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| **Submodule** | **Class** | **Methods** | **Descriptions** |
| breed.arch | BreedingGraph | self.graph | Access to the underlying graph structure |
| breed.arch | BreedingNode | self.gen\_cur  self.gen\_max  self.pop  self.bval  self.gmod  self.bval\_true  self.gmod\_true | Current generation number of the breeding node  Maximum generation number of the breeding node  Main breeding population  Breeding values for main population  Genomic model for main population  True breeding values for main population  True genomic model for main population |
| breed.arch | BreedingProgram (Breeding Node) | self.pop\_queue  self.bval\_queue  self.gmod\_queue  self.bval\_queue\_true  self.gmod\_queue\_true  self.pop\_kw  self.bval\_kw  self.gmod\_kw  self.bval\_kw\_true  self.gmod\_kw\_true  self.pselop  self.mateop  self.evalop  self.calop  self.sselop  pselect()  mate()  evaluate()  calibrate()  sselect()  evolve() | Queue breeding populations (list)  Queue breeding values (list)  Queue genomic models (list)  True queue breeding values (list)  True queue genomic models (list)  Keyword (special) populations (dict)  Keyword (special) breeding values (dict)  Keyword (special) genomic models (dict)  True keyword (special) breeding values (dict)  True keyword (special) genomic models (dict)  Parental selection operator  Mating operator  Evaluation operator  Genomic model calibration operator  Survivor selection operator  Parental selection  Parental mating  Performance evaluation  Calibrate genomic model  Survivor selection  Evolve the breeding program |
| breed.arch | GermplasmBank |  |  |
| breed.arch | BreedingEdge |  |  |
| breed.arch | ImmigrationOperator (BreedingEdge) | immigrate() | Immigrate individuals |
| breed.arch | EmigrationOperator (BreedingEdge) | emigrate() | Emigrate individuals |
| breed.eval | PerformanceTrial | evaluate() | Evaluate individuals in a single trial |
| breed.eval | EvaluationOperator | evaluate() | Evaluate individuals |
| breed.mate | MatingOperator | mate() | Mate individuals |
| breed.calibr | GenomicModelCalibrationOperator | calibrate() | Calibrate genomic model (factory function) |
| breed.calibr | LinearGenomicModelCalibrationOperator |  |  |
| breed.calibr | NonlinearGenomicModelCalibrationOperator |  |  |
| breed.sel | SelectionOperator | select() | Select individuals |