

HMMoC



# HMMs – powerful but tedious...

## Implementing from scratch

- + Flexibility
- + Efficient
- Optimal efficiency usually not reached
- Expertise required
- Long implementation time
- Bugs
- Pitfall: hard-code model/optimization choices

## Libraries

- + Lower level of expertise required
- + Short implementation time
- + Bug free
- + Model change easy
- Restricted to library features
- Suboptimal efficiency

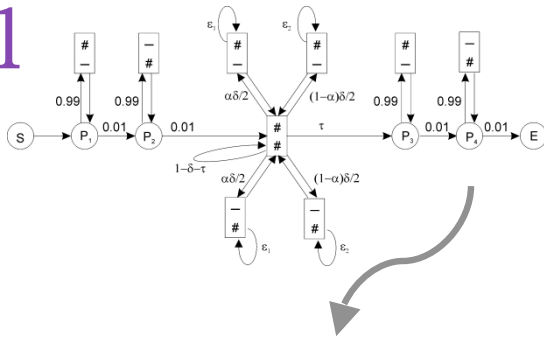
# HMMoC

Aims to combine the advantages of both

“Hidden Markov Model Compiler” (really, a parser-generator):

- Describe structure of HMM in XML
- Transition and emission probabilities: C snippets
- Generates C++ code / header file
- Feature-rich
- Documentation + examples

# Model



```

- <graph>
  <cliq idref="block1" />
  <cliq idref="block2withbanding" />
  <cliq idref="block3" />
</graph>
<!-- Define all emissions for this HMM; relates output tape and code that calculates
+ <emission id="emit12">
+ <emission id="emit1">
+ <emission id="emit2">
+ <emission id="empty">
- <!--

  Define all transitions: "from" and "to" states, transition probability, and emiss
  It is permissible to assign emissions to states (see the end state). In th
  all transitions going to that state should have no "emission" attribute.

-->
- <transitions id="transitions">
  <transition id="trSE" from="start" to="end" probability="probSE" emission="empty" />
  <transition id="trSM" from="start" to="match" probability="probSM" emission="emit12" />
  <transition id="trSI" from="start" to="insert" probability="probSI" emission="emit1" />
  <transition id="trSD" from="start" to="delete" probability="probSD" emission="emit2" />
  <transition id="trMM" from="match" to="match" probability="probMM" emission="emit12" />
  <transition id="trMI" from="match" to="insert" probability="probMI" emission="emit1" />
  <transition id="trMD" from="match" to="delete" probability="probMD" emission="emit2" />
  <transition id="trME" from="match" to="end" probability="probME" emission="empty" />
  <transition id="trIM" from="insert" to="match" probability="probIM" emission="emit12" />
  <transition id="trII" from="insert" to="insert" probability="probII" emission="emit1" />
  <transition id="trID" from="insert" to="delete" probability="probID" emission="emit2" />
  <transition id="trIE" from="insert" to="end" probability="probIE" emission="empty" />
  <transition id="trDM" from="delete" to="match" probability="probDM" emission="emit12" />
  <transition id="trDI" from="delete" to="insert" probability="probDI" emission="emit1" />
  <transition id="trDD" from="delete" to="delete" probability="probDD" emission="emit2" />
  <transition id="trDE" from="delete" to="end" probability="probDE" emission="empty" />
</transitions>
</hmm>
+ <hmm id="Align">
  <!-- Code generation -->
+ <forward outputTable="yes" baumWelch="no" name="Forward" id="fw">
+ <backward outputTable="no" baumWelch="transitions" name="BackwardBaumWelch" id="bwbw">
+ <backward outputTable="yes" baumWelch="no" name="Backward" id="bw">
  
```

XML

```

else {
  iSymbol[0] = 'A' /* dummy value */;
}
if ((iPos0+0<=iLen1+1)) {
  iSymbol[1] = iSequence1[iPos0+0];
}
else {
  iSymbol[1] = 'A' /* dummy value */;
}
CurStateMemoryblock2To = dp.StateMemoryblock2.write((iPos0-(0))-0), (iPos1-(0))-0);
CurStateMemoryblock2Secondary = dp2.StateMemoryblock2.read((iPos0-(0))-0), (iPos1-(0))-0);
iTempResult[0] = iEquilibriumDistribution[ iTranslate[ iSymbol[0] ] ];
iEmission[0] = iTempResult[0];
if ((iPos1+1<=iLen2+0)) {
  CurStateMemoryblock2From = dp.StateMemoryblock2.read((iPos0-(0))-0), (iPos1-(-1))-0);
  CurStateMemoryblock2To[1] = iTempProb[1] = ((iTransition[14])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[14] += iTempProb[1] * CurStateMemoryblock2Secondary[1];
  CurStateMemoryblock2To[0] = iTempProb[1] = ((iTransition[6])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[6] += iTempProb[1] * CurStateMemoryblock2Secondary[0];
  CurStateMemoryblock2To[2] = iTempProb[1] = ((iTransition[10])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[10] += iTempProb[1] * CurStateMemoryblock2Secondary[2];
}
iTempResult[0] = iEquilibriumDistribution[ iTranslate[ iSymbol[1] ] ];
iEmission[0] = iTempResult[0];
if ((iPos0+1<=iLen1+0)) {
  CurStateMemoryblock2From = dp.StateMemoryblock2.read((iPos0-(-1))-0), (iPos1-(0))-0);
  CurStateMemoryblock2To[1] += iTempProb[1] = ((iTransition[13])*iEmission[0])*CurStateMemoryblock2
  bw.transitionBaumWelchCount00[13] += iTempProb[1] * CurStateMemoryblock2Secondary[1];
  CurStateMemoryblock2To[0] += iTempProb[1] = ((iTransition[5])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[5] += iTempProb[1] * CurStateMemoryblock2Secondary[0];
  CurStateMemoryblock2To[2] += iTempProb[1] = ((iTransition[9])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[9] += iTempProb[1] * CurStateMemoryblock2Secondary[2];
}
iTempResult[0] = iEquilibriumDistribution[ iTranslate[ iSymbol[1] ] ] * (iSubstitutionMatrix[ iTranslat
iEmission[0] = iTempResult[0];
if ((iPos0+1<=iLen1+0) && (iPos1+1<=iLen2+0)) {
  CurStateMemoryblock2From = dp.StateMemoryblock2.read((iPos0-(-1))-0), (iPos1-(-1))-0);
  CurStateMemoryblock2To[1] += iTempProb[1] = ((iTransition[12])*iEmission[0])*CurStateMemoryblock2
  bw.transitionBaumWelchCount00[12] += iTempProb[1] * CurStateMemoryblock2Secondary[1];
  CurStateMemoryblock2To[0] += iTempProb[1] = ((iTransition[4])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[4] += iTempProb[1] * CurStateMemoryblock2Secondary[0];
  CurStateMemoryblock2To[2] += iTempProb[1] = ((iTransition[8])*iEmission[0])*CurStateMemoryblock2F
  bw.transitionBaumWelchCount00[8] += iTempProb[1] * CurStateMemoryblock2Secondary[2];
}
iEmission[0] = 1.0;
if ((iPos0+0>=iLen1+0) && (iPos1+0>=iLen2+0)) {
  
```

C++



HMMoC

# HMMoC - Features

- Single, pair, triple, quadruple HMMs
- Forward, Backward, Viterbi, posterior sampling, Baum-Welch
- Silent states (“wing folding”) fully supported.
- Higher-order HMMs
- Emissions associated to states (Moore) or transitions (Mealy); mixing allowed.
- Position-dependent transition and emission probabilities
- Banded recursion by providing a DP table iterator
- Transparent memory+time efficient implementation of banded DP table
- Probabilities: double, logspace, or extended-exponent float (“bfloats”)
- Both reals and DP tables are implemented by templates; can be adapted if desired.

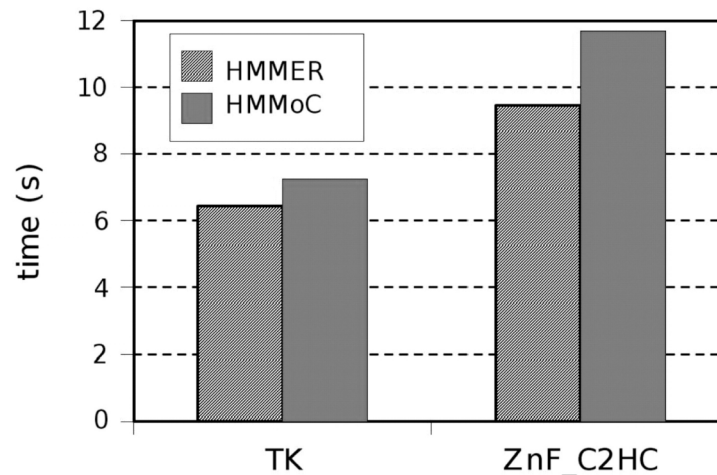
# HMMoC - Efficiency

## Time:

- No table lookups; loops over transitions/emissions are unrolled
- Probabilities are computed early and re-used
- Calculations are ordered to minimize DP table lookups
- Silent state ordering to minimize dimension of matrix inversions

## Memory:

- Special states (start, end, ...) have their own DP tables
- Supports folded DP tables if not required for output



# HMMoC – Handy features

- **Macro facility** to reduce repetitiveness of XML
- DP table / Baum-Welch counts access by **name** and **numerical ID**
- **Python** interface (prototype, using pyrex/cython)
  
- Negative probabilities cause run-time warnings
- **Informative compiler errors**
- **Sanity checks** on HMM
  - e.g. consistent order of states;
  - consistent mixing of Mealy/Moore views
- Reasonably **readable** (indented) **C++ output**

# HMMoC - Examples

- Published:
  - Probabilistic whole-genome re-alignment  
Lunter, Rocco, Mimouni, Heger, Caldeira, Hein; Gen Res 18; 2008
  - Identification of viral overlapping reading frames  
de Groot et al., BMC Bioinformatics (accepted)
- Toy examples included with HMMoC:
  - Occasionally dishonest casino
  - CpG island detection
  - Simple pairwise aligner
  - HMMER implementation
  - Several more
- Download
  - <http://genserv.anat.ox.ac.uk/downloads/software/hmmoc>
  - Google “hmmoc”