Taking the derivative of (29) with respect to b and setting it to 0 we get:

$$\begin{aligned}
0 &= -2\mathbf{V}^{-1}(\mathbf{Y} - \mathbf{X}\boldsymbol{\beta} - b) + \frac{2}{\eta}\boldsymbol{\Phi}^{-1}b \\
&= -\mathbf{V}^{-1}(\mathbf{Y} - \mathbf{X}\boldsymbol{\beta}) + \left(\mathbf{V}^{-1} + \frac{1}{\eta}\boldsymbol{\Phi}^{-1}\right) b \\
\widehat{b} &= \left(\mathbf{V}^{-1} + \frac{1}{\widehat{\eta}}\boldsymbol{\Phi}^{-1}\right)^{-1} \mathbf{V}^{-1}(\mathbf{Y} - \mathbf{X}\widehat{\boldsymbol{\beta}}) \\
&= \left(\mathbf{U}\widetilde{\mathbf{D}}^{-1}\mathbf{U}^T + \frac{1}{\widehat{\eta}}\mathbf{U}\mathbf{D}^{-1}\mathbf{U}^T\right)^{-1} \mathbf{U}\widetilde{\mathbf{D}}^{-1}\mathbf{U}^T(\mathbf{Y} - \mathbf{X}\widehat{\boldsymbol{\beta}}) \\
&= \left(\mathbf{U}\left[\widetilde{\mathbf{D}}^{-1} + \frac{1}{\widehat{\eta}}\mathbf{D}^{-1}\right]\mathbf{U}^T\right)^{-1} \mathbf{U}\widetilde{\mathbf{D}}^{-1}(\widetilde{\mathbf{Y}} - \widetilde{\mathbf{X}}\widehat{\boldsymbol{\beta}}) \\
&= \mathbf{U}\left[\widetilde{\mathbf{D}}^{-1} + \frac{1}{\widehat{\eta}}\mathbf{D}^{-1}\right]^{-1} \mathbf{U}^T\mathbf{U}\widetilde{\mathbf{D}}^{-1}(\widetilde{\mathbf{Y}} - \widetilde{\mathbf{X}}\widehat{\boldsymbol{\beta}})
\end{aligned}$$

where $\mathbf{V}^{-1}$ is given by (11), and $(\widehat{\boldsymbol{\beta}}, \widehat{\eta})$ are the estimates obtained from Algorithm 1.

3.7 Choice of the optimal tuning parameter

In order to choose the optimal value of the tuning parameter λ, we use the generalized information criterion (34) (GIC):

$$GIC_\lambda = -2\ell(\widehat{\boldsymbol{\beta}}, \widehat{\sigma}^2, \widehat{\eta}) + a_n \cdot \widehat{df}_\lambda \tag{30}$$

where $\widehat{df}_\lambda$ is the number of non-zero elements in $\widehat{\boldsymbol{\beta}}_\lambda$ (35) plus two (representing the variance parameters η and σ^2). Several authors have used this criterion for variable selection in mixed models with $a_n = \log N_T$ (31, 36), which corresponds to the BIC. We instead choose the high-dimensional BIC (37) given by $a_n = \log(\log(N_T)) * \log(p)$. This is the default choice in our `ggmix` R package, though the interface is flexible to allow the user to select their choice of a_n.

If X and + SNPs in $\widetilde{\Phi}$ were identical what would happen?

You still need to address how the algorithm treats SNPs in both X + $\widetilde{\Phi}$ explicitly