# CS 215 — Assignment 2

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## 1: Pool Testing

## (a) Disjoint pools of size s.

**Step 1:** We split n people into n/s disjoint pools, each of size s.

**Step 2:** Round 1: test the n/s pools.

Step 3: Round 2: test individually everyone who was not in a negative pool.

We are given that the disease prevalence is p, i.e in the entire population (not just in these n people) percentage of affected people is p, hence for these n people currenty being tested, each person has a chance p of being affected.

#### (a-i) Expected total tests T(s):

A pool is positive iff it contains  $\geq 1$  diseased person:

 $Pr(\text{pool positive}) = r = 1 - (1 - p)^s$ 

Say M is the number of positive pools among the m = n/s pools.

Because pools are disjoint and each pool is positive with probability r,

$$M \sim \text{Binomial}(m, r), \qquad \Pr(M = k) = \binom{m}{k} r^k (1 - r)^{m - k} \quad (k = 0, 1, \dots, m).$$

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$$E[M] = \sum_{k=0}^{m} k \binom{m}{k} r^k (1-r)^{m-k}$$

$$= \sum_{k=1}^{m} m \binom{m-1}{k-1} r^k (1-r)^{m-k} \qquad \left(\text{since } k \binom{m}{k} = m \binom{m-1}{k-1}\right)$$

$$= mr \sum_{k=1}^{m} \binom{m-1}{k-1} r^{k-1} (1-r)^{(m-1)-(k-1)}$$

$$= mr \sum_{t=0}^{m-1} \binom{m-1}{t} r^t (1-r)^{(m-1)-t} \qquad (t=k-1)$$

$$= mr (r+1-r)^{m-1}$$

$$= mr.$$

With m = n/s and  $r = 1 - (1 - p)^s$ , we obtain

Expected Number of positive pools =  $E[M] = \frac{n}{s} [1 - (1-p)^s].$ 

Therefore, the expected number of people re-tested in round 2 is

$$s \cdot E[M] = n [1 - (1-p)^s].$$

Total expected number of tests = T(s)

T(s) = Expected number of tests in round 1 + Expected number of tests in round 2:

$$T(s) = \underbrace{E[\text{round 1 tests}]}_{= n/s} + \underbrace{E[\text{round 2 tests}]}_{= n [1 - (1 - p)^s]}.$$

The first term is exactly the number of pools, n/s. The second term follows from the above calculation and is equal to  $n[1-(1-p)^s]$  tests expectated for round 2. Therefore,

$$T(s) = \frac{n}{s} + n[1 - (1-p)^s].$$

(a-ii) Very small p approximation: For small p, we know  $(1-p)^s \approx 1-sp$ . Then

$$T(s) \approx \frac{n}{s} + nsp.$$

Treating s as continuous:

T(s) is minimum when  $\frac{d}{ds}(\frac{n}{s} + nsp) = -\frac{n}{s^2} + np = 0 \Rightarrow s^* \approx \frac{1}{\sqrt{p}}$  (round to nearest integer).

$$T_{\rm min} \approx 2n\sqrt{p}$$

(a-iii) When is pooling better than individual testing: We want T(s) < n:

$$\frac{n}{s} + n[1 - (1-p)^s] < n \implies (1-p)^s > \frac{1}{s} \implies p < 1 - s^{-1/s}$$

Maximizing the threshold  $1 - s^{-1/s}$  over integers  $s \ge 2$  gives s = 3, with

$$p_{\text{max}} = 1 - 3^{-1/3} \approx 0.30664.$$

So for values of P greater than this, no number of pools will give expected number of tests with pooling better than individual testing, hence for values greater than this there is no point in pooling.

#### (b) Setup:

We have n subjects; the prevalence of the disease is  $p \in [0,1]$  (I assume that in the whole population p is the prevalence rate and not that there are exactly np diseased people), and the tests are perfect. In round 1 there are  $T_1$  pools. Each subject independently joins each pool with probability  $\pi$  (so the pool memberships overlap and the pool sizes are random). Round 2 individually tests all subjects who did not participate in a negative pool in Round 1.

For a fixed healthy subject X and a fixed pool, the pool is negative for X iff none of the other n-1 people are *both* infected and included in that pool. Each other person independently contaminates the pool with probability  $p\pi$ , hence

$$\Pr(X \text{ joins a specific pool and that pool is negative}) = h(\pi) = \pi (1 - p\pi)^{n-1}.$$
 (1)

## (b-i) Probability that a healthy subject participates in a pool that tests negative:

Across the  $T_1$  pools, the events "X joins & the pool is negative" are independent, each with probability  $h(\pi)$ . Therefore,

Pr(Healthy subject(X) participates in a negative pool)

= 
$$\Pr(X \text{ is } cleared \text{ in round } 1)$$
  
=  $1 - \Pr(\text{none of the } T_1 \text{ pools both joined and negative})$   
=  $1 - (1 - h(\pi))^{T_1}$   
=  $1 - \left[1 - \pi(1 - p\pi)^{n-1}\right]^{T_1}$ 

#### (b-ii) Choice of $\pi$ that maximizes this probability: We want to maximize

$$1 - \left[1 - \pi(1 - p\pi)^{n-1}\right]^{T_1}$$

Since the outer expression is  $1 - (1 - (\cdot))^{T_1}$ , maximizing this probability is the same as maximising  $\pi (1 - p\pi)^{n-1}$ 

Maximizing  $\pi(1-p\pi)^{n-1}$  is equivalent to setting  $\frac{d}{d\pi}\Big(\pi(1-p\pi)^{n-1}\Big)=0$ .

$$\frac{d}{d\pi} \Big( \pi (1 - p\pi)^{n-1} \Big) = 0 \implies (1 - p\pi)^{n-2} \Big[ 1 - pn\pi \Big] = 0 \implies \pi = \frac{1}{np}$$

Clipping to the feasible range gives

$$\pi_{optimal} = \min\{1, 1/(np)\}$$
 (2)

(Second derivative is negative at this point; hence it is a maximizer.)

#### (b-iii) Probability all pools a healthy subject joins are positive for $\pi_{optimal}$ :

The event "all joined pools are positive" occurs exactly when none of the  $T_1$  pools is simultaneously joined-and-negative. Thus

Pr(all joined pools test positive) = 
$$(1 - h(\pi))^{T_1} = \left[1 - \pi(1 - p\pi)^{n-1}\right]^{T_1}$$
 (3)  
Plugging in  $\pi = \frac{1}{np}$  gives (if  $np > 1$ )

$$\Pr(\text{all joined pools test positive}) = \left[1 - \frac{1}{np} \left(1 - \frac{1}{n}\right)^{n-1}\right]^{T_1}$$

#### (b-iv) Expected total number of tests:

Round 1 contributes  $T_1$  tests.

Round 2 contributions:

- Truly positive subjects: an infected person is never cleared by Round 1. Hence *all* infected are tested in Round 2.
- Truly healthy subjects: a healthy person is tested in Round 2 iff they are not cleared in Round 1.

 $Pr(\text{not cleared in Round 1} \mid Sick) = 1$ 

Pr(not cleared in Round 1 | Healthy) =  $(1 - h(\pi))^{T_1}$ 

 $\Pr(A \text{ specific person is tested in Round 2}) = \Pr(\text{tested in round 2} \mid Infected) \Pr(Infected) + \Pr(A \text{ specific person is tested in Round 2}) = \Pr(\text{tested in round 2} \mid Infected) + \Pr(A \text{ specific person is tested in Round 2}) = \Pr(\text{tested in round 2} \mid Infected) + \Pr(A \text{ specific person is tested in Round 2}) = \Pr(\text{tested in round 2} \mid Infected) + \Pr(A \text{ specific person is tested in Round 2}) = \Pr(\text{tested in round 2} \mid Infected) + \Pr(A \text{ specific person 2}) = \Pr(A \text{ specific person 2}) + \Pr(A \text{ specific person 2}) = \Pr(A \text{ specific person 2}) = \Pr(A \text{ specific person 2}) + \Pr(A \text{ specific person 2}) = \Pr(A \text{ specific person 2}) = \Pr(A \text{ specific person 2}) + \Pr(A \text{ specific person 2}) = \Pr(A \text{ speci$ 

Pr(tested in round 2 | Healthy) Pr(Healthy)

$$= 1 \cdot p + (1 - h(\pi))^{T_1} (1 - p)$$

 $E[\text{No. of people tested in round 2}] = n \left[ p + \left(1 - h(\pi)\right)^{T_1} (1 - p) \right]$ 

$$E[\text{total tests}] = T_1 + E[N_2] = T_1 + n \left[ p + (1 - h(\pi))^{T_1} (1 - p) \right].$$

So the expected number of test being done is

$$E[\text{tests}](T_1, \pi) = T_1 + np + n(1-p) \left( \left[ 1 - \pi (1-p\pi)^{n-1} \right]^{T_1} \right).$$
 (4)

(b-v) Minimizing the expected number of tests over  $T_1$ .

Let 
$$B := 1 - \pi (1 - p\pi)^{n-1} \in (0, 1)$$
.

Treating  $T_1$  as continuous,

$$\frac{\partial}{\partial T_1} E[\text{tests}] = 1 + n(1-p) B^{T_1} \ln B.$$

Setting the derivative to zero gives

$$1 + n(1-p) B^{T_1^{\star}} \ln B = 0 \implies B^{T_1^{\star}} = -\frac{1}{n(1-p) \ln B}.$$

Taking logs (note  $\ln B < 0$  since 0 < B < 1), the closed-form optimizer is

$$T_1^{\star} = \frac{\ln\left(-\frac{1}{n(1-p)\ln(1-\pi(1-p\pi)^{n-1})}\right)}{\ln(1-\pi(1-p\pi)^{n-1})}.$$

A meaningful solution exists only when n(1-p) ( $-\ln B$ ) > 1;(from the above expression) otherwise, the objective is minimized at the boundary  $(T_1 = 1)$ .

(c) Plot construction: We evaluate the expected number of tests for prevalence values

$$p \in \{10^{-4}, 5 \times 10^{-4}, 0.001, 0.005, 0.01, 0.02, 0.05, 0.08, 0.1, 0.2\}.$$

**Method (a):** For each s, we calculate the expected tests  $T(s) = \frac{n}{s} + n(1 - (1-p)^s)$ , and choose s which minimizes it.

**Method (b):** For  $T_1$  in  $\{1, \lfloor T_1^{\star} \rfloor - 2, \dots, \lceil T_1^{\star} \rceil + 2\}$ , we compute the expected tests by plugging in in  $\pi = \pi_{optimal}$  and choose  $T_1$  which minimizes it.

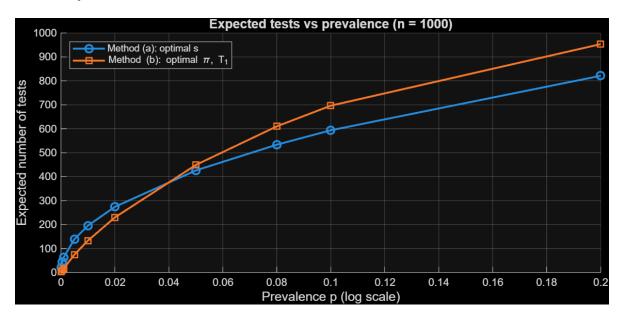
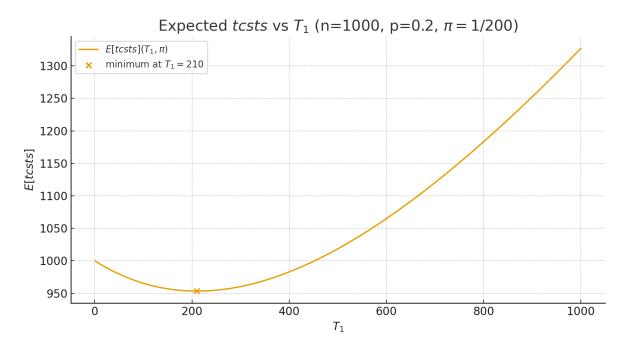


Figure 1: Expected No. of tests vs p

P	MethodA_MinTests	s_opt	MethodB_MinTests	T1_star	pi_opt
0.0001	19.951	101	3.9594	3	1
0.0005	44.476	45	8.9535	7	1
0.001	62.759	32	16.56	13	1
0.005	139.1	15	74.735	57	0.2
0.01	195.57	11	133.05	96	0.1
0.02	274.24	8	230.05	156	0.05
0.05	426.22	5	449.08	264	0.02
0.08	533.61	4	610.24	313	0.0125
0.1	593.9	4	696.51	325	0.01
0.2	821.33	3	953.37	210	0.005
>>					

Figure 2: Values which minimize Expected number of tests

**Note:** This is the graph of Expected number of tests vs  $T_1$ , for  $n = 1000, p = 0.2, \pi = 1/np$ . (Just to illustrate) (Generated with matplotlib)



#### Comments

- Overall trend. As prevalence p increases, the expected total tests for both methods grow and approach n; for small p, both are far below n.
- Disjoint pools (a): low-p scaling. The optimizer follows  $s^* \approx 1/\sqrt{p}$ , yielding  $T_{\min} \approx 2n\sqrt{p}$  for  $p \ll 1$ .
- Overlapping design (b). With first-round settings near the analytic optimum (e.g., inclusion rate  $\pi \approx 1/(np)$  and a tuned  $T_1$ ), round 1 clears many true negatives. This makes (b) essentially coincide with (a) for very small p, and often slightly outperform it for mid-range p.
- **High-**p **regime.** As  $p \to 1$ , both strategies converge to individual testing  $(T \to n)$ .

#### How to run the code

The implementation is in the file q1.m which can be executed to generate the plot and the values which minimize the expected number of tests. The code can be executed by running q1.

## 2: PDF of a new Random Variable

$$Z = X \cdot Y$$

Probability that  $a \le X \le a + da = p_X(a) da = F_X(a + da) - F_X(a)$ .

If  $a \le X \le a + da$  and  $X \cdot Y \le z$ :

$$(a > 0)$$
  $Y \le \frac{z}{a}$ , which has probability  $F_Y\left(\frac{z}{a}\right)$ 

$$(a < 0)$$
  $Y \ge \frac{z}{a}$ , whose probability is  $1 - F_Y\left(\frac{z}{a}\right)$ 

Hence, for the  $p_X(a)$  da chance that X lies in [a, a + da], there is a  $F_Y\left(\frac{z}{a}\right)$   $\left[\text{or } 1 - F_Y\left(\frac{z}{a}\right)\right]$  chance that  $XY \leq z$ . So the contribution is (casewise)

$$p_X(a) F_Y\left(\frac{z}{a}\right) da$$
 or  $p_X(a)\left(1 - F_Y\left(\frac{z}{a}\right)\right) da$ 

Since a can be anything we integrate to get the CDF  $F_Z(z)$ :

$$F_Z(z) = \int_{-\infty}^0 p_X(a) \left[ 1 - F_Y\left(\frac{z}{a}\right) \right] da + \int_0^\infty p_X(a) F_Y\left(\frac{z}{a}\right) da \tag{5}$$

#### Differentiate to obtain the PDF

$$p_Z(z) = \frac{d}{dz} F_Z(z) = \int_{-\infty}^0 p_X(a) \frac{d}{dz} \left( 1 - F_Y\left(\frac{z}{a}\right) \right) da + \int_0^\infty p_X(a) \frac{d}{dz} F_Y\left(\frac{z}{a}\right) da$$

By the chain rule,

$$\frac{d}{dz}F_Y\left(\frac{z}{a}\right) = F_Y'\left(\frac{z}{a}\right) \cdot \frac{1}{a} = p_Y\left(\frac{z}{a}\right) \cdot \frac{1}{a}$$

Therefore,

$$p_Z(z) = \int_{-\infty}^0 p_X(a) \left( -\frac{1}{a} p_Y\left(\frac{z}{a}\right) \right) da + \int_0^\infty p_X(a) \left( \frac{1}{a} p_Y\left(\frac{z}{a}\right) \right) da$$

$$= \int_{-\infty}^0 p_X(a) p_Y\left(\frac{z}{a}\right) \frac{da}{|a|} + \int_0^\infty p_X(a) p_Y\left(\frac{z}{a}\right) \frac{da}{|a|}$$

$$= \int_{-\infty}^\infty p_X(a) p_Y\left(\frac{z}{a}\right) \frac{da}{|a|}$$

Equivalently, by conditioning on Y,

$$p_Z(z) = \int_{-\infty}^{\infty} p_X(a) \, p_Y\left(\frac{z}{a}\right) \, \frac{da}{|a|} \, = \int_{-\infty}^{\infty} p_Y(a) \, p_X\left(\frac{z}{a}\right) \, \frac{da}{|a|}$$

## 3: Correct Estimator

Let  $X_1, \ldots, X_n \stackrel{\text{iid}}{\sim} f_X$  and suppose we want to estimate E[X].

Correct estimator. Use the sample mean

$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} X_i.$$

By linearity of expectation,

$$E[\hat{\mu}] = \frac{1}{n} \sum_{i=1}^{n} E[X_i] = E[X],$$

so  $\hat{\mu}$  is an unbiased estimator of E[X] (and  $Var(\hat{\mu}) = Var(X)/n$ ).

What the "weighted" estimator is actually estimating: Consider instead

$$\tilde{\mu} = \frac{1}{n} \sum_{i=1}^{n} f_X(x_i) X_i.$$

This is the sample average of the transformed variable  $h(X) = x f_X(x)$ . Hence

$$E[\tilde{\mu}] = E[Xf_X(x)] = \int x f_X(x) f_X(x) dx = \int x f_X(x)^2 dx,$$

which is not E[X] in general.

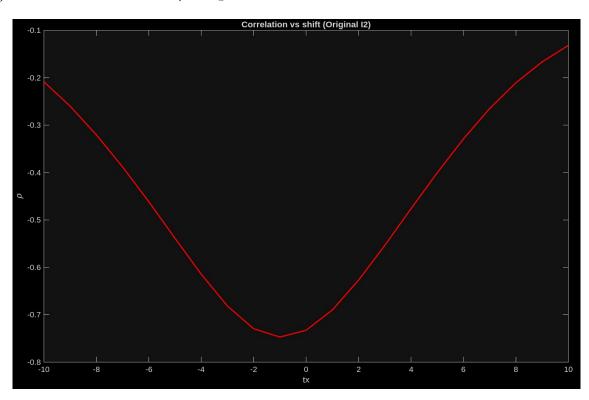
So  $\tilde{\mu}$  is correct estimator only in the special case where  $f_X$  is constant (e.g., a uniform density).

**Conclusion.** The correct choice is the plain sample mean  $\hat{\mu} = \frac{1}{n} \sum X_i$ . The weighted choice  $\tilde{\mu}$  is biased and instead estimates  $E[xf_X(x)]$ .

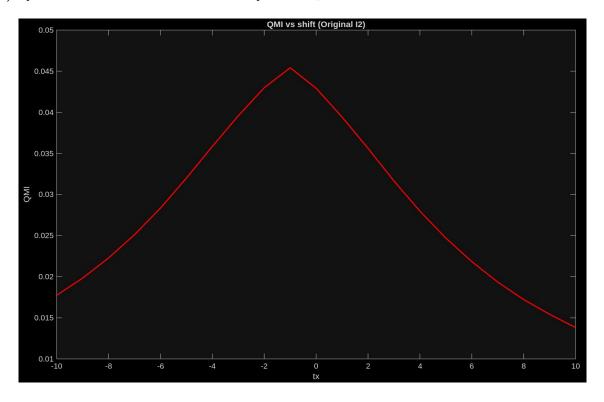
## 4: Brain Matters

## Original I2:

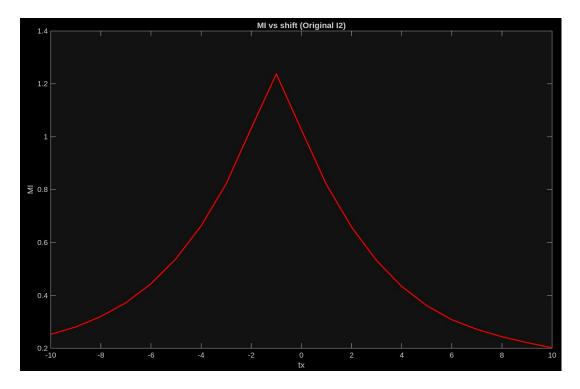
1) Correlation coefficient  $\rho$  vs  $t_x$ :



#### 2) Quadratic Mutual Information QMI vs $t_x$ :



## 3) Mutual Information MI vs $t_x$ :

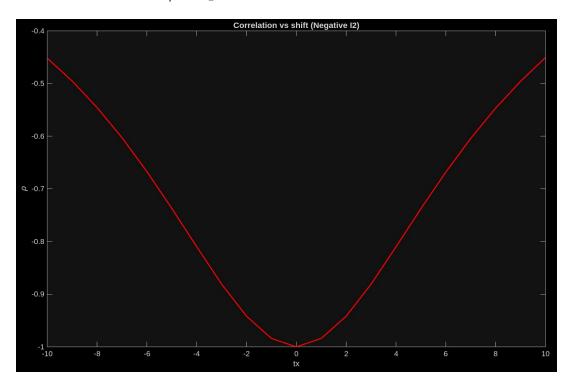


#### Comments:

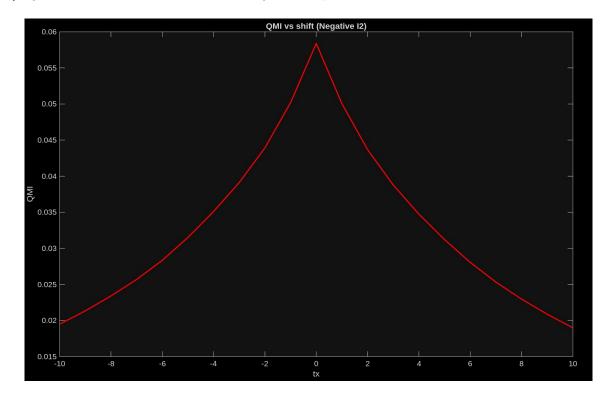
The Correlation  $\rho$  vs  $t_x$  plot is minimum at  $t_x = -1$ . So, I1 and I2 actually best aligned when shifted by 1 pixel. The magnitude is negative because the linear relationship is negative here. The QMI vs  $t_x$  plot peaks at  $t_x = -1$ , which indicates alignment. It detects the alignment better than correlation because it has a sharper peak. The MI vs  $t_x$  plot has a sharper peak than QMI at  $t_x = -1$ , which confirms the alignment. Just like QMI, MI detects the alignment more effectively than correlation because it has a sharper peak.

**Negative I2**  $(I_2 = 255 - I_1)$ :

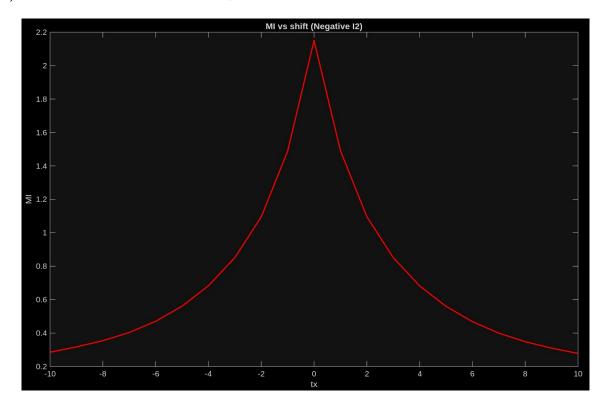
# 1) Correlation coefficient $\rho$ vs $t_x$ :



# 2) Quadratic Mutual Information QMI vs $t_x$ :



## 3) Mutual Information MI vs $t_x$ :

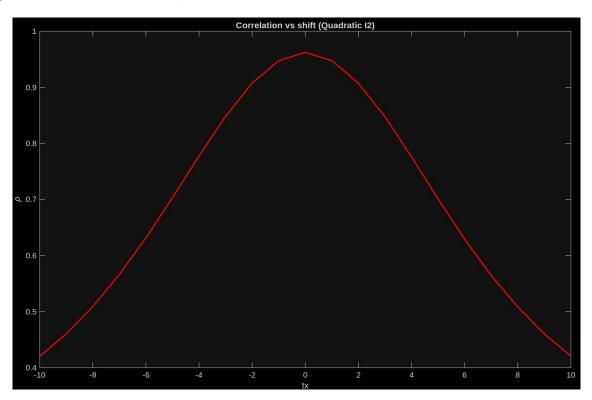


#### **Comments:**

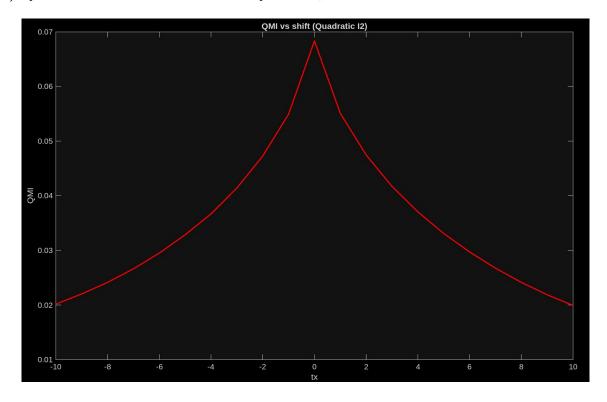
The Correlation  $\rho$  vs  $t_x$  plot is minimum at  $t_x = 0$ . This shows that the best alignment is at zero shift. It is highly negative because the image is the inverted version of the original I2. The QMI vs  $t_x$  plot peaks at  $t_x = 0$ . This indicates the correct alignment. The MI vs  $t_x$  plot peaks at  $t_x = 0$ , which confirms the alignment. Like before, MI detects the alignment more effectively because of its sharper peak.

Quadratic I2 
$$(I_2 = 255(I_1)^2/max((I_1)^2) + 1)$$
:

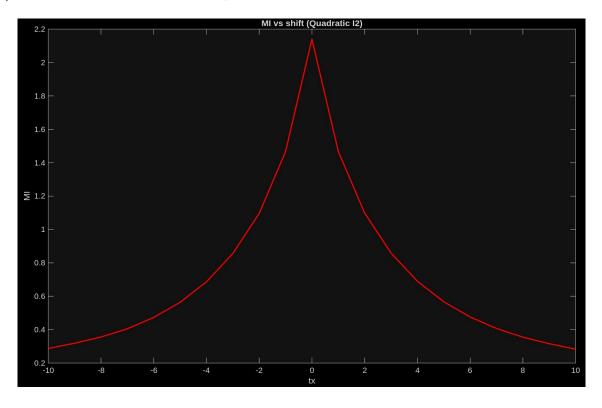
## 1) Correlation coefficient $\rho$ vs $t_x$ :



## 2) Quadratic Mutual Information QMI vs $t_x$ :



## 3) Mutual Information MI vs $t_x$ :



#### **Comments:**

The Correlation  $\rho$  vs  $t_x$  plot is minimum at  $t_x = 0$ , indicating the best alignment is at zero shift. The values are positive because its a quadratic transformation. The QMI vs  $t_x$  plot peaks at  $t_x = 0$ , which shows the correct alignment. The MI vs  $t_x$  plot peaks at  $t_x = 0$ , which confirms the alignment. Like before, MI detects the alignment more effectively because of its sharper peak.

#### How to run the code

The implementation is in the file q4.m which can be executed to generate the three plots for each case. The code can be executed by running q4.

# 5: Probability Bound

Markov's inequality:

$$P(Y \ge a) \le \frac{E(Y)}{a}, \quad Y \ge 0, \ a > 0$$

Let  $Y = e^{tX}$  for some random variable X. For t > 0,

$$P(X \ge x) \le P(e^{tX} \ge e^{tx}) \le \frac{E(e^{tX})}{e^{tx}}$$

Since the MGF of X is  $E(e^{tX}) = \varphi_X(t)$ 

$$P(X \ge x) \le e^{-tx} \, \varphi_X(t), \quad t > 0$$

Similarly, for t < 0,

$$P(X \le x) \le P(e^{tX} \ge e^{tx}) \le \frac{E(e^{tX})}{e^{tx}}$$

$$P(X \le x) \le e^{-tx} \varphi_X(t), \quad t < 0$$

Let X denote the sum of n independent Bernoulli random variables  $X_1, X_2, ..., X_n$  where  $E(X_i) = p_i$ .

$$X = \sum_{i=1}^{n} X_i, \quad \mu = \sum_{i=1}^{n} p_i$$

From the above inequality,

$$P(X \ge (1+\delta)\mu) \le \frac{\varphi_X(t)}{e^{t(1+\delta)\mu}}, \quad t \ge 0, \quad \delta > 0$$

Since the  $X_i$ 's are independent,

$$\varphi_X(t) = \prod_{i=1}^n E(e^{tX_i})$$

$$E(e^{tX_i}) = (1 - p_i) + p_i e^t = 1 + p_i (e^t - 1)$$

$$\varphi_X(t) = \prod_{i=1}^n \left(1 + p_i(e^t - 1)\right)$$

Using  $1 + x \le e^x$  where  $x = p_i(e^t - 1)$ ,

$$1 + p_i(e^t - 1) \le e^{\left(p_i(e^t - 1)\right)}$$

$$\varphi_X(t) \le e^{\left(\sum_{i=1}^n p_i(e^t - 1)\right)} = e^{\left(\mu(e^t - 1)\right)}$$

Therefore,

$$P(X \ge (1+\delta)\mu) \le \frac{e^{\left(\mu(e^t-1)\right)}}{e^{\left(t(1+\delta)\mu\right)}}$$

$$P(X \ge (1+\delta)\mu) \le e^{(\mu(e^t-1)-(t(1+\delta)\mu))}$$

The exponent is

$$f(t) = e^t - 1 - t(1 + \delta)$$

$$f'(t) = e^t - (1 + \delta)$$

Solving f'(t) = 0 gives  $e^t = 1 + \delta \implies t' = \ln(1 + \delta)$ . At  $t' = \ln(1 + \delta)$ ,

$$P(X \ge (1+\delta)\mu) \le e^{\left(\mu\left((1+\delta)-1-(1+\delta)\ln(1+\delta)\right)\right)}$$

$$P(X \ge (1+\delta)\mu) \le e^{\left(-\mu\left((1+\delta)\ln(1+\delta)-\delta\right)\right)}$$

## 6: Expected First Success

Let the random variable T denote the trial number of the first head.

The probability of getting the first head after (t-1) throws is

$$P(T = t) = p(1 - p)^{t-1}$$
 for  $t = 1, 2, ..., n$ 

$$E(T) = \sum_{t=1}^{n} t \, p (1-p)^{t-1}$$

$$E(T) = p \sum_{t=1}^{n} t(1-p)^{t-1} - - - - (1)$$

Multiplying both sides of (1) by (1 - p):

$$(1-p)E(T) = p\sum_{t=1}^{n} t(1-p)^{t} ---- (2)$$

(1) - (2) gives:

$$E(T) - (1-p)E(T) = p\left(\sum_{t=1}^{n} (1-p)^{t-1} - n(1-p)^n\right)$$

$$pE(T) = p\left(\sum_{t=1}^{n} (1-p)^{t-1} - n(1-p)^n\right)$$

$$E(T) = \frac{1 - (1 - p)^n}{p} - n(1 - p)^n$$