

Predicting time to ovarian carcinoma recurrence using protein markers

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J Clin Invest. 2013;123(12):5410-5410. <https://doi.org/10.1172/JCI74035>.

Erratum

Original citation: *J Clin Invest.* 2010;123(9):3740–3750. doi:10.1172/JCI68509. Citation for this erratum: *J Clin Invest.* 2013;123(12):5410. doi:10.1172/JCI74035. 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 (β) maximizes the objective function given below: (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). PROVAV 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 ($j = 1, \dots, m$), β_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. (Equation 2) The JCI regrets the error.

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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

Derek E. Byers, Jennifer Alexander-Brett, Anand C. Patel, Eugene Agapov, Geoffrey Dang-Vu, Xiaohua Jin, Kangyun Wu, Yingjian You, Yael Alevy, Jean-Philippe Girard, Thaddeus S. Stappenbeck, G. Alexander Patterson, Richard A. Pierce, Steven L. Brody, and Michael J. Holtzman

Original citation: *J Clin Invest.* 2013;123(9):3967–3982. doi:10.1172/JCI65570.

Citation for this corrigendum: *J Clin Invest.* 2013;123(12):5410. doi:10.1172/JCI74125.

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.