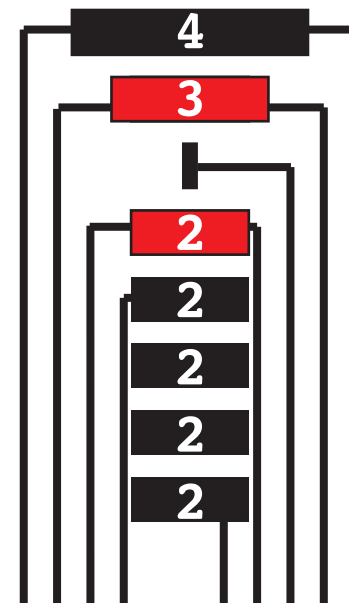


yeast	human	cow	mouse
U C	U C	U C	U C
U G	U G	U G	U G
C·G	G·C	A·U	U·A
U·A ^C	C·G ^U	C·G ^C	C·G ^U
G·C	G·C	G·C	G·C

time

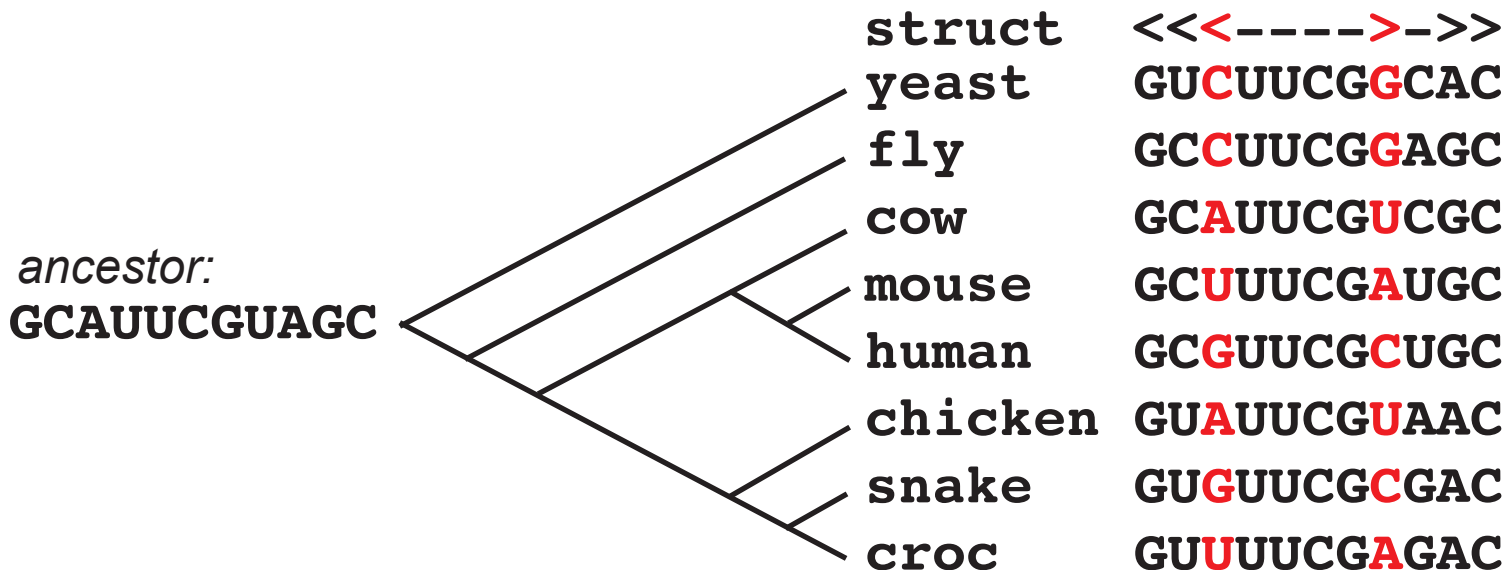
sequence + **structure**
 profile: 17 bits

Base-paired columns
 are not independent

Maximum **extra** info:
 2 bits per base pair

$\log_2 (16/4) = 2$ bits

sequence profile:
 14 bits



expect a match by chance: 1 in 2^{17} nt \approx 130 Kb
 reducing expected false positives by $2^3 = 8$ -fold