



Erratum

Predicting time to ovarian carcinoma recurrence using protein markers

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Some expressions and notations related to Equations 1 and 2 were presented incorrectly. The correct text and equations are below.

The coefficients (β) in Cox's regression model are estimated by maximizing the partial likelihood function subject to a constraint on the L1-norm of the coefficients. The lasso estimator ($\hat{\beta}$) maximizes the objective function given below:

$$l(\beta) - \lambda \|\beta\|_1 \quad (\text{Equation 1})$$

Here $l(\beta)$ is the log partial likelihood in the Cox model; for the exact form of this function, see ref. 41. The tuning parameter, λ in Equation 1, was chosen by 10-fold cross-validation. For the implementation, we used the R package "glmnet" (39).

PROVAR was defined for each of the 222 TCGA samples as the sum of the estimated coefficients multiplied by protein expression levels, as shown below. Here i represents patients ($i = 1, \dots, 222$), j represents proteins with nonzero coefficients ($j = 1, \dots, m$), $\hat{\beta}_j$ is the lasso coefficient of the j th protein marker, and X_{ij} is the expression level of the j th protein for the i th patient.

$$\text{PROVAR} = \sum_{j=1}^m \hat{\beta}_j X_{ij} \quad (\text{Equation 2})$$

The *JCI* regrets the error.

Corrigendum

Long-term IL-33-producing epithelial progenitor cells in chronic obstructive lung disease

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The author list for reference 83 was incorrect. The correct reference is below.

83. Cairns JM, Dunning MJ, Ritchie ME, Russell RC, Lynch AG. BASH: a tool for managing BeadArray spatial artefacts. *Bioinformatics.* 2008;24(24):2921–2922.

The authors regret the error.