|  |  |  |  |
| --- | --- | --- | --- |
| **Submodule** | **Class** | **Methods** | **Description** |
| breed.arch | BreedingGraph | self.graph | Access to the underlying graph structure |
| breed.arch | BreedingNode | self.t\_cur  self.t\_max  self.pop  self.bval  self.gmod | Current generation number of the breeding node  Maximum generation number of the breeding node  Breeding populations (dict)  Breeding values for populations (dict)  Genomic model for populations (dict) |
| breed.arch | BreedingProgram (Breeding Node) | self.a\_max  self.initop  self.pselop  self.mateop  self.evalop  self.calop  self.sselop  initialize()  pselect()  mate()  evaluate()  calibrate()  sselect()  evolve() | Maximum age allowable to be considered as a candidate.  Initialization operator  Parental selection operator  Mating operator  Evaluation operator  Genomic model calibration operator  Survivor selection operator  Initialize breeding program  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 |

Minimum required fields for BreedingProgram.pop (dict)

|  |  |  |
| --- | --- | --- |
| **Field** | **Type** | **Description** |
| “main” | PhasedGenotypeMatrix | Main breeding population |
| “queue” | List of PhasedGenotypeMatrix | Breeding populations on queue to be added to main population |
| … | PhasedGenotypeMatrix or other | Special breeding populations specific to special operators, program structures, etc. |

Minimum required fields for BreedingProgram.bval (dict)

|  |  |  |
| --- | --- | --- |
| **Field** | **Type** | **Description** |
| “main” | BreedingValueMatrix | Breeding values for main population |
| “main\_true” | BreedingValueMatrix | True breeding values for main population |
| “queue” | List of BreedingValueMatrix | Breeding values for queue populations |
| “queue\_true” | List of BreedingValueMatrix | True breeding values for queue populations |
| … | BreedingValueMatrix | Breeding values for special populations |

Minimum required fields for BreedingProgram.gmod (dict)

|  |  |  |
| --- | --- | --- |
| **Field** | **Type** | **Description** |
| “main” | GenomicModel | Genomic model for main population |
| “true” | GenomicModel | True genomic model for trait(s) |
| “queue” | List of GenomicModel | Genomic models for queue populations |
| … | GenomicModel | Genomic models for special populations |