 sec)

BEST SCORE FOUND : -5292.432

WARNING: bootstrap analysis did not converge. You should rerun with higher number of iterations (-nm option)

Creating bootstrap support values...

Split supports printed to NEXUS file speech.splits.nex

Total tree length: 0.197

Total number of iterations: 1001

CPU time used for tree search: 35.186 sec (0h:0m:35s)

Wall-clock time used for tree search: 35.403 sec (0h:0m:35s)

Total CPU time used: 35.333 sec (0h:0m:35s)

Total wall-clock time used: 35.550 sec (0h:0m:35s)

Computing bootstrap consensus tree...

Reading input file speech.splits.nex...

11 taxa and 199 splits.

Consensus tree written to speech.contree

Reading input trees file speech.contree

Log-likelihood of consensus tree: -5292.432

Analysis results written to:

IQ-TREE report: speech.iqtree

Maximum-likelihood tree: speech.treefile

Likelihood distances: speech.mldist

Ultrafast bootstrap approximation results written to:

Split support values: speech.splits.nex

Consensus tree: speech.contree

Screen log file: speech.log

Date and Time: Wed May 13 16:13:24 2020

**tab1020@js-157-183**:**~/finalproj**$ cat speech.contree

(chimp\_1:0.0030186767,gorilla\_1:0.0037951440,(((((((human\_1:0.0000024411,human\_2:0.0000063817)42:0.0000024426,human\_3:0.0000024411)49:0.0000024426,human\_6:0.0000024411)28:0.0000024426,human\_5:0.0000024411)56:0.0000024426,human\_4:0.0000024411)35:0.0000179195,human\_7:0.0000024411)28:0.0014782544,(monkey\_1:0.0066705703,parrot\_1:0.1752429477)64:0.0067517029)34:0.0000024411);

**tab1020@js-157-183**:**~/finalproj**$ cat gibbon\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ cat mouse\_unwrap\_gene.fa

**tab1020@js-157-183**:**~/finalproj**$ grep "CNTNAP2" -A 1 mouse\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ head mouse\_unwrap.fa

>ENSMUSP00000142955.1 pep chromosome:GRCm38:14:54122226:54122241:1 gene:ENSMUSG00000096176.1 transcript:ENSMUST00000177564.1 gene\_biotype:TR\_D\_gene transcript\_biotype:TR\_D\_gene gene\_symbol:Trdd2 description:T cell receptor delta diversity 2 [Source:MGI Symbol;Acc:MGI:4439546]

IGGIR

>ENSMUSP00000142546.1 pep chromosome:GRCm38:14:54113468:54113476:1 gene:ENSMUSG00000096749.2 transcript:ENSMUST00000196221.1 gene\_biotype:TR\_D\_gene transcript\_biotype:TR\_D\_gene gene\_symbol:Trdd1 description:T cell receptor delta diversity 1 [Source:MGI Symbol;Acc:MGI:4439547]

MAY

>ENSMUSP00000141764.1 pep chromosome:GRCm38:6:41533201:41533212:1 gene:ENSMUSG00000095668.1 transcript:ENSMUST00000178537.1 gene\_biotype:TR\_D\_gene transcript\_biotype:TR\_D\_gene gene\_symbol:Trbd1 description:T cell receptor beta, D region 1 [Source:MGI Symbol;Acc:MGI:4439571]

GTGG

>ENSMUSP00000141312.1 pep chromosome:GRCm38:6:41542163:41542176:1 gene:ENSMUSG00000094569.1 transcript:ENSMUST00000178862.1 gene\_biotype:TR\_D\_gene transcript\_biotype:TR\_D\_gene gene\_symbol:Trbd2 description:T cell receptor beta, D region 2 [Source:MGI Symbol;Acc:MGI:4439727]

GTGG

>ENSMUSP00000142153.1 pep chromosome:GRCm38:12:113430528:113430538:-1 gene:ENSMUSG00000094028.1 transcript:ENSMUST00000179520.1 gene\_biotype:IG\_D\_gene transcript\_biotype:IG\_D\_gene gene\_symbol:Ighd4-1 description:immunoglobulin heavy diversity 4-1 [Source:MGI Symbol;Acc:MGI:4439801]

LTG

**tab1020@js-157-183**:**~/finalproj**$ grep "CASPR2" -A 1 mouse\_unwrap.fa

**tab1020@js-157-183**:**~/finalproj**$ packet\_write\_wait: Connection to 149.165.157.183 port 22: Broken pipe

Thomass-MacBook-Pro-4:~ thomasbouchard$