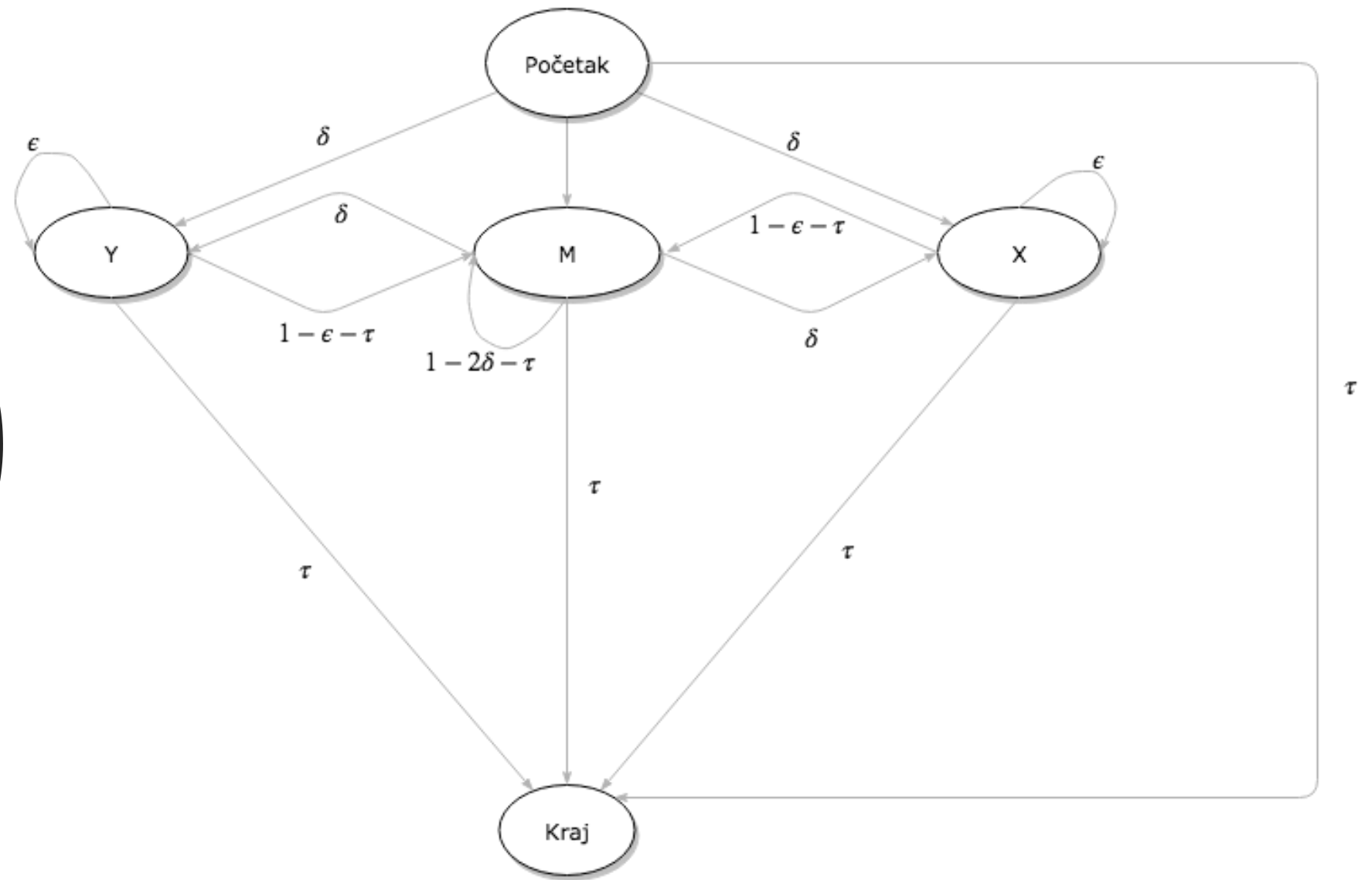


Određivanje poravnanja parova sljedova korištenjem HMM

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Hidden Markov Model



Optimalno poravnanje logaritamskim kvotama

Algoritam: optimalno poravnanje logaritamskih kvota [3]

Inicijalizacija:

$$V^M(0,0) = -2\log(\eta), V^X(0,0) = V^Y(0,0) = -\infty$$

$$V^\bullet(i, -1) = V^\bullet(-1, j) = -\infty$$

Korak:

za svaki $i = 0, \dots, n, j = 0, \dots, m$ osim $(0,0)$:

$$V^M(i, j) = s(x_i, y_j) + \max \begin{cases} V^M(i-1, j-1) \\ V^X(i-1, j-1) \\ V^Y(i-1, j-1) \end{cases} \quad (4)$$

$$V^X(i, j) = \max \begin{cases} V^M(i-1, j) - d \\ V^X(i-1, j) - e \end{cases} \quad (5)$$

$$V^Y(i, j) = \max \begin{cases} V^M(i, j-1) - d \\ V^Y(i, j-1) - e \end{cases} \quad (6)$$

Uvjet zaustavljanja: $V = \max(V^M(n, m), V^X(n, m) + c, V^Y(n, m) + c)$

Pri čemu su:

$$s(a, b) = \log \frac{p_{ab}}{q_a q_b} + \log \frac{1-2\delta-\tau}{(1-\eta)^2}$$

$$d = -\log \frac{\delta(1-\epsilon-\tau)}{(1-\eta)(1-2\delta-\tau)}$$

$$e = -\log \frac{\epsilon}{1-\eta}$$

$$c = \log(1-2\delta-\tau) - \log(1-\epsilon-\tau)$$

Procjena parametara

- Maximum Likelihood Estimation
- Smoothing level = 1

$$e(\alpha, \beta) = \frac{E(\alpha, \beta) + \text{smoothing}}{\sum_{\alpha, \beta} E(\alpha, \beta) + 2 \cdot \text{smoothing}}$$

$$t(X, Y) = \frac{T(X, Y) + \text{smoothing}}{\sum_{X, Y} T(X, Y) + 2 \cdot \text{smoothing}}$$

Rezultati

<i>Sekvenca</i>	<i>Pairwise HMM score</i>	<i>MAFFT score</i>
HIV:Ref.A1.RW.92.92RW008.AB253421, Ref.A1.UG.92.92UG037.AB253429	46609	49486
HIV:Ref.A1.RW.92.92RW008.AB253421, Ref.A2.CD.97.97CDKTB48.AF286238	36264	42534
Tropomyosin : Homo sapiens cDNA, Soares Thymus Mus musculus cDNA	855	1761
Hepatitis B virus isolate G376-A6, complete genome, Hepatitis C virus genotype 1, complete genome	-3273	2691
Nasumične sekvenca duljine 101 i 105 znakova	102	187
Nasumične sekvenca duljine 5097 i 5053 znakova	4300	9516

Tablica 7: Usporedba rezultata poravnanja modela učenog na bazi HIV-a poravnatoj s *ClustalW*-om

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