

Using Spatial Order to Boost the Elimination of Incorrect Feature Matches

Supplementary Material

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In this document we complete the missing proofs of the paper, and present a synthetic experiment to test the algorithm's robustness to deviations from assumption A1.

1. Proof for $E(\hat{K}_B) = 1/2$ (Line 358)

Proposition 1. Assuming A2, $E(\hat{K}_B) = 1/2$.

Proof. Let $C = C_2^{N_B}$ be the number of incorrect matches. From Eq. 1, Eq. 4 & Eq. 5, and the linearity of the expectation, we get

$$\begin{aligned} E(\hat{K}_B) &= E[\frac{K_B}{C}] \\ &= E[\frac{1}{C} \sum_{i \in N_B} \sum_{j \in N_B} \eta_\sigma(i, j)] \\ &= \frac{1}{C} \sum_{i \in N_B} \sum_{j \in N_B} E[\eta_\sigma(i, j)]. \end{aligned}$$

Using the definition of η_σ , the expectation, $E[\eta_\sigma(i, j)]$, is given by

$$\begin{aligned} E[\eta_\sigma(i, j)] &= 1 \cdot P[\sigma(j) < \sigma(i)] + 0 \cdot P[\sigma(j) > \sigma(i)] \\ &= P[\sigma(j) < \sigma(i)]. \end{aligned}$$

Since we assume A2 (The spatial order of incorrect matches is random) for $i, j \in B$, it follows that $P[\sigma(j) < \sigma(i)] = P[\sigma(j) > \sigma(i)]$. (Otherwise it implies that there is a prior for the order of $\sigma(i)$ or $\sigma(j)$, and consequently either $\sigma(i)$ or $\sigma(j)$ are not random.) Since $P[\sigma(j) < \sigma(i)] = 1 - P[\sigma(j) > \sigma(i)]$, it follows that $P[\sigma(j) < \sigma(i)] = 1/2$. Putting it all together, we obtain

$$\begin{aligned} E(\hat{K}_B) &= \frac{1}{C} \sum_{i \in N_B} \sum_{j \in N_B} E[\eta_\sigma(i, j)] \\ &= \frac{1}{C} \sum_{i \in N_B} \sum_{j \in N_B} \frac{1}{2} = \frac{1}{2} \frac{C}{C} = \frac{1}{2}. \end{aligned}$$

□

2. Proof for $\max_{\omega} N_G(\omega) = N_G(\omega^*)$ (Claim 2)

We first state our main assumption:

A4: The estimated N_G from Eq. 10 is the true number of correct matches in the case where ω defines fully overlapped subsequences (and only in this case).

Proposition 2. Assuming A4, $\max_{\omega} N_G(\omega) = N_G(\omega^*)$.

Proof. We first consider the case where $\omega^* = (j_L^1, j_H^1, 1, N)$. In this case, we also set $\omega = (i_L^1, i_H^1, 1, N)$. For simplicity we write $\omega_1^* = (j_L^1, j_H^1)$ and $\omega_1 = (i_L^1, i_H^1)$. Let us consider three sub-cases: (i) ω_1 is fully contained in ω_1^* , i.e., $j_L^1 \leq i_L^1$ and $j_H^1 \geq i_H^1$. (ii) $\omega_1^* \cap \omega = \emptyset$, that is ω_1^* has no overlapping with ω_1 . (iii) ω_1 “intersects” ω_1^* , but neither are contained in each other, i.e., w.l.g. $j_L^1 \leq i_L^1$ and $j_H^1 \leq i_H^1$.

Let $N_G^* = N_G(\omega^*)$ be the true number of correct matches and $N_G = N_G(\omega)$ be the estimated number of correct matches in the subsequences defined by ω . Let us consider sub-case (i). Since ω_1 is contained in ω_1^* , the subsequences defined by ω are fully overlapped; therefore, using Assumption A4, N_G is the true number of correct matches in the fully overlapped subsequences defined by ω . In this case, it is given that $N_G \leq N_G^*$, since the fully overlapped subsequences defined by ω contain no more correct matches than ω^* , by the definition of ω .

Let us consider sub-case (ii) using Assumption A4, N_G is the true number of correct matches in the fully overlapped subsequences defined by ω . Since there are no inliers in the region, we obtain $0 = N_G < N_G^*$.

Let us consider the last sub-case (iii). Let N_G' be the true number of correct matches in the subsequences defined by ω . Consider the expected number of inversions for the incorrect matches in the margins outside ω_1^* , i.e., $[i_L^1, j_L^1]$ and $[j_H^1, i_H^1]$. The term K_B remains the same, since it depends only on N_B and not on the distribution of $i \in G$ and $i \in B$. In contrast, $E(\hat{K}_{GB}) = 1/3$ (claim 1), does not hold for these incorrect matches. Instead, it can be shown that it is

given that $E(\hat{K}_{GB}) = 1/2$ for these incorrect matches. If we take this new term into account in Eq. 10, we get an estimation of N_G as a function of \hat{K}_N and the number of matches outside ω_1^* , N_M , as an additional variable:

$$0 = -\frac{1}{6}N_G^2 + \left(\frac{1}{2} - \frac{1}{3}N + \frac{1}{3}N_M\right)N_G + N(N-1)\left(\frac{1}{2} - \hat{K}_N\right). \quad (1)$$

From this equation it is clear that increasing N_M , increases N_G (for one of the solutions of the equation); therefore, if we set N_M to its true value, i.e., $N_M = |i_L^1 - j_L^1| + |j_H^1 - i_H^1|$, we get a higher value for N_G than in the case where $N_M = 0$ (the case for ω), and consequently $N_G \leq N_G^*$.

Finally, the general case where $\omega^* = (j_L^1, j_H^1, k_L^1, k_H^1)$, is similar and follows the same reasoning. To see that, consider that if $k_L^1 > 1$ or $k_H^1 < N$, the same reasoning from sub-case (ii), where $E(\hat{K}_{GB}) = 1/2$, can be applied to the incorrect matches in $[1, k_L^1]$ or $[k_H^1, N]$. \square

3. Matching Probabilities (Sec. 5)

We next describe our estimation of $P(H_\sigma(i)|i \in G)$ and $P(H_\sigma(i)|i \notin G)$. Consider $\beta = (\beta_1^l, \beta_1^r, \beta_2^l, \beta_2^r)$ (defined in Sec. 4.2). Since β is unknown, we compute $P(H_\sigma(i)|i \in G)$ by:

$$P(H_\sigma(i)|i \in G) = P(H_\sigma(i)|i \in G, \beta)P(\beta).$$

Let $B(n, p)$ be a binomial probability density function (PDF), where n is the number of binomial trials and p is the probability of success. Let $B_B(i-1, \hat{N}_B)$ describe the PDF that there are $\beta_1^l \in \{0, \dots, i-1\}$ incorrectly matched features to the left of i , where $\hat{N}_B = N_B/N$. Similarly, $B_B(\sigma(i)-1, \hat{N}_B)$ corresponds to β_2^l . We compute $P(\beta)$ as the product of these two binomial PDFs:

$$P(\beta) = B_B(i-1, \hat{N}_B)B_B(\sigma(i)-1, \hat{N}_B).$$

Let $B_H(\beta_1^l, p_1)$ describe the PDF that $H_\sigma^1(i) \in \{0, \dots, \beta_1^l\}$ order inversions occur out of the β_1^l order inversions possible, given the number incorrectly matched features to the right of $\sigma(i)$, where $p_1 = 1 - \beta_1^l/N_B$. Similarly, $B_H(\beta_2^l, p_2)$ corresponds to β_2^l , where $p_2 = 1 - \beta_2^l/N_B$. The probability $P(H_\sigma(i)|i \in G, \beta)$ can be described as a product of these two binomial PDFs:

$$P(H_\sigma(i)|i \in G, \beta) = B_H(\beta_1^l, p_1)B_H(\beta_2^l, p_2).$$

Similarly, although with one difference which is described next, it is given that:

$$P(H_\sigma(i)|i \notin G) = P(H_\sigma(i)|i \notin G, \beta)P(\beta).$$

For $i \notin G$, i.e., $i \in B$, the number of order inversions with the correct matches needs to be taken into account when considering the number of order inversions in

\hat{K}_G	0	0.002	0.005	0.02	0.05	0.1	0.15
$\mu(N_G)$	4	4.1	4.4	5	6.2	8.5	10.7

Table 1. The mean normalized absolute error (percentage) in the estimation of N_G for the synthetic experiment ‘‘Exp1’’, when deviations from assumption A1 (values $\hat{K}_G \neq 0$ are considered.)

$P(H_\sigma(i)|i \notin G, \beta)$. Specifically, p_1 and p_2 of $B_H(\beta_1^l, p_1)$ and $B_H(\beta_2^l, p_2)$ needs to be corrected. We consider two cases. The first is when $i > \sigma(i)$; in this case, the corrected values are given by $p_1' = p_1 + |\gamma_1^l - \gamma_2^l|$ and $p_2' = p_2$, where γ_1^l and γ_2^l are the number of correct matches to the left of i and $\sigma(i)$, respectively. Similarly, in the second case it is given that ($i < \sigma(i)$), $p_1' = p_1$ and $p_2' = p_2 + |\gamma_1^l - \gamma_2^l|$.

Since computing these PDFs is time-consuming (tens of seconds for 1000 matches), we use several approximations. First, we consider only a few values of β_1^l , β_1^r , β_2^l and β_2^r around the means, $\hat{N}_B(i-1)$ and $\hat{N}_B(\sigma(i)-1)$, respectively. Second, the binomial distributions are approximated using Gaussian distributions with means and standard deviations of the respective binomial distributions. Finally, computing $P(H_\sigma(i)|i \notin G, \beta)$ is more time-consuming than computing $P(H_\sigma(i)|i \in G, \beta)$, since $\gamma_1^l = \gamma_2^l$ for the latter; hence, β_1^l and β_2^l are constrained. We approximate $P(H_\sigma(i)|i \notin G, \beta)$ as a uniform distribution (different for each i). This uniform distribution is obtained by calculating the range, d , which is given by the difference between the maximal and minimal values of $H_\sigma(i)$. The uniform probability is then given by $1/d$. The maximal value is given by $\sigma(i) = 1$ when $i > N - i$ and by $\sigma(i) = N$ otherwise. The minimal value is given when $i = \sigma(i)$.

4. Deviation From A1 Assumption

We used in our analysis the assumption that the order of correct matches is preserved (A1). Clearly, in real data, this assumption does not strictly hold. For systematically testing the effect of the deviation from this assumption on the computation of N_G , we repeated the synthetic experiments of Sec. 7.1, with inversions between correct matches. We parametrized the number of inversions by the normalized Kendall distance of the correct matches, \hat{K}_G , which is not available to the algorithm. (In the original experiment we used $\hat{K}_G = 0$.) The results show that our method is robust to a relatively large deviation from assumption A1 (Tab. 1). For example, in the synthetic experiment ‘‘Syn1’’, where $N_G = 300$ out of $N = 1000$ matches, in our original experiment, $\hat{K}_G = 0$ and the error was $\mu(N_G) = 4$. In the new experiment we considered $\hat{K}_G = 0.002$ and $\hat{K}_G = 0.02$ which correspond to 90 and 900 inversions, respectively. Note that if one third of the correct matches are switched with their correct neighbor, than we will obtain approximately 100 inversions. The errors are $\mu(N_G) = 4.1$ and $\mu(N_G) = 5$, respectively.