Using Irizarry et al. (2003) (Biostatistics 4: 249-264),we fit the following model to the normalized, background corrected data:

$$Y_{ijn} = \mu_{in} + \alpha_{jn} + e_{ijn}$$

where Y_{ijn} is the 'raw' expression data for the ith array $(i = 1, , , .I)$, j^{th} probe and n^{th} gene. RMA or expresso can be used to fit the model. Either of these approaches yields an estimate of the expression of the nth gene on the ith array, i.e., $\widehat{\mu}_{in}$. If I want to compute a test statistic based on the $\widehat{\mu}_{in}$ I could construct a summary of the $\widehat{\mu}'_{in}$s,say $\widehat{\mu}_{.n}$, the mean of the $\widehat{\mu}'_{in}$s for the nth gene. I could normalize the data using the sample standard deviation for the nth gene

$$s_n = \sqrt{\frac{1}{(I-1)} \sum \left(\widehat{\mu}_{in} - \widehat{\mu}_{.n}\right)^2}$$

Here s_n^2 estimates the variance of the individual expression estimates, i.e. $Var\left(\widehat{\mu}_{in}\right)$, so that the variance estimate of $\widehat{\mu}_{.n}$ is

$$Var\left(\widehat{\mu}_{.n}\right) = s_n^2/I$$

s_n^2/I. Alternatively I could use an estimate of the standard error based on the fitted model. However, I'm not sure now what se.exprs, used after expresso, gives me.