

Competitor landscape: multiple imputation / missing-data tools in R

| Package | Approach (MI / missing-data engine) | Random effects / multilevel support | Variable types (imputation) | Most relevant reference / URL |
|-------------------------|--|--|---|---|
| <code>mice</code> | Fully Conditional Specification (FCS) / chained equations MI | Primarily single-level FCS; provides dedicated <i>two-level</i> methods (e.g., <code>2l.pan</code> , <code>2l.lmer</code>) for clustered settings | Broad at single level (continuous, binary, unordered/ordered categorical); multilevel methods more limited in scope | CRAN: mice; van Buuren & Groothuis-Oudshoorn 2011 (JSS) |
| <code>miceadds</code> | Extensions for <code>mice</code> (incl. multilevel engines) | <code>mice.impute.ml.lmer</code> : described for hierarchical <i>or cross-classified</i> structures; supports arbitrary levels and random slopes (lme4-based; see docs for scope/limits) | Mainly continuous / lmer-style settings (see function docs; nominal missing not covered in that function per docs) | CRAN: miceadds; docs: <code>mice.impute.ml.lmer</code> |
| <code>micemd</code> | Add-on methods for <code>mice</code> aimed at multilevel data | Explicitly designed for <i>two-level</i> data; distinguishes sporadically vs systematically missing patterns | Continuous, binary, count (two-level focus) | CRAN: micemd |
| <code>pan</code> | Joint-model-based MI for multivariate panel/clustered data | Targets clustered/panel settings (multivariate linear mixed-model machinery) | Primarily continuous / linear mixed-model context | CRAN: pan |
| <code>jomo</code> | Multilevel <i>joint modelling</i> MI | Designed for <i>multilevel</i> MI; supports cluster structure and substantive-model compatible MI (per package description) | Continuous plus binary/categorical via latent-normal formulations (per package description) | CRAN: jomo |
| <code>mitml</code> | Workflow / interface layer for multilevel MI | User-facing tools + pooling; interfaces with <code>pan</code> and <code>jomo</code> rather than providing a new MI engine | Inherits capabilities of underlying engines (<code>pan/jomo</code>) | CRAN: mitml |
| <code>hmi</code> | Hierarchical MI “driver” that translates models | Translates an analysis model into imputation calls; can use engines such as <code>mice</code> and <code>MCMCglmm</code> (per description) | Broad (depends on underlying engines and supported translations) | Speidel et al. 2020 (JSS; hmi); CRAN: hmi |
| <code>mdmb</code> | Model-based missing-data methods (Bayesian estimation + MI options) | States availability of multilevel models with missing predictors for Bayesian estimation; also supports substantive-model compatible MI (per description) | Regression-family oriented; scope described in package manual | CRAN: mdmb |
| <code>JointAI</code> | Bayesian <i>joint analysis + imputation</i> (JAGS-based) | Supports mixed models; documentation discusses grouping factors and notes no practical distinction in formula form between nested vs crossed specifications | Broad GLM/GLMM-style families (see manual); imputation integrated into model fitting (not classic FCS MI datasets) | Erler et al. (JointAI; JSS); CRAN: JointAI |
| <code>smcfcs</code> | Substantive-model compatible FCS MI | SMC-FCS emphasis; commonly used in single-level settings (focus is substantive-model compatibility) | Depends on substantive-model support; see package manual | CRAN: smcfcs |
| <code>phylomice</code> | Phylogeny-augmented <code>mice</code> methods | Uses phylogenetic covariance inputs; not primarily positioned as general multilevel/cross-classified MI | Phylogeny-informed MI methods (docs note development/experimental status) | GitHub: pdrhlik/phylomice |
| <code>Rphylopars</code> | Phylogenetic comparative imputation/prediction under evolutionary models | Phylogenetic model-based missing-data handling (not general-purpose FCS MI with arbitrary random effects) | Primarily continuous-trait PCM framework; see manual for scope | CRAN: Rphylopars |

Note: For “complex random factors” (multi-level and/or cross-classified structures), the most direct R-package comparator in an MI workflow is typically `miceadds` (lme4-based multilevel imputation). For a Bayesian joint modelling alternative where imputation is integrated with analysis, `JointAI` is a prominent option.