

(Re)Discovering “profile” HMMs
i.e. adapt HMM to multiple sequence alignment

- **Q1: Could we use HMM to get multiple alignments?**
- **Q2: None of the previously exposed multiple alignment (MA) methods is supported by a fully probabilistic approach. Could we do better?**

profile

Remark: If Q1 is positively answered, so is Q2!

- **Either**
 - directly answer Q1, i.e. design from scratch a HMM for MA
- **or (thinking of Q2...)**
 - we shouldn't really start from scratch...
 - (because profiles can be thought as being not far from the idea of emitting symbols: one state/table for each column in a MA profile)
 - Q2': What about inserts?
 - Q2'': What about gaps?
 - Q2''': Could we put all these together?
- **or**
 - Q3: could pair HMM be extended/adapted to do multiple alignments?
(because HMMs were successfully applied to pairwise alignment (PA), and MA is a generalisation of PA)
 - Q4: How should the probability parameters be set for a “profile” HMM?
 - Q4': Are these all the parameters needed for a profile HMM? Q4'': If no, could we cope well with it?...
 - Q5: Could we adapt (pair) HMM basic algorithms to the profile HMM model?
 - Q6: Given a profile HMM and a new sequence, how should we proceed to align the sequence (to the model represented by the profile HMM)?
 - Q7: Is it possible to get a profile HMM without starting from a profile (multiple alignment)?