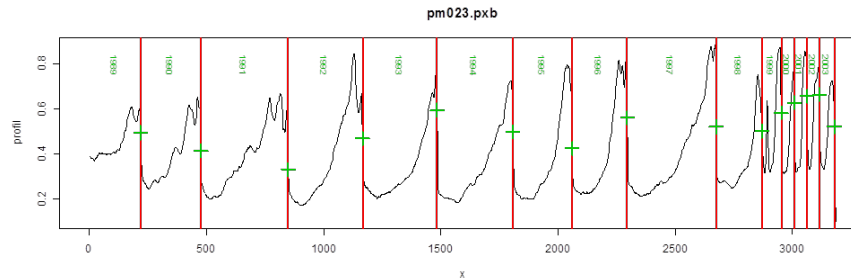


Longitudinal traits



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Function-valued traits

- Many traits in tree breeding are recorded on the same individuals along a continuous scale, such as time.
- These are often call “function-valued traits” (Pletcher and Geyer 1999).
- Classical studies fit such traits using a multivariate mixed model through discrete ages or states, although the underlying process is intrinsically continuous.
- A negative consequence of treating each age as discrete traits is the undesirable loss of information.

Function-valued traits

- An alternative is the linear mixed model with random regression (RR) coefficients (e.g. Jamrozik and Schaeffer 1997).
- RR comes with the following advantages:
 - 1) to predict BLUPs at any (unmeasured) point along a continuous (age) scale;
 - 2) to estimate (co)variances smoothly and with less bias, within and across the trajectory.

Statistical model – the random regression model

- RR mixed models estimates the coefficients of a covariance function (equivalent to the (co)variance matrix in the multivariate mixed model) as the covariance among the RR coefficients, using orthogonal polynomials or basis functions of B-splines, among others base functions.

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\Phi} \mathbf{a} + \mathbf{w} + \mathbf{e}$$

\mathbf{y} = observations

\mathbf{X} = incidence matrix of systematic effects

$\boldsymbol{\beta}$ = parameters vector

$\boldsymbol{\Phi}$ = matrix of Legendre orthogonal polynomials (or other functions)

\mathbf{a} = regression coefficients for additive genetic effects

\mathbf{w} = vector of serial environmental effects

\mathbf{e} = residuals