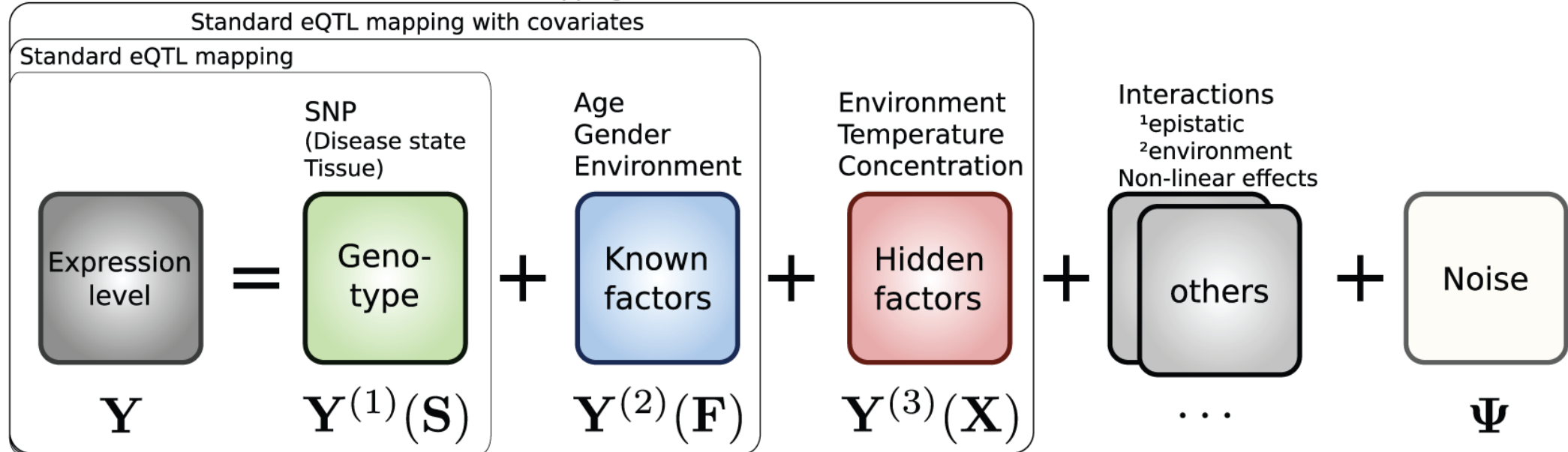
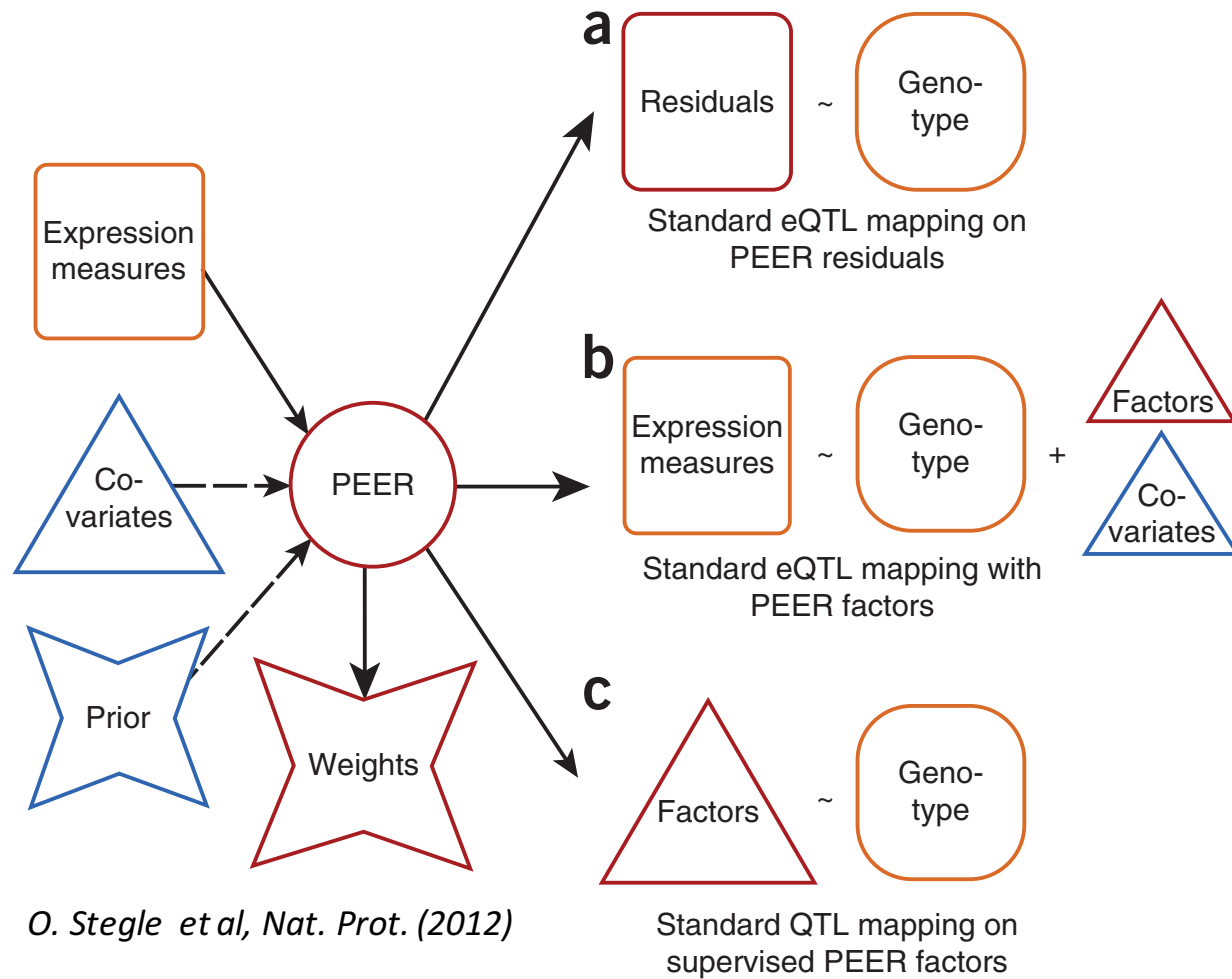


Standard eQTL mapping with covariates and hidden factors

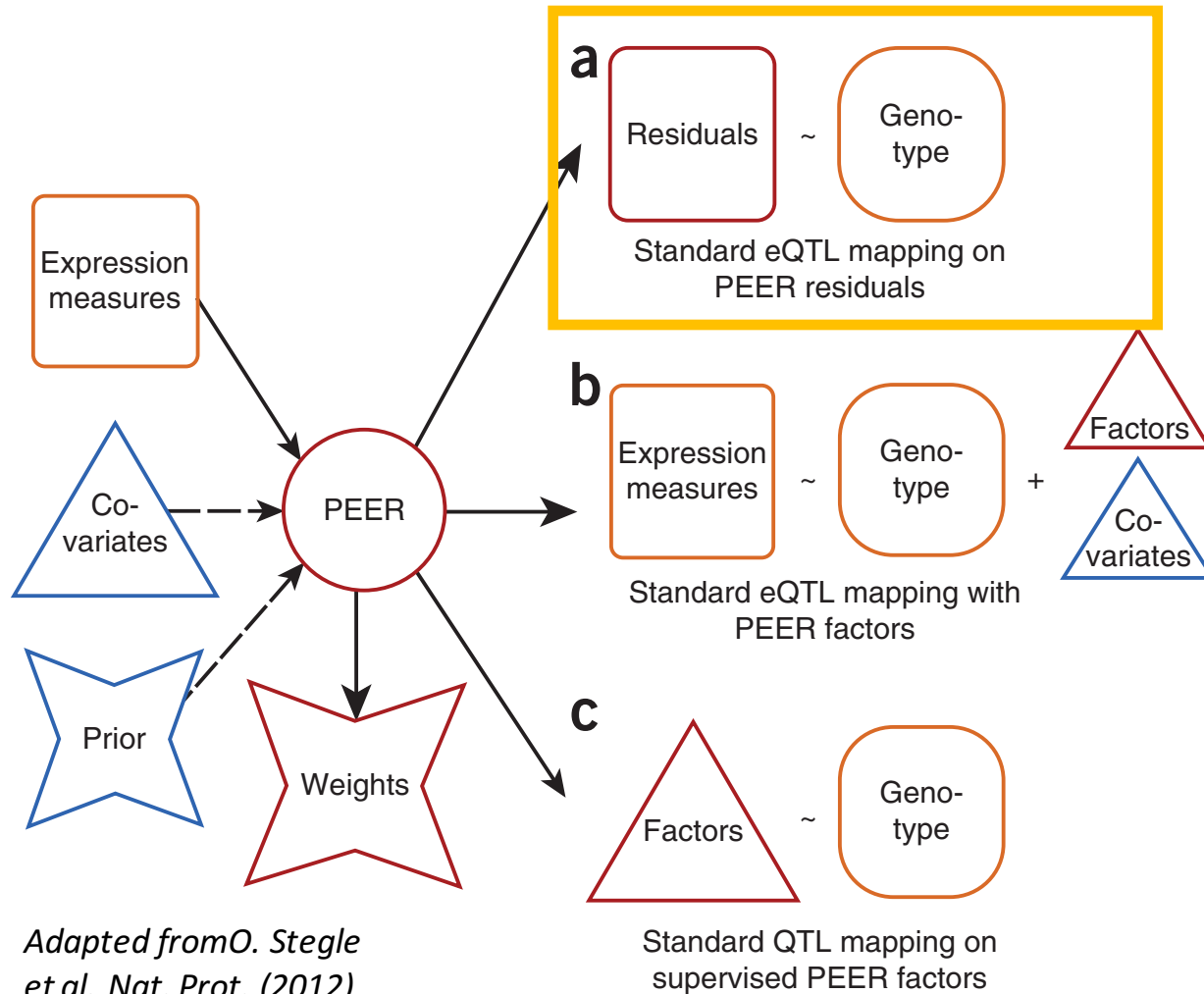


O. Stegle et al, PLoS Comp. Biol. (2010)



*“PEER produces learned factor activations, their effects on each gene and a residual data set of the expression values after subtracting the factor contribution (Fig. 1). eQTLs can then be mapped on the residuals directly (Fig. 1a), or on original data, treating the learned factors as covariates in the association tests (Fig. 1b).”*

*“eQTLs can be mapped on the residuals directly (Fig. 1a)”*

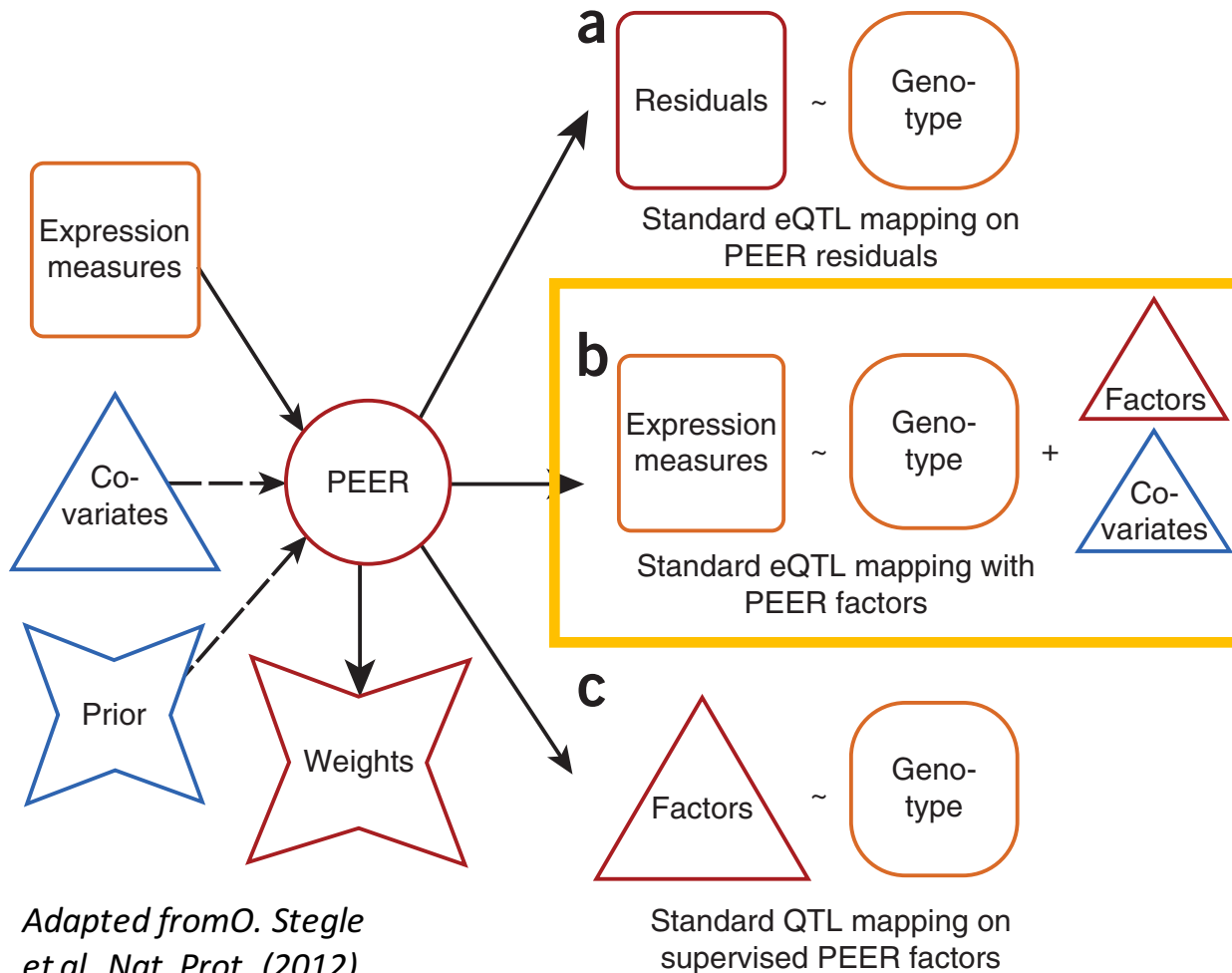


*Adapted from O. Stegle et al, Nat. Prot. (2012)*

**Method 1** : use residuals & genotype data only (without any explicit covariates)

→ produced NO eQTLs at an FDR threshold of less than 5%

*“eQTLs can be mapped on original data, treating the learned factors as covariates in the association tests (Fig. 1b)”*



**Method 2** : subtract residuals from original gene expression data, and calculate eQTLs using the resultant (updated) gene expression matrix, without any explicit covariates added during eQTL detection (assumed to be implicitly represented by residuals).

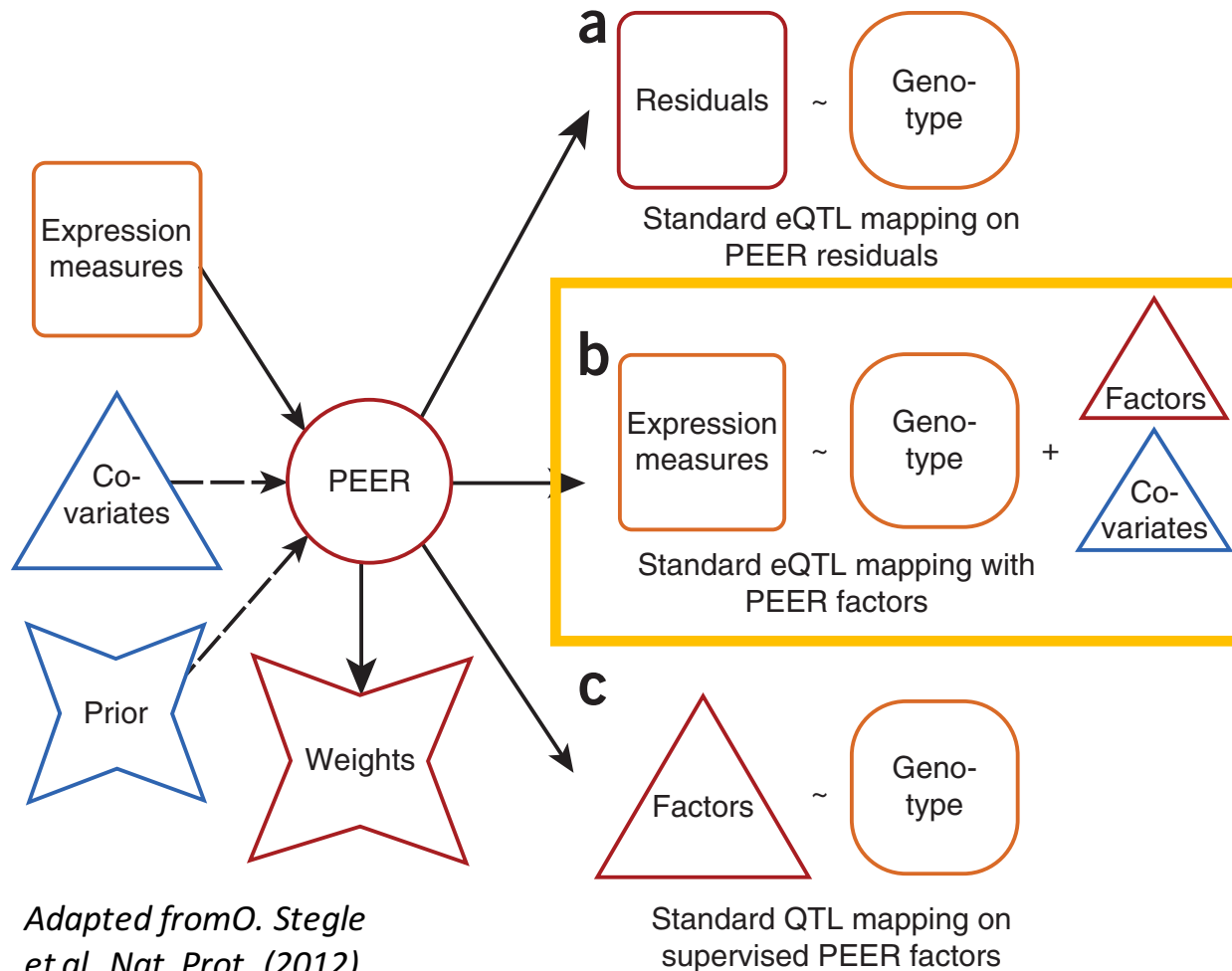
Compare resultant eQTLs w/those produced by applying the approach in **panel b**

**# eQTLs from Method 2: 2921**

**# eQTLs from panel b: 4877**

**Jaccard similarity of eQTLs btwn the 2 sets of eQTLs: 0.37**

*“eQTLs can be mapped on original data, treating the learned factors as covariates in the association tests (Fig. 1b)”*



**Method 3** : add residuals to original gene expression data, and calculate eQTLs using the resultant (updated) gene expression matrix, without any explicit covariates added during eQTL detection (assumed to be implicitly represented by residuals).

Compare resultant eQTLs w/those produced by applying the approach in **panel b**

**# eQTLs from Method 3: 3179**

**# eQTLs from panel b: 4877**

**Jaccard similarity of eQTLs btwn the 2 sets of eQTLs: 0.41**