**Important shortcuts in AliView (Linux)**

Physalia Transposable Elements Course 2018

**View options:**

Look at two alignment regions: O*pen the file twice*

*Go to a specific position:* **View > Goto sequence position (Ctrl + G)**

**Import/export/copy/paste sequences:**

Import fasta sequence from outside AliView: ***File > Open file (Ctrl + O)***

Export fasta sequence for outside AliView: ***Edit > Copy selection as fasta (Ctrl + C)***

Copy sequence within AliView: ***Edit > Copy selection as fasta (Ctrl + C)***

Paste sequence within AliView: ***Edit > Paste (fasta-sequences) (Ctrl + V)***

Delete sequence: ***Ctrl + Delete***

Copy only sequence titles: ***Edit > Copy name(s) only***

Copy only sequence itself: *Click on first and last position while holding* ***Shift****, then:* ***Edit > Copy selection as characters (Ctrl + Shift + C)***

**Select sequences:**

Select specific sequences: Click on title(s) (with ***Ctrl*** for multiple*)* or drag mouse over multiple titles

Select all sequences: ***Ctrl + A***

Select specific positions: Click on position(s) (with ***Shift*** for multiple*)* or drag mouse over multiple positions

Select from current position until beginning of sequence: ***Selection >* Expand selection left (Alt + Shift + Left)**

Select from current position until end of sequence: ***Selection >* Expand selection right (Alt + Shift + Right)**

**Manual realignment modes:**

Manually realign sequences: *Copy the sequences in a new AliView window and select them, then:* ***Align > Realign selected sequence(s)***

**Manipulate sequences:**

Reverse complement sequence: ***Edit > Reverse Complement Selected Sequences***

Display all sequences as upper case characters:***View > Always display as Upper case character***

Insert gap(s): ***Align > Insert Gap move right (Space)***

Replace selected base-pair(s) with gap(s): *Select base-pair(s), then:* ***Edit > Clear selected bases (Delete)***

Delete selected base-pair(s): *Select base-pair(s), then:* ***Edit > Delete selected (Ctrl + Delete)***

Replace char (?) into gaps: ***Edit > Replace missing char (?) into GAP (-)***

Rename sequence: ***Edit > Rename sequence (double click sequence name)***

**Search for patterns:**

Find pattern in sequence: ***Ctrl + F***