

Are conservation scores trustworthy ?

- Good quality alignments
 - Conservation == probable molecular similarity
- Poor alignments
 - Conservation == random noise
- How do you measure MSA reliability ?
 - Try different methods. Vary parameters
 - Compare the results.

Consistent Pairwise Alignments

Score = 740 Length = 17

PID = 100%

Q93Z60_ARATH MASTA**LSSA**IVSTSFLR

|||||

FER2_ARATH MASTA**LSSA**IVSTSFLR

Score = 160 Length = 17

PID=29.41

FER1_MAIZE LGSPR**APAF**FFSSSSLR

..| .. . |. | |

Q93Z60_ARATH MASTA**LSSA**IVSTSFLR

Score = 160 Length = 17

PID=29.41%

FER1_MAIZE LGSPR**APAF**FFSSSSLR

..| .. . |. | |

FER2_ARATH MASTA**LSSA**IVSTSFLR

Score = 310 Length = 12

PID = 58.33%

O80429_MAIZE MAATA**LSMS**ILR

||.|||| .|.

Q93Z60_ARATH MASTA**LSSA**IVS

Score = 310 Length = 12

PID=58.33%

O80429_MAIZE MAATA**LSMS**ILR

||.|||| .|.

FER2_ARATH MASTA**LSSA**IVS

Major inconsistency: +4 Shift

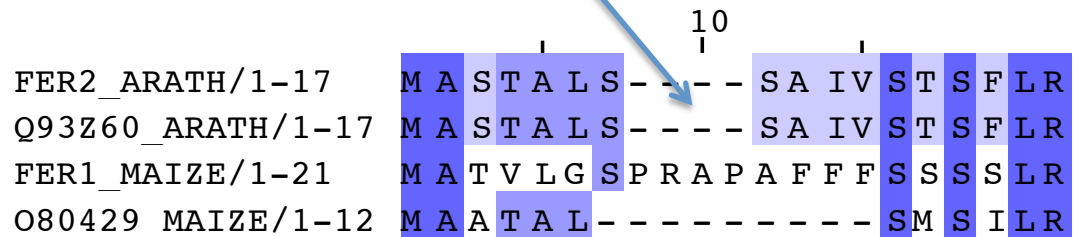
Score = 120 Length = 12

PID = 41.67%

O80429_MAIZE MAATA**LSMS**ILR

.| .| | |

FER1_MAIZE **APAF**FFSSSSLR



- Calculate ‘shift’ between all pairwise alignments and the multiple sequence alignment
 - Higher shifts are less reliable

Consistent Pairwise Alignments

Score = 740 Length = 17

PID = 100%

```
Q93Z60_ARATH MASTALSSAIVSTSFLR
|||||
FER2_ARATH MASTALSSAIVSTSFLR
```

Score = 160 Length = 17

PID=29.41

```
FER1_MAIZE LGSPRAPAFFFSSSSLR
..| .. . |. | ||
Q93Z60_ARATH MASTALSSAIVSTSFLR
```

Score = 160 Length = 17

PID=29.41%

```
FER1_MAIZE LGSPRAPAFFFSSSSLR
..| .. . |. | ||
FER2_ARATH MASTALSSAIVSTSFLR
```

Score = 310 Length = 12

PID = 58.33%

```
O80429_MAIZE MAATALSMSILR
||. ||| .|.
Q93Z60_ARATH MASTALSSAIVS
```

Score = 310 Length = 12

PID=58.33%

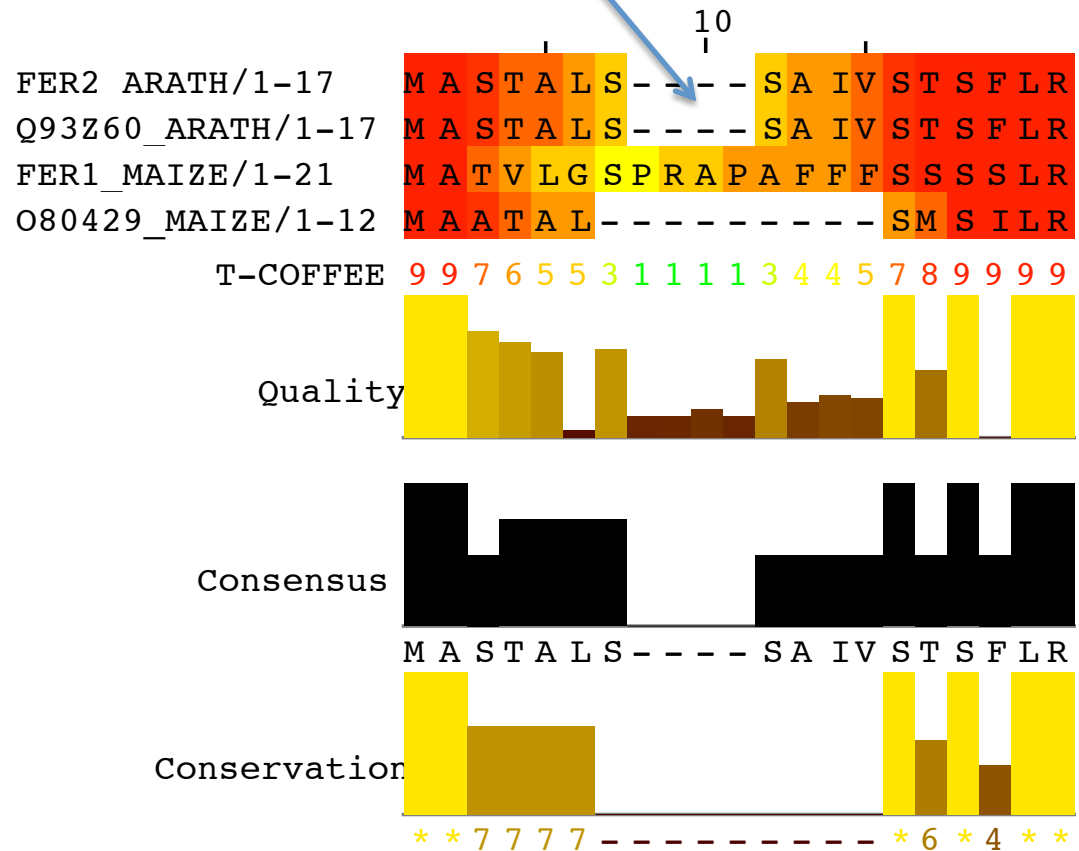
```
O80429_MAIZE MAATALSMSILR
||. ||| .|.
FER2_ARATH MASTALSSAIVS
```

Major inconsistency: +4 Shift

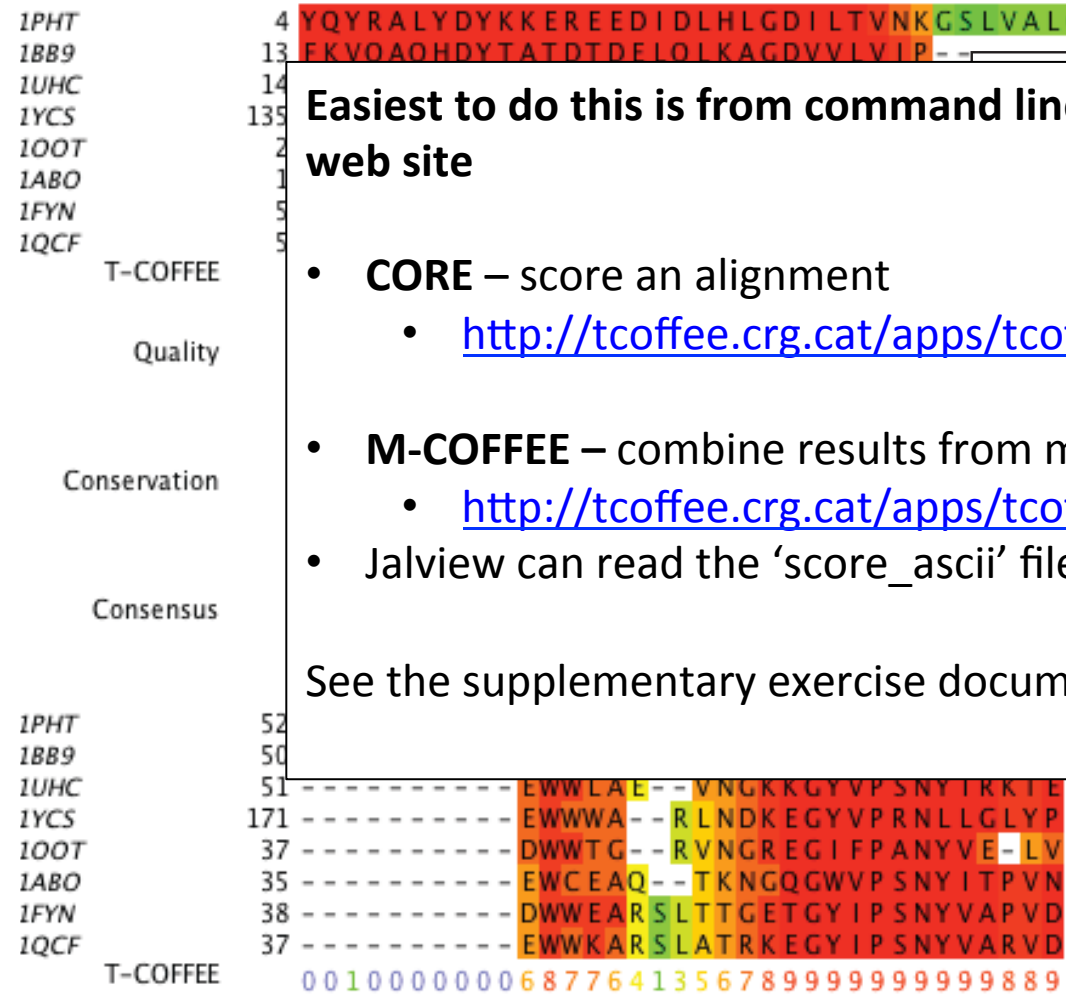
Score = 120 Length = 12

PID = 41.67%

```
O80429_MAIZE MAATALSMSILR
. | . | | | |
FER1_MAIZE APAFFFSSSSLR
```



T-COFFEE alignment reliability scores



Easiest to do this is from command line, or from the T-COFFEE web site

- **CORE** – score an alignment
 - <http://tcoffee.crg.cat/apps/tcoffee/do:core>
- **M-COFFEE** – combine results from many ‘popular aligners’
 - <http://tcoffee.crg.cat/apps/tcoffee/do:mcoffee>
- Jalview can read the ‘score_ascii’ file for an alignment

See the supplementary exercise document for a worked exercise.

es
nment
OFFEE
reliable
blue.

