

Multiple sequence alignments and phylogenetic trees

Multiple sequence alignment (MSA)

B9SI54 | B9SI54_RICCO_263_570
 Q01I60 | Q01I60_ORYSA_160_476
 C5Y8S2 | C5Y8S2_SORBI_153_466
 B4FRR6 | B4FRR6_MAIZE_154_469
 D7U4G4 | D7U4G4_VITVI_82_394
 D7M270 | D7M270_ARALY_263_574
 Q8L7Q7 | PME64_ARATH_283_601
 D8QSM2 | D8QSM2_SELML_242_541
 A9TZ89 | A9TZ89_PHYP_A_262_575
 D8SH72 | D8SH72_SELML_209_529

```

-----DAVVAAD-----GSGQFKTIGEALNSYKLNTK--GWYVIYVKAGVYNEHVFIS
--TLRAHATVCNAPSPATTQRCDYSTVQAAIDAAPNHTA--GHFVIKVAAGIYKENVVIP
---IRPDATVCK--PNSGAEP CGYSTVQAAVDAAPNYTA--GHFVIAVAAGTYKENIVIP
---IRPDATVCK--PNSGVKPCGYSTVQAAVDAAPNHTAGAGHFAIAVGAGTYKENVVIP
--SPQPNATVCKG-----GDGCYKTVQEA VNAAPDNDS--SRKFVIRIQEGVYEETVRVP
-SGLKEDVTVC KD-----GKCGYKTVQDAVNAAPEDNG--MRKFVIRISEGVYEENVVIP
-SGLTEDVTVC KN----GGKDKYKTVQEA VDSAPDTNR--TVKFVIRIREGVYEETVRVP
-----SVV-----VGKSGSFKTIQE AID SAPSNSK--ERFSIYIQEGIYDERIYVS
---SPSVTVDI-----YSAFSSIQRAVDLAPDWST--QRYVIYIKTGVYNEVVRIP
ASLISPSAIVSRT--PDQPQLTIFTSIQAAVDHAPNHCT--ARYVIYIKAGVYAENVVRIP
      .                : : :      * : :                : * :      * * * : :
  
```

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```

RILT NVMYGDGIDRTIISGSKHTM-DGLPAYRTATVAVLGDGFVCKSMTIQNSATSD-K
YEKTNILLVGDGIGATVITASRSVGIDGIGTYETATVAVIGDGFRAKDITFENGAGAGAH
YEKTNILLMGE MGATVITASRSVGIDGLGTHETATVAVIGDGFRAKDITFENSAGARAH
YEKANILLMGE MGATVITASRSVGIDGLGTYETATVDVIGDGFRAKDITFENSAGAGAH
LEKKNVVF LIGDGMGKTVITGSLNVGQPGISTYNSATVGVAGDGFMA SGLTMENTAGPDEH
FEKKNVVF LIGDGMGKTVITGSLNAGMPGITTYNTATVGVVGDGFMA HDLTFQNTAGPDAH
FEKKNVVF LIGDGMGKTVITGSLNVGQPGMTTFESATVGVLDGDFMARDLTIENTAGADAH
DSKSMIMLVGAGARKTIIISGNNYVR-EGVTTMDTATVLVAGDGFVARDLTIRNTAGPELH
KQKTNLMFLGDGTDKTIITGSLSDSQPGMITWATATVAVSGSGFIARGITFQNTAGPAGR
LQKSMLMFVGDGMDKTIIRGSM SVSKGGTTTFASATLAVNGKGFLARDLTVENTAGPEGH
      : : * *      * : * . .      * :      : * : * * . . : * . * * :
  
```

Software to generate MSAs

- MAFFT
(very good, very fast)
<http://mafft.cbrc.jp/alignment/software/>
- Clustal Omega
(very good, very fast)
<http://www.ebi.ac.uk/Tools/msa/clustalo/>
- PRANK
(extremely good, very slow)
<http://wasabiapp.org/software/prank/>

File formats: FASTA (holds any sequence data)

label (1 line) sequence (multiple lines)

>human
MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLLIVLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA

>domestic_cat
MNGTEGPNFYVPFSNKTGVVRSPFEYPQYYLAEPWQFSMLAAYMFLLIVLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLG
YNPVIYIMMNKQFRNCMLTTLCCGKNPLGDDEASTTASKTETSQVAPA

>chimpanzee
MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLLIVLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA

File formats: Clustal (holds an alignment)

CLUSTAL O(1.2.1) multiple sequence alignment

labels sequences

```
human      MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLIVLGFPINFLTLY
chimpanzee MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLIVLGFPINFLTLY
domestic_cat MNGTEGPNFYVPFSNKTGVVRSPFEYPQYYLAEPWQFSMLAAYMFLIVLGFPINFLTLY
*****

human      VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
chimpanzee VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
domestic_cat VTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTTLYTSLHGYFVFGPTGCNLEGFFATLG
*****

human      YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA
chimpanzee YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA
domestic_cat YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASTASKTETSQVAPA
*****
```

consensus indicators:

* = no variation

: = highly similar amino acids

. = somewhat similar amino acids

File formats: Phylip (holds an alignment)

of sequences

↓
3 168

sequence length
labels

sequences

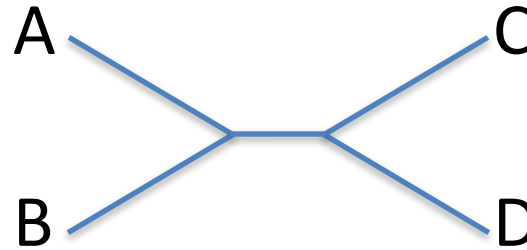
human	MNGTEGPNFY	VPFSNATGVV	RSPFEYPQYY	LAEPWQFSML	AAYMFLLIVL
chimpanzee	MNGTEGPNFY	VPFSNATGVV	RSPFEYPQYY	LAEPWQFSML	AAYMFLLIVL
domestic_c	MNGTEGPNFY	VPFSNKTGVV	RSPFEYPQYY	LAEPWQFSML	AAYMFLLIVL
	GFPINFLTLY	VTVQHKKLRT	PLNYILLNLA	VADLFMVLGG	FTSTLYTSLH
	GFPINFLTLY	VTVQHKKLRT	PLNYILLNLA	VADLFMVLGG	FTSTLYTSLH
	GFPINFLTLY	VTVQHKKLRT	PLNYILLNLA	VADLFMVFGG	FTTTLYTSLH
	GYFVFGPTGC	NLEGFFATLG	YNPVIYIMMN	KQFRNCMLTT	ICCGKNPLGD
	GYFVFGPTGC	NLEGFFATLG	YNPVIYIMMN	KQFRNCMLTT	ICCGKNPLGD
	GYFVFGPTGC	NLEGFFATLG	YNPVIYIMMN	KQFRNCMLTT	LCCGKNPLGD
	DEASATVSKT	ETSQVAPA			
	DEASATVSKT	ETSQVAPA			
	DEASTTASKT	ETSQVAPA			

Tools exist to convert from one sequence format to another

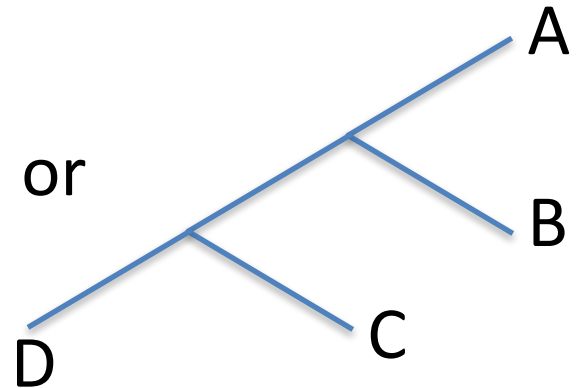
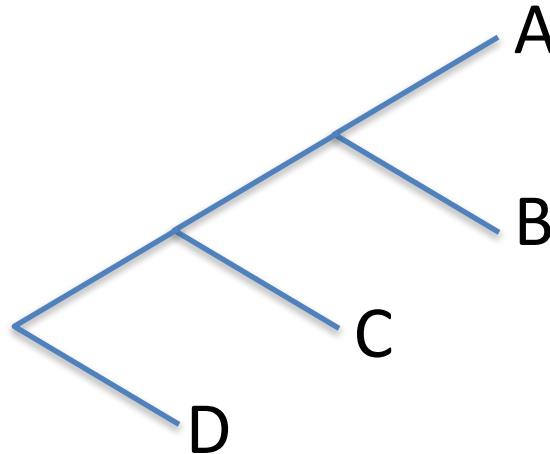
- Online:
<http://www.ebi.ac.uk/Tools/sfc/readseq/>
- In a script:
Use biopython SeqIO

Storing trees: The Newick format

$((A,B),(C,D))$



$((A,B),C),D)$

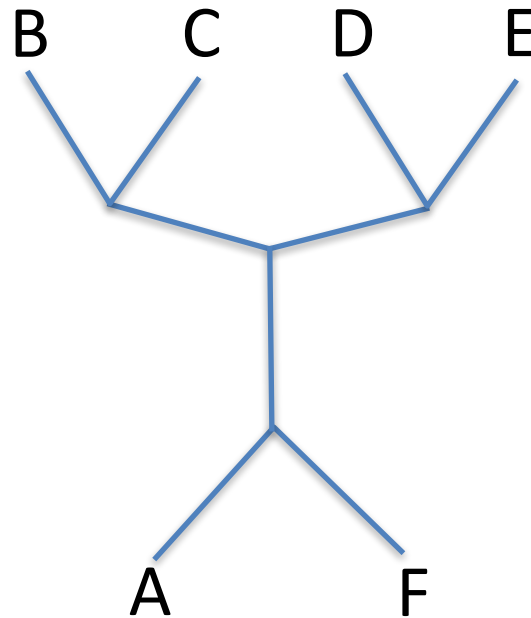


What does this tree look like?

$(A, ((B, C), (D, E)), F)$

What does this tree look like?

$(A, ((B, C), (D, E)), F)$



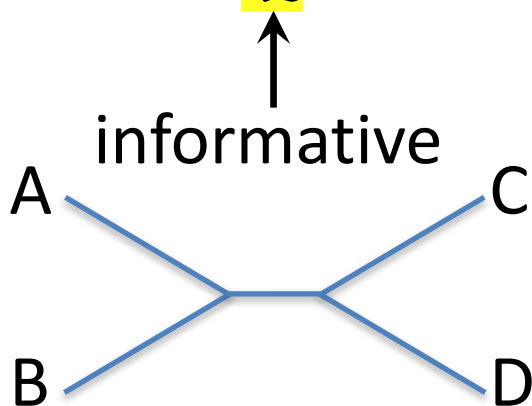
Not all sites in an alignment contain information about the tree topology

A	M	N	G	T	E	G
B	M	N	G	Y	E	R
C	M	Q	G	Y	D	K
D	M	Q	G	T	D	I

↑
uninformative

Not all sites in an alignment contain information about the tree topology

A	M	N	G	T	E	G
B	M	N	G	Y	E	R
C	M	Q	G	Y	D	K
D	M	Q	G	T	D	I



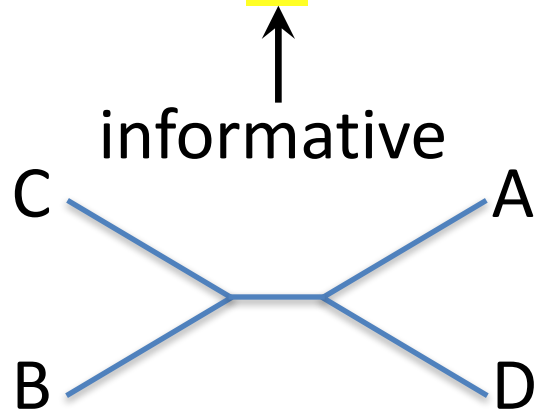
Not all sites in an alignment contain information about the tree topology

A	M	N	G	T	E	G
B	M	N	G	Y	E	R
C	M	Q	G	Y	D	K
D	M	Q	G	T	D	I

↑
uninformative

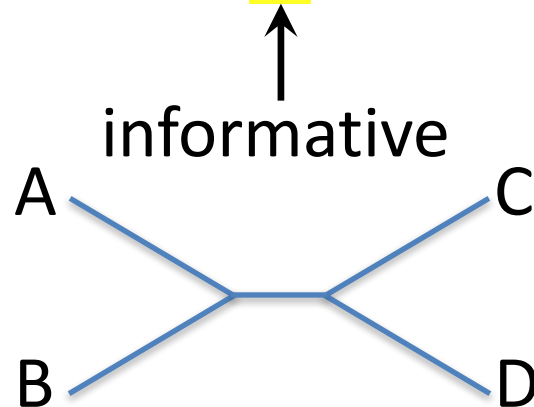
Not all sites in an alignment contain information about the tree topology

A	MNGTEG
B	MNGYER
C	MQGYDK
D	MQGTDI



Not all sites in an alignment contain information about the tree topology

A	MNGTEG
B	MNGYER
C	MQGYDK
D	MQGTDI



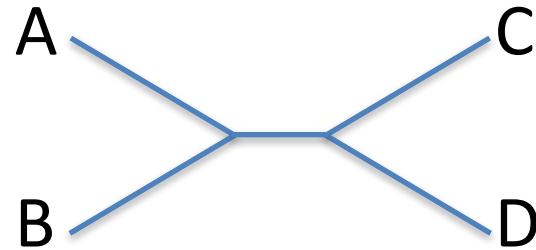
Not all sites in an alignment contain information about the tree topology

A	MNGTEG
B	MNGYER
C	MQGYDK
D	MQGTDI

↑
uninformative (in simplest model)

Not all sites in an alignment contain information about the tree topology

A	MNGTEG
B	MNGYER
C	MQGYDK
D	MQGTDI



by majority rule

How confident are we in a given tree topology?

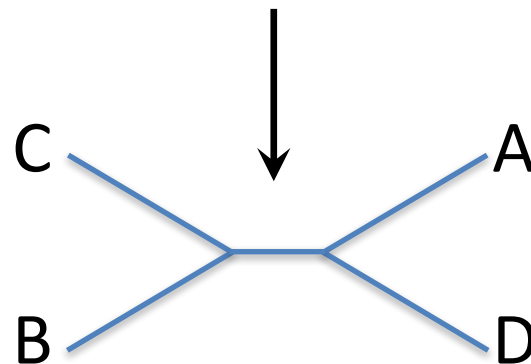
Bootstrap: a method to assess confidence in tree topology

Randomly re-sample columns from the alignment, count frequency of topologies

A MNGTEG
B MNGYER
C MQGYDK
D MQGTDI



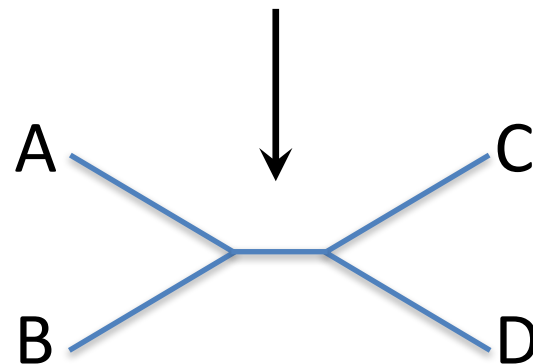
A GMGTMG
B GMRYMR
C GMKYMK
D GMITMI



Bootstrap: a method to assess confidence in tree topology

Randomly re-sample columns from the alignment, count frequency of topologies

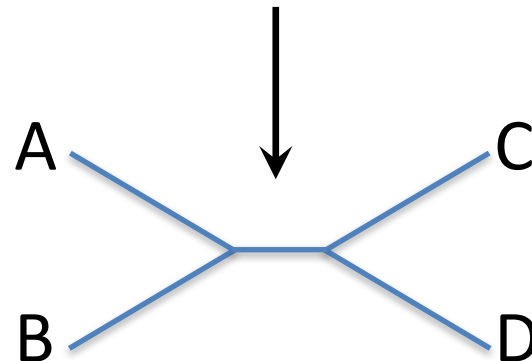
A	MNGTEG		A	NMNTMG
B	MNGYER	→	B	NMNYMG
C	MQGYDK		C	QMQYMG
D	MQGTDI		D	QMQTMG



Bootstrap: a method to assess confidence in tree topology

Randomly re-sample columns from the alignment, count frequency of topologies

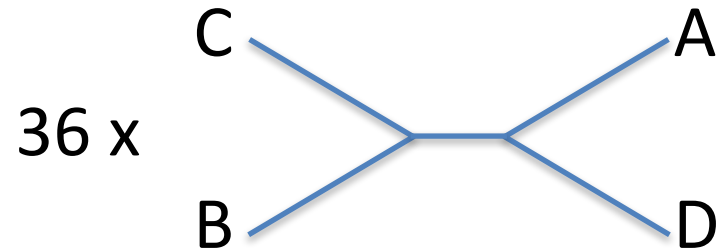
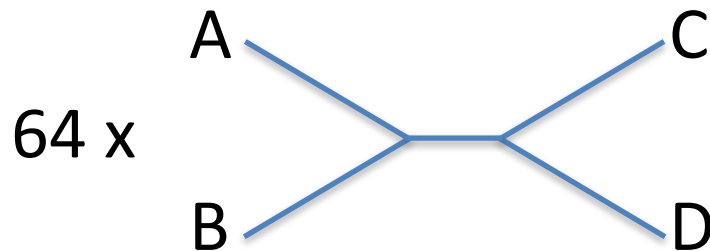
A	MNGTEG		A	MTNGEG
B	MNGYER	→	B	MYNREG
C	MQGYDK		C	MYQKDG
D	MQGTDI		D	MTQIDG



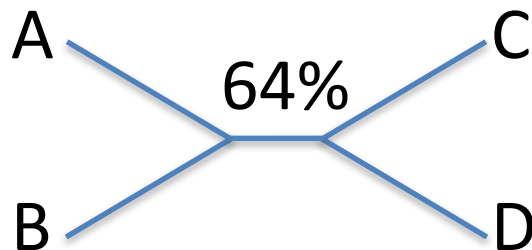
Bootstrap: a method to assess confidence in tree topology

Randomly re-sample columns from the alignment,
count frequency of topologies

Bootstrapped trees (100 x):



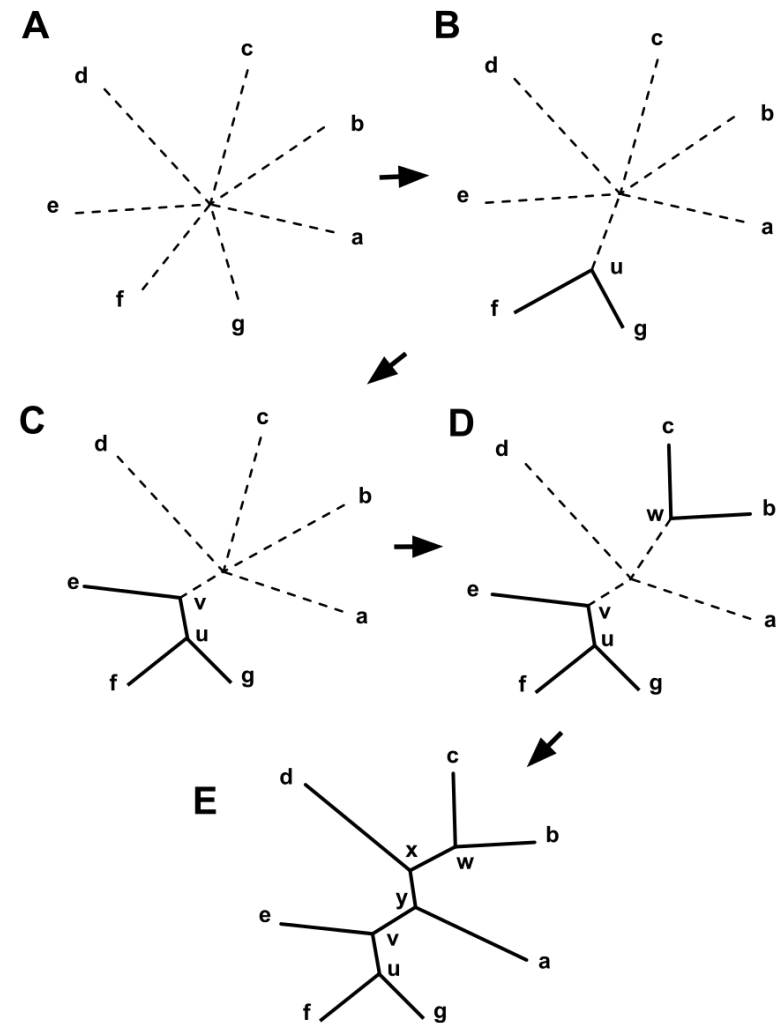
Final result:



Tree-building methods:

1. Neighbor-joining

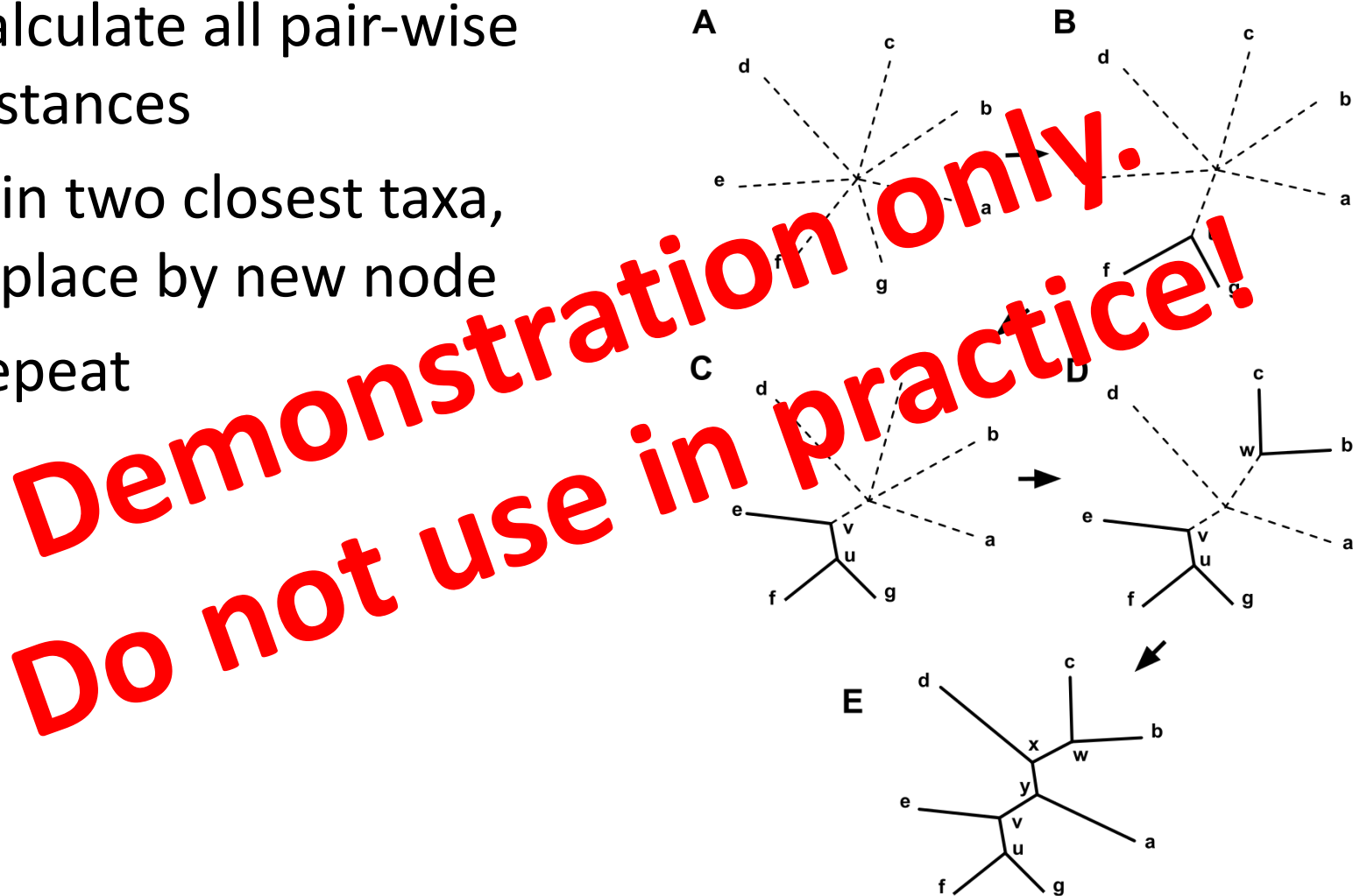
- Calculate all pair-wise distances
- Join two closest taxa, replace by new node
- Repeat



Tree-building methods:

1. Neighbor-joining

- Calculate all pair-wise distances
- Join two closest taxa, replace by new node
- Repeat



Tree-building methods:

2. Maximum likelihood

- Builds likelihood model of molecular evolution
- Finds tree that maximizes:
 $\text{Pr}(\text{sequence data} \mid \text{tree})$
- Commonly used software:
RAxML, FastTree2

Tree-building methods:

3. Bayesian

- Builds likelihood model of molecular evolution
- Calculates:
 $\text{Pr}(\text{tree} \mid \text{sequence data})$
- Commonly used software:
MrBayes, BEAST