

	Name of Method	link of codes	Real Data	High-dim?	mixed effect?	Penalized mixed effect? type?	Do they apply penalties to the fixed or random effects or both in their model?	Linear/Generalized
main references	<a href="#">lmlasso</a>	<a href="#">Fun in R</a>	Gene Expression	Yes	Yes	Yes Lasso	Fixed-effect	Yes/Yes
	<a href="#">lmmscad</a>	<a href="#">Fun in R</a>	Gene Expression	Yes	Yes	Yes SCAD	Fixed-effect	Yes/No
	<a href="#">splmm</a>	<a href="#">R package</a>	not molecular	Yes	Yes	Yes lasso, scad, Group lasso, Group	Both	Yes/Yes
	<a href="#">cluster splmm</a>	<a href="#">R package</a>	not molecular	Yes	Yes	Yes lasso, scad, Group lasso, Group scad	Both	Yes/Yes
	<a href="#">SCAD penalty for mixed-effect models</a>	not available	not molecular	Yes	Yes	Yes SCAD	Fixed-effect	Yes/No
	<a href="#">pglm</a>	<a href="#">Julia package</a>	GWAS	Yes	Yes	Yes Lasso	Fixed-effect	No/Yes
Mixed-effect in high-dimensional	<a href="#">glmPen</a>	<a href="#">R package</a>	Gene Expression	Yes	Yes	Yes Lasso, SACD, MCP Group Lasso, Group SCAD, Group MCP, Group SCAD, Group Lasso	Both	Yes/Yes
	<a href="#">penalizedLM</a>	<a href="#">R package</a>	GWAS	Yes	Yes	Yes elastic net, MCP SCAD	Fixed-effect	Yes/No
	<a href="#">seagull</a>	<a href="#">R package</a>	DNA mythelation	Yes	Yes	Yes Lasso, Group Lasso Sparse-Group Lasso	random-effect	Yes/No
	<a href="#">glmTree</a>	<a href="#">Fun in R</a>	OTU	Yes	Yes	Yes tree-guided penalty	random-effect	No/Yes
	<a href="#">A Quasi-Likelihood Approach</a>	<a href="#">Fun in R</a>	GWAS	Yes	Yes	Yes Lasso	Fixed-effect	Yes/No
	<a href="#">ggmix</a>	<a href="#">R package</a>	GWAS	Yes	Yes	Yes Lasso; Group Lasso	Fixed-effect	Yes/No
	<a href="#">SGL-LMM</a>	not available	GWAS	Yes	Yes	Yes Group Lasso	Fixed-effect	Yes/No
	<a href="#">PMLMM</a>	not available	GWAS	Yes	Yes	Yes Group MCP	Fixed-effect	Yes/No
	<a href="#">Lasso-MLR screening+GLM screening+Lasso</a>	not available	OTU	Yes	Yes	Yes Lasso	Fixed-effect	No/Yes
	<a href="#">glmlasso</a>	<a href="#">R package</a>	not molecular	Yes	Yes	yes Lasso	Fixed-effect	Yes/Yes
	<a href="#">Procedures for Generalized Linear Mixed Models in Longitudinal</a>	not available	not molecular	Yes	Yes	Yes SCAD	Fixed-effect	No/Yes
	<a href="#">penalized quasi-likelihood (PQL)</a>	not available	not molecular	No	Yes	Yes SCAD, adaptive Lasso, adaptive group Lasso	Both	Yes/Yes
	<a href="#">high-dimensional generalized additive mixed model (GAMM)</a>	not available	Gene Expression	Yes	Yes	Yes SCAD	Fixed-effect	Yes/Yes
	<a href="#">lmlasso(an implemetation)</a>	not available	not molacular	Yes	Yes	Yes Lasso	Fixed-effect	Yes/Yes
	<a href="#">MMS</a>	<a href="#">R package</a>	metabolic data	Yes	Yes	Yes Lasso	Fixed-effect	Yes/No
	<a href="#">LMMconvexLASSO</a>	<a href="#">Fun in</a>	Simulated data	Yes	Yes	Yes Lasso, Ridge	Both	Yes/No
	<a href="#">HDLMMnaive</a>	<a href="#">MATLAB</a>						
	<a href="#">mixed-effects ODE model</a>	not available	Gene Expression	Yes	Yes	Yes SCAD	Fixed-effect	Yes/No
Penalized high-dimensional Models (not Mixed-effect Model)	<a href="#">SGL</a>	<a href="#">R package</a>	Simulated data	Yes	No	Yes Lasso, Group Lasso	---	Yes/Yes
	<a href="#">grplasso</a>	<a href="#">R package</a>	RNA splicing signals	Yes	No	Yes Lasso, Group Lasso	----	Yes/Yes
	<a href="#">gglasso</a>	<a href="#">R package</a>	Gene Expression	Yes	No	yes Lasso, Group Lasso	----	Yes/Yes (logistic model)
	<a href="#">grpreg</a>	<a href="#">R package</a>	Gene Expression SNP	Yes	No	yes Group penalties(lasso SCAD, MCP, Bridge)	----	Yes/Yes
	<a href="#">ncvreg</a>	<a href="#">R package</a>	Gene Expression	Yes	No	Yes Lasso, Scad, MCP	----	Yes/Yes
effect model in Low-dimensional	<a href="#">mixed effects models using maximum penalized likelihood (MPDL)</a>	not Available	not molecular	No	Yes	Yes SCAD, adlasso	Fixed-Random	No/Yes
	<a href="#">Re-parameterized Linear Mixed Effects Model</a>	not Available	not molecular data	No	Yes	Yes adlasso	Fixed-effect	Yes/No
	<a href="#">two-stage model selection procedure for the linear mixed-effects models</a>	<a href="#">Fun in R</a>	not molecular data	No	Yes	Yes adaptiveLasso,	Both	Yes/No
	<a href="#">Variable selection in linear mixed model for longitudinal data</a>	not Available	not molecular data	No	Yes	Yes SCAD	Fixed	Yes/No
	<a href="#">regularized REML</a>	not Available	not molecular data	No	Yes	Yes lasso, ridge	Both	Yes/No

Mixed-effect Model not penalized	Mixed-effect	<a href="#">Adaptive mixed LASSO</a>	<a href="#">R package (amltest)</a>	SNP	No	Yes	Yes Lasso, adLasso	Fixed-Random	Yes/No
		<a href="#">glmseq</a>	<a href="#">R package</a>	Gene Expression	No	yes	No ----	-----	Yes/Yes
	Model	<a href="#">lme4</a>	<a href="#">R package</a>	not molecular (sleepy study)	No	Yes	No ---	----	Yes/Yes
		<a href="#">nlme</a>	<a href="#">R package</a>	not molecular (several datasets)	No	Yes	No ----	-----	Yes/Yes
		<a href="#">glmmTMB</a>	<a href="#">R package</a>	General	Yes	Yes	No ---		
	Julia Package	<a href="#">MixedModels.jl</a>	<a href="#">Julia package</a>	not molecular	No	Yes	No -----	-----	Yes/Yes
		<a href="#">pglm</a>	<a href="#">Julia package</a>	not molecular (sleepy study)	No	Yes	No -----	-----	Yes/Yes
		<a href="#">pglm</a>	<a href="#">Julia package</a>	GWAS	Yes	Yes	Yes Lasso	Fixed-effect	No/Yes