## 1 Derivation of *EAD* recurrences given in the main text Section 3.2

Beyond the notations introduced in section 3.2 of the main text, the derivation below uses the following additional ones:

**A** the **set** of all possible alignments between  $\langle S, T \rangle$ .

 $\mathbf{A}_{(i,j)}$  the set of all possible alignments of their prefixes  $\langle S_{1...i}, T_{1...j} \rangle$  of the sequences.

 $\mathbf{A}_{(i,j)}^{\mathtt{m}}$  the subset of all alignments of prefixes that end in a match(m) state at cell (i,j).

 $\mathbf{A}_{(i,j)}^{\mathbf{i}}$  the subset of all alignments of prefixes that end in a insert(i) state at cell (i, j).

 $\mathbf{A}_{(i,j)}^{\mathsf{d}}$  the subset of all alignments of prefixes that end in a delete(d) state at cell (i, j).

 $\mathcal{A}_{(i,j)}^{\mathtt{m}}$  any **alignment** of prefixes that ends in a match(m) state at (i,j).

 $\mathcal{A}_{(i,j)}^{i}$  any **alignment** of prefixes that ends in a insert(i) state at (i,j).

 $\mathcal{A}_{(i,j)}^{d}$  any alignment of prefixes that ends in a delete(d) state at (i,j).

 $\mathcal{A}_{(i,j)}^{m|m}$  any **alignment** of prefixes that ends in a match(m) state at (i, j) given a match(m) state at (i-1, j-1). (Similar notation for all 9 possible transitions going between any two states of {match, insert, delete}.)

 $Pr(\mathbf{m}|\mathbf{m})$  the transition probability of going into a match given a previous match state.

(Similar notation for all 9 possible transitions going between any two states of {match, insert, delete}.)

 $\Pr(\langle s_i, t_j \rangle)$  the joint probability of matching a pair of amino acids,  $s_i \in S$  and  $t_j \in T$ .

## Derivation

Starting with recurrence (6) in the main text, by the definition of  $EAD^{m}(i, j)$ , we have:

$$EAD^{\mathfrak{m}}(i,j) = \sum_{\forall \mathcal{A}_{(i,j)}^{\mathfrak{m}} \in \mathbf{A}_{(i,j)}^{\mathfrak{m}}} \Pr(\mathcal{A}_{(i,j)}^{\mathfrak{m}}, \langle S_{1...i}, T_{1...j} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathfrak{m}}, \mathcal{A}_{\operatorname{ref}}),$$
(1)

But all alignments  $\mathbf{A}_{(i,j)}^{m}$  that end in a match (m) state at (i, j) are derived by extending all alignments arriving at the cell (i - 1, j - 1) in any of the three alignment states ({match, insert, delete}), that is the set of alignments  $\mathbf{A}_{(i-1,j-1)} = \mathbf{A}_{(i-1,j-1)}^{m} \cup \mathbf{A}_{(i-1,j-1)}^{i} \cup \mathbf{A}_{(i-1,j-1)}^{d}$ , by a pair of matched amino acids corresponding to the cell (i, j), that is,  $\langle s_i, t_j \rangle$ .

Therefore, Equation 1, can be decomposed based on the above observation as:

$$EAD^{\mathbf{m}}(i,j) = \sum_{\forall \mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{m}} \in \mathbf{A}_{(i,j)}^{\mathbf{m}}} \Pr(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{m}}, \langle S_{1...i}, T_{1...j} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{m}}, \mathcal{A}_{\operatorname{ref}}) + \sum_{\forall \mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{i}} \in \mathbf{A}_{(i,j)}^{\mathbf{m}}} \Pr(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{i}}, \langle S_{1...i}, T_{1...j} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{i}}, \mathcal{A}_{\operatorname{ref}}) + \sum_{\forall \mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{d}} \in \mathbf{A}_{(i,j)}^{\mathbf{m}}} \Pr(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{d}}, \langle S_{1...i}, T_{1...j} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathbf{m}|\mathbf{d}}, \mathcal{A}_{\operatorname{ref}})$$
(2)

where the component joint probability terms in the r.h.s of Equation 2 are equivalent to:

$$\begin{aligned} \Pr(\mathcal{A}_{(i,j)}^{\mathfrak{m}|\mathfrak{m}}, \langle S_{1...i}, T_{1...j} \rangle) &= \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{m}) \times \Pr(\langle s_i, t_j \rangle) \\ \Pr(\mathcal{A}_{(i,j)}^{\mathfrak{m}|\mathfrak{i}}, \langle S_{1...i}, T_{1...j} \rangle) &= \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{i}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{i}) \times \Pr(\langle s_i, t_j \rangle) \\ \Pr(\mathcal{A}_{(i,j)}^{\mathfrak{m}|\mathfrak{d}}, \langle S_{1...i}, T_{1...j} \rangle) &= \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{d}) \times \Pr(\langle s_i, t_j \rangle) \end{aligned}$$

Further, the component distance terms in the r.h.s of Equation 2 can be expanded as:

$$\begin{aligned} \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathtt{m}|\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) &= \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) + \delta(i+j-1) + \delta(i+j) \\ \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathtt{m}|\mathtt{i}}, \mathcal{A}_{\operatorname{ref}}) &= \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{i}}, \mathcal{A}_{\operatorname{ref}}) + \delta(i+j-1) + \delta(i+j) \\ \operatorname{distance}(\mathcal{A}_{(i,j)}^{\mathtt{m}|\mathtt{d}}, \mathcal{A}_{\operatorname{ref}}) &= \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{d}}, \mathcal{A}_{\operatorname{ref}}) + \delta(i+j-1) + \delta(i+j) \end{aligned}$$

This holds because any alignment ending in a match state at (i, j) must arrive from (i - 1, j - 1), and in doing so, will cross two skew-diagonals (see Figure 1. Also cf. Figure 1 in the main text)

- 1. one skew-diagonal indexed by i + j 1 and
- 2. the other skew-diagonal indexed by i + j.

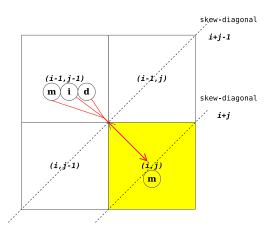


Figure 1: All alignments ending in a match state at (i, j) cross two skew-diagonals, along which their additional distances has to be accounted for during dynamic programming

Thus, for all alignments going from (i - 1, j - 1) to (i, j), the component distance terms at (i - 1, j - 1) get augmented by a  $\delta(i + j - 1) + \delta(i + j)$ , accounting for their widths/slacks with respect to the reference alignment  $\mathcal{A}_{ref}$  along the above two skew-diagonals.

Substituting the expanding the component joint probability and distance terms shown above into Equation 2, after rearranging yields:

$$\begin{split} EAD^{\mathtt{m}}(i,j) &= \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) \times \Pr(\mathtt{m}|\mathtt{m}) \times \Pr(\langle s_{i}, t_{j} \rangle)}_{EAD^{\mathtt{m}}(i-1,j-1)} \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{Pr}(\mathtt{m}|\mathtt{m}) \times \Pr(\langle s_{i}, t_{j} \rangle) \times [\delta(i+j-1)+\delta(i+j)]}_{EAD^{\mathtt{m}}(i-1,j-1)} \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) \times \Pr(\mathtt{m}|\mathtt{n}) \times \Pr(\mathtt{m}|\mathtt{n}) \times \Pr(\mathtt{m}|\mathtt{n}) \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{Pr}(\mathtt{m}|\mathtt{n}) \times \Pr(\langle s_{i}, t_{j} \rangle) \times [\delta(i+j-1)+\delta(i+j)]}_{EAD^{\mathtt{m}}(i-1,j-1)} \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) \times \Pr(\mathtt{m}|\mathtt{n}) \times \Pr(\langle s_{i}, t_{j} \rangle) \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) \times \Pr(\mathtt{m}|\mathtt{n}) \times \Pr(\langle s_{i}, t_{j} \rangle) \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \mathcal{A}_{\operatorname{ref}}) \times \Pr(\mathtt{m}|\mathtt{n}) \times \Pr(\langle s_{i}, t_{j} \rangle) \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{i}, t_{j} \rangle) \times \Pr(\langle s_{i}, t_{j} \rangle) \\ &+ \underbrace{\sum_{\forall A_{(i-1,j-1)}^{\mathtt{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{i}, t_{j} \rangle) \times [\delta(i+j-1)+\delta(i+j)] \\ &= \underbrace{\sum_{\forall A_{i}^{\mathtt{m}} \in \mathbf{A}_{i}^{\mathtt{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathtt{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \operatorname{distance}(\mathcal{A}_{i}, t_{j} \rangle) \times [\delta(i+j-1)+\delta(i+j)]$$

By grouping all even terms on the r.h.s. of Equation 3 together, we get the recurrence:

$$\begin{split} EAD^{\mathfrak{m}}(i,j) &= EAD^{\mathfrak{m}}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{m}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ EAD^{1}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{i}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ EAD^{\mathfrak{d}}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{d}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ \left( \sum_{\forall \mathcal{A}_{(i-1,j-1)}^{\mathfrak{m}} \in \mathbf{A}_{(i-1,j-1)}^{\mathfrak{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{m}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{m}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ \sum_{\forall \mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}} \in \mathbf{A}_{(i-1,j-1)}^{\mathfrak{m}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{i}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ \sum_{\forall \mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}} \in \mathbf{A}_{(i-1,j-1)}^{\mathfrak{d}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{d}) \times \Pr(\langle s_{i},t_{j} \rangle) \\ &+ \sum_{\forall \mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}} \in \mathbf{A}_{(i-1,j-1)}^{\mathfrak{d}}} \Pr(\mathcal{A}_{(i-1,j-1)}^{\mathfrak{d}}, \langle S_{1...i-1}, T_{1...j-1} \rangle) \times \Pr(\mathfrak{m}|\mathfrak{d}) \times \Pr(\langle s_{i},t_{j} \rangle) \right) \\ &\times [\delta(i+j-1) + \delta(i+j)] \end{split}$$

But the last term on the r.h.s. is the marginal probability over all alignments ending in a match at (i, j), resulting in the final form of recurrence (6) used in the main text:

$$EAD^{\mathfrak{m}}(i,j) = EAD^{\mathfrak{m}}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{m}) \times \Pr(\langle s_{i},t_{j}\rangle) + EAD^{1}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{i}) \times \Pr(\langle s_{i},t_{j}\rangle) + EAD^{d}(i-1,j-1) \times \Pr(\mathfrak{m}|\mathfrak{d}) \times \Pr(\langle s_{i},t_{j}\rangle) + \Pr_{\mathrm{marginal}}(\langle S_{1...i},T_{1...j}\rangle | \mathtt{match}\mathfrak{Q}(i,j)) \times [\delta(i+j-1) + \delta(i+j))$$
(5)

Recurrences (7) and (8) in the main text follow identical lines of derivations, with the only difference that they account for all alignments coming into (i, j) in a insert(i) and delete(d) states, respectively. Also, all such alignment transitions only cross a single skew-diagonal, indexed by i + j, therefore those recurrences will contain only the  $\delta(i + j)$  term.