Frali: Frame based multiple sequence alignment

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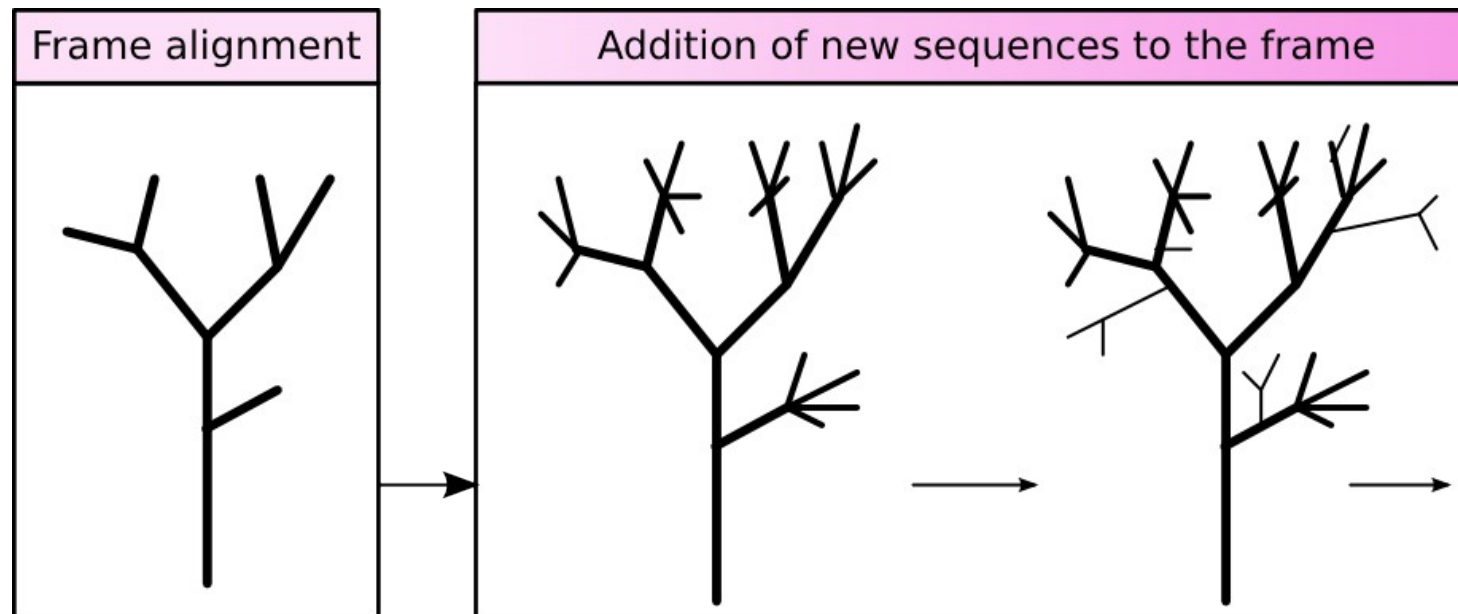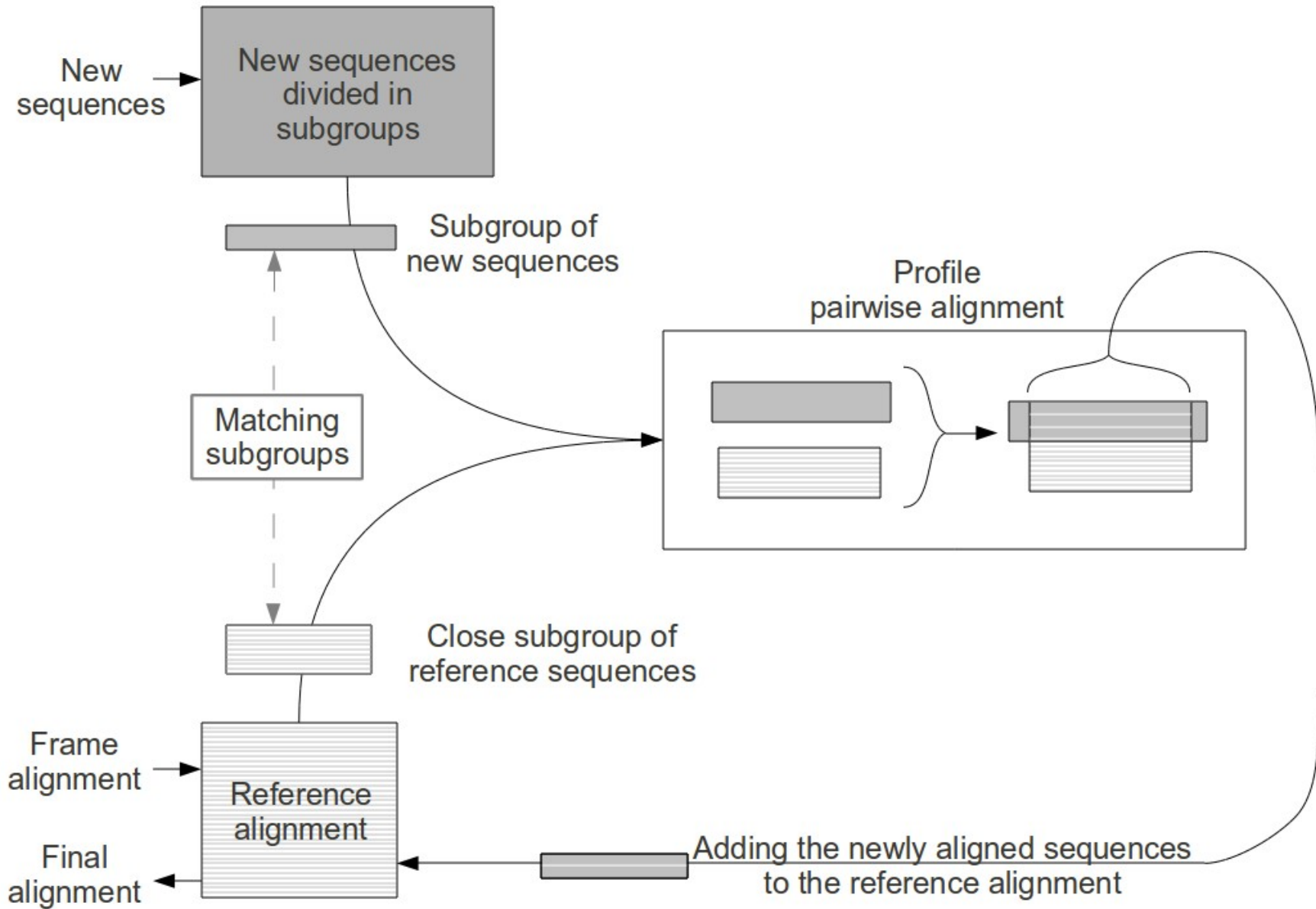
Poster 2

Protein families and multiple sequence alignment

- Building a multiple sequence alignment

- Automatic methods: Tcoffee, Muscle, ClustalW...

- New sequences available at high rate

- Manual curation

Principle:

- Instead of recreating the whole alignment every time: direct addition of sequences to an initial high quality multiple sequence alignment called "Frame"

New sequences

New sequences divided in subgroups

Subgroup of new sequences

Matching subgroups

Profile pairwise alignment

Close subgroup of reference sequences

Frame alignment

Reference alignment

Final alignment

Adding the newly aligned sequences to the reference alignment

Conclusion

- Several filters: identity threshold, indels size, etc.

- No pre-treatment needed especially for mutiple domain proteins

- High quality and representative (diversified) Frame alignment needed, but easy and fast update

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