

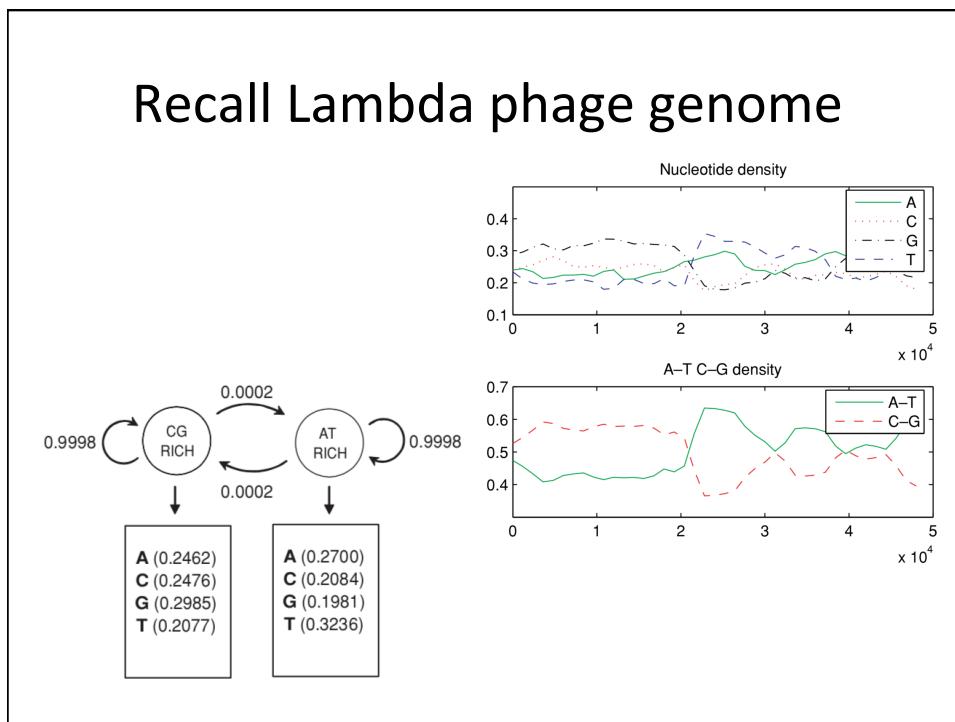
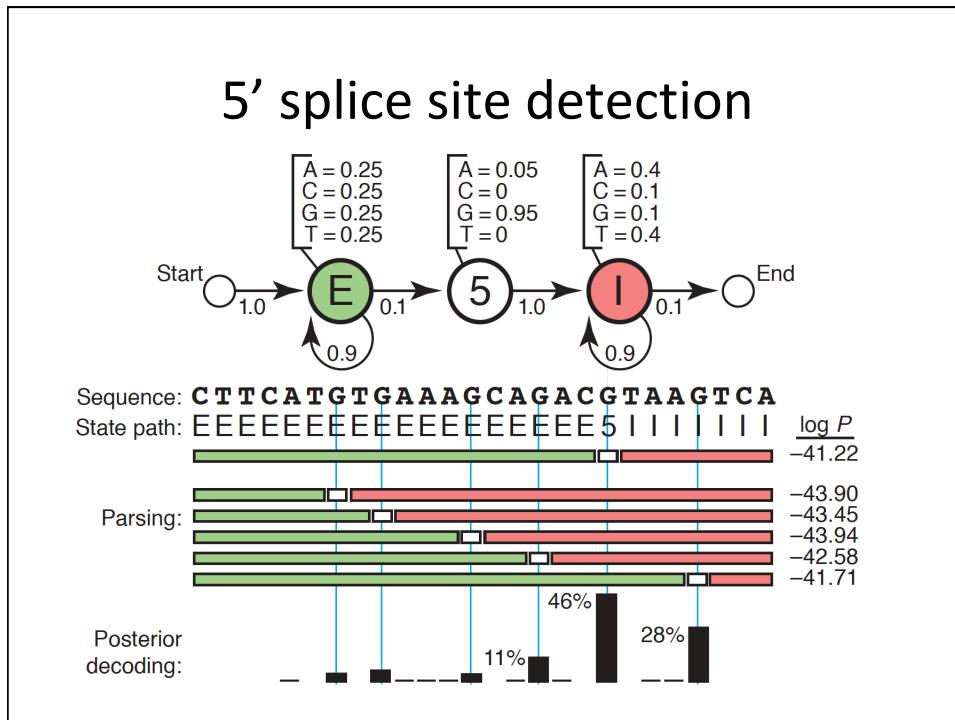
Typical HMM Problems

Scoring Given a model M , an observed string S and a path through the model (H), determine the joint probability of the sequence and path.

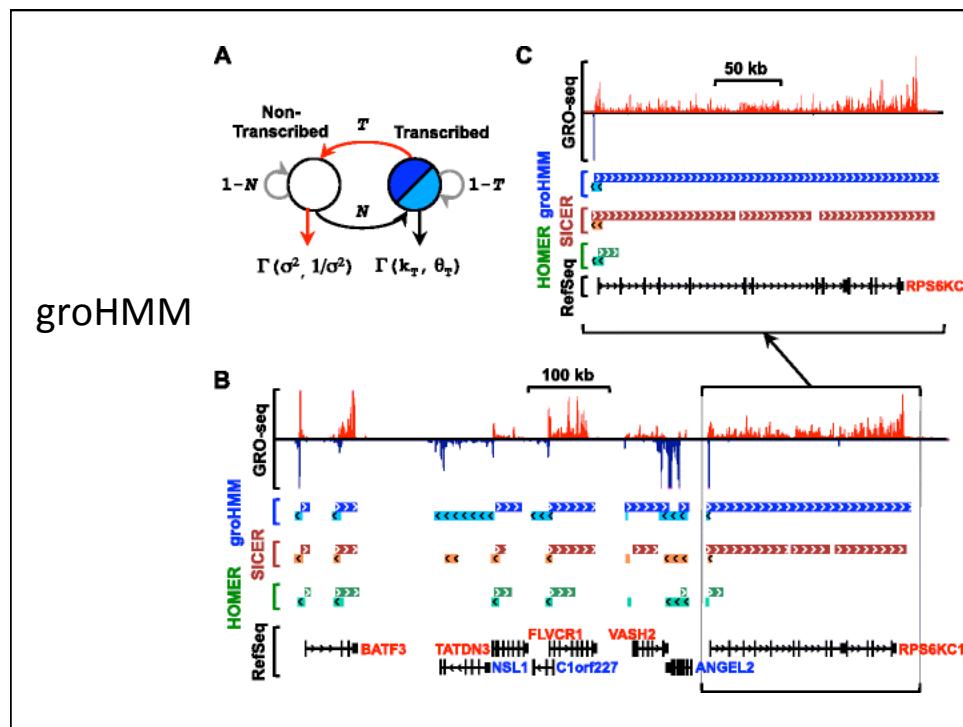
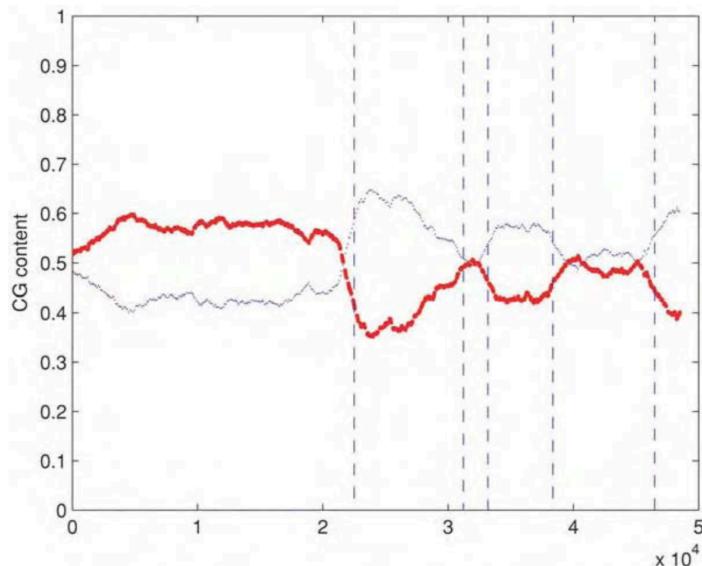
Viterbi Given a model M and an observed string S , what is the most probable path through M generating S .

Forward Given a model M and an observed string S , what is the total probability of S under M

Training Given a set of strings and a model structure, find transition and emission probabilities assigning high probabilities to the strings



Segmentation of lambda phage genome



Multiple Alignment

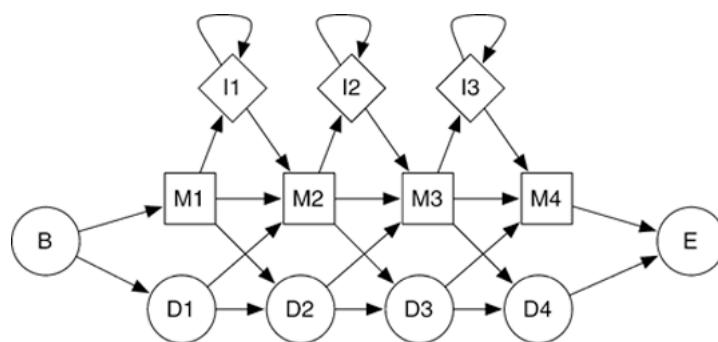
(a) Sequence Alignment

Seq 1	5' → T	C	-	G	A	3'
Seq 2	5' → T	C	A	C	A	3'
Seq 3	5' → T	G	A	G	T	3'
Seq 4	5' → T	C	A	C	-	3'
Seq 5	5' → -	C	A	C	T	3'

(b) Ungapped HMM



Profile HMMs



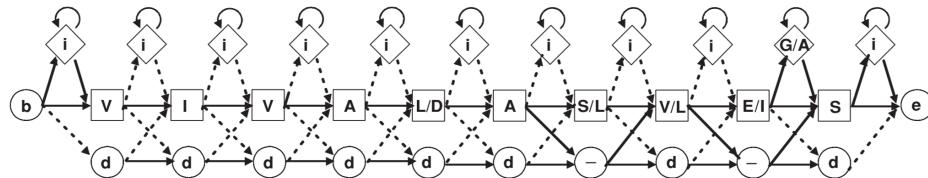
Profile HMMs

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V I V A L A S V E G A S
V I V A D A - V I - - S
V I V A D A L L - - A S

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position-specific information about the frequency of particular amino acids as well as the frequency of insertions and deletions in the alignment.

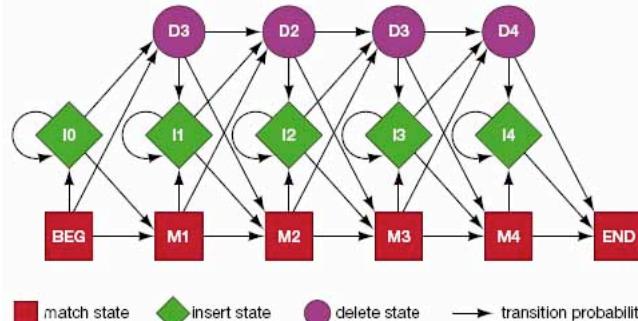


A. Sequence alignment

N	•	F	L	S
N	•	F	L	S
N	K	Y	L	T
Q	•	W	-	T

RED POSITION REPRESENTS ALIGNMENT IN COLUMN
 GREEN POSITION REPRESENTS INSERT IN COLUMN
 PURPLE POSITION REPRESENTS DELETE IN COLUMN

B. Hidden Markov model for sequence alignment



Pfam

welcome trust sanger institute

Family: **Piwi** (PF02171)

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Pfam keyword search Go

18 architectures 842 sequences 0 interactions 215 species 46 structures

Summary

Domain organisation Clans Alignments HMM logo Trees Curation & models Species Interactions Structures

Jump to... ↴

enter ID/acc

Summary

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

Wikipedia: Piwi Pfam Interpro

The Pfam group coordinates the annotation of Pfam families in Wikipedia. This family is described by a Wikipedia entry entitled "Piwi". More...

Piwi Edit Wikipedia article

The piwi (sometimes also PIWI; originally P-element induced wimpy testis in *Drosophila*^[2]) class of genes was originally identified as encoding regulatory proteins responsible for maintaining incomplete differentiation in stem cells and maintaining the stability of cell division rates in germ line cells.^[3] Piwi proteins are highly conserved across evolutionary lineages and are present in both plants and animals.^[4] One of the major human homologs, whose upregulation is implicated in the formation of tumors such as seminomas, is called hiwi.^[5] Other variants on the theme include the miwi protein in mice.^[6]

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- 2 piRNAs and transposon silencing
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Role in RNA interference

The piwi domain^[7] is a protein domain homologous to piwi proteins and present in a large number of nucleic acid-binding proteins, especially in the germ line of insects. The largest family of proteins is the argonaute family; argonautes are ribose-H-like enzymes that carry out the catalytic functions of the RNA-induced silencing complex (RISC). In the well-known cellular process of RNA interference, the argonaute protein in the RISC complex binds small interfering RNA (siRNA) generated from exogenous double-stranded RNA or microRNA (miRNA) generated from endogenous non-coding RNA, both the ribonuclease dicer. The RNA duplex binds to the argonaute protein, which then cleaves the siRNA, destroying it at the 3' end preventing its transition into a protein. Crystallized piwi domains have a conserved binding site for the 5' end of bound RNA; in the case of argonaute proteins binding siRNA strands, the last unpaired nucleotide base of the siRNA is also stabilized by base stacking interactions between the base and neighboring tyrosine residues.^[8]

Recent evidence suggests that the germ-line determination function of piwi proteins relies on their interaction with miRNAs, which are known to play a key role in early development and morphogenesis of *Drosophila melanogaster* embryos, in which germ-line maintenance has been extensively studied.^[9]

piRNAs and transposon silencing

Recently, a novel class of longer-than-average miRNAs known as Piwi-interacting RNAs (piRNAs) has been defined in mammalian cells, about 26-31 nucleotides long as compared to the more typical miRNA or siRNA of about 21 nucleotides. These miRNAs are processed independently of the miRNA pathway and function as

Piwi domain

Structure of *Pyrococcus furiosus* Argonaute.^[1]

Identifiers

Symbol	Piwi
Pfam	PF02171
InterPro	IPR003165
PROSITE	PS50922

Available protein structures: [show]

PDB	RCSB PDB
PDBsum	structure summary

Piwi RCSB PDB | PDB

Piwi structure summary