

Edit parameters for Align with MafftWS



Current parameter set name :

- Delete
- Revert
- Create
- Update

Details

Options

- Shared 6mers distance calculation
- Output sequences order
- Sequence type
- Pairwise alignment computation...

--nuc - Assume the sequences are nucleotide. --amino - Assume the sequences are amino acid.
[?Link](#)

Parameters

Max iteration number

Partsize

- Start Job
- Cancel Job