Simulation to estimating alpha 2

2019-09-11

Kullback-Leibler divergence

For distributions F_1 and F_2 of a continuous random variable, the KL divergence is defined as:

$$D_{KL}(F_1||F_2) = \int_{-\infty}^{+\infty} f_1(x) \log(\frac{f_1(x)}{f_2(x)}) dx$$
 (1)

where f_1 and f_2 denote the probability density of F_1 and F_2 .

Therefore, we defined the *puirty* as

$$\int log(f_1)f_1 - \int log(f_2)f_1 + \int log(f_2)f_2 - \int log(f_1)f_2$$

$$= \left(-\frac{p}{2}log(2\pi) - \frac{1}{2}log(|D_1|) - \frac{p}{2}\right)$$

$$- \left(-\frac{p}{2}log(2\pi) - \frac{1}{2}log(|D_2|) - \frac{1}{2}\left(tr(D_2^{-1}D_1) + (\mu_1 - \mu_2)'D_2^{-1}(\mu_1 - \mu_2)\right)\right)$$

$$+ \left(-\frac{p}{2}log(2\pi) - \frac{1}{2}log(|D_2|) - \frac{p}{2}\right)$$

$$- \left(-\frac{p}{2}log(2\pi) - \frac{1}{2}log(|D_1|) - \frac{1}{2}\left(tr(D_1^{-1}D_2) + (\mu_1 - \mu_2)'D_1^{-1}(\mu_1 - \mu_2)\right)\right)$$

$$= -p + \frac{1}{2}tr(D_2^{-1}D_1) + \frac{1}{2}tr(D_1^{-1}D_2) + \frac{1}{2}(\mu_1 - \mu_2)'(D_1^{-1} + D_2^{-1})(\mu_1 - \mu_2)$$

where $\mu_1 = \beta_1 + \Gamma_1 \alpha' x$, $\mu_2 = \beta_2 + \Gamma_2 \alpha' x$.

That is:

KL purity
$$= -p + \frac{1}{2}tr(D_2^{-1}D_1) + \frac{1}{2}tr(D_1^{-1}D_2) + \frac{1}{2}(\mu_1 - \mu_2)'(D_1^{-1} + D_2^{-1})(\mu_1 - \mu_2)$$

The optimization of α :

$$\alpha = -2B^{-1}A'$$

where

•
$$A = \sum_{i} (\Gamma_1 - \Gamma_2)' (D_1^{-1} + D_2^{-1}) (\beta_1 - \beta_2) x_i'$$

•
$$B = \sum_{i} x_i ((\Gamma_1 - \Gamma_2))' (D_1^{-1} + D_2^{-1}) ((\Gamma_1 - \Gamma_2)) x_i'$$

Simulation Setting

Sample size:

• 200 subjects in each group, 400 in total.

Dimensions:

• p = 4. (4 baseline biosignature)

Angle between Γ_1 and Γ_3 :

• scenario: 0, 30, 60, 90, 120, 150, 180 degrees.

Initial value: True α Simulation time: 500

Parameters

• Each subject has 7 time points: $2 \times 100 \times 7 = 1400$

• True $\alpha = [0.5, 0.5, 0.5, 0.5]'$

• $\beta_{pbo} = [0, 3, 0.9]', \beta_{drg} = [0, 3.1, 1]'$

• $\Gamma_{drg} = [0, 1, 0]'$, angle between the two Γ lines can be 0, 30, 60, 90, 120, 150, and 180 degrees.

• $|\Gamma_{drg}| = |\Gamma_{pbo}| = 1$

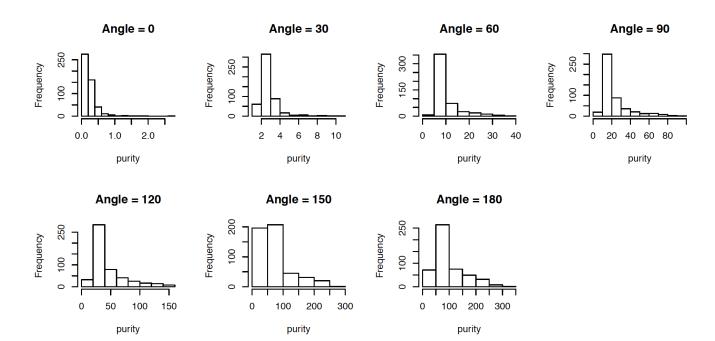
Result

 α calculated by $\hat{\beta}_{drg}, \hat{\beta}_{pbo}, \hat{\Gamma}_{drg}, \hat{\Gamma}_{pbo}, \hat{D}_{drg}, \hat{D}_{pbo}$

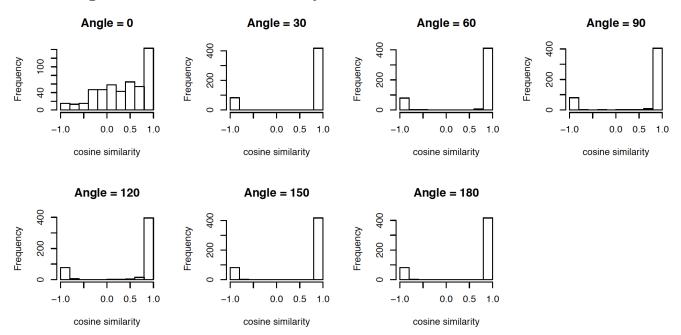
Angle	Mean KL dif	Mean KL	SD KL	Mean cosine	SD cosine
0	0.24	0.24	0.24	0.35	0.54
30	0.70	2.79	1.07	0.66	0.73
60	3.37	10.18	5.64	0.66	0.72
90	9.47	22.76	15.26	0.65	0.73
120	21.22	44.90	30.80	0.64	0.72
150	35.49	75.20	49.32	0.67	0.73
180	44.41	96.89	57.38	0.66	0.74

- Mean_KL_dif: the mean absolute differences between true *purity* and the estimated *purity* during the 500 times replication.
- $\bullet\,$ Mean_KL: The mean value of the estimated purity
- ullet SD_KL: The standard deviation value of the estimated purity
- Mean_cosine: the mean value of the cosine_similarity.
- SD_cosine: The standard deviation value of the cosine_similarity

The histogram of purity



The histogram of the consine similarity



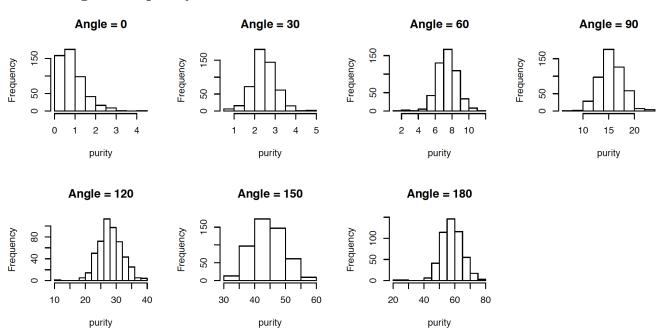
 α calculated by $\hat{\beta}_{drg}, \hat{\beta}_{pbo}, \hat{\Gamma}_{drg}, \hat{\Gamma}_{pbo}$, true D_{drg}, D_{pbo}

Angle	Mean KL dif	Mean KL	SD KL	Mean cosine	SD cosine
0	0.88	0.88	0.60	0.28	0.41
30	0.46	2.46	0.58	0.62	0.67
60	0.82	7.40	1.24	0.67	0.72
90	1.50	15.45	2.28	0.66	0.75
120	2.38	28.04	3.79	0.67	0.74
150	3.16	44.26	5.25	0.67	0.74

Angle	Mean KL dif	Mean KL	SD KL	Mean cosine	SD cosine
180	3.75	58.16	6.71	0.67	0.74

- Mean_KL_dif: the mean absolute differences between true *purity* and the estimated *purity* during the 500 times replication.
- Mean_KL: The mean value of the estimated purity
- SD_KL: The standard deviation value of the estimated purity
- Mean_cosine: the mean value of the cosine_similarity.
- SD_cosine: The standard deviation value of the cosine_similarity

The histogram of purity



The histogram of the consine similarity

