|  |  |  |  |
| --- | --- | --- | --- |
| **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.geno  self.bval  self.gmod | Current generation number of the breeding node  Maximum generation number of the breeding node  Breeding population genotypes (dict)  Breeding values for populations (dict)  Genomic model for populations (dict) |
| breed.arch | BreedingProgram (Breeding Node) | self.initop  self.pselop  self.mateop  self.evalop  self.intgop  self.calop  self.sselop  evolve() | Initialization operator  Parental selection operator  Mating operator  Evaluation operator  Integration operator  Genomic model calibration operator  Survivor selection operator  Evolve the breeding program for a number of generations. |
| breed.arch | GermplasmBank |  |  |
| breed.arch | BreedingEdge |  |  |
| breed.arch | ImmigrationOperator (BreedingEdge) | immigrate() | Immigrate individuals |
| breed.arch | EmigrationOperator (BreedingEdge) | emigrate() | Emigrate individuals |
| breed.init | InitializationOperator | initialize() | Initialize breeding populations |
| breed.sel | ParentSelectionOperator | pselect() | Select parents |
| breed.mate | MatingOperator | mate() | Mate individuals |
| breed.eval | PerformanceTrial | evaluate() | Evaluate individuals in a single trial |
| breed.eval | EvaluationOperator | evaluate() | Evaluate individuals |
| breed.intg | IntegrationOperator | integrate() | Integrate progeny into geno and bval |
| breed.calibr | GenomicModelCalibrationOperator | calibrate() | Calibrate genomic model (factory function) |
| breed.calibr | LinearGenomicModelCalibrationOperator |  |  |
| breed.calibr | NonlinearGenomicModelCalibrationOperator |  |  |
| breed.sel | SurvivorSelectionOperator | sselect() | Select survivors |

Minimum required fields for BreedingProgram.geno (dict)

|  |  |  |
| --- | --- | --- |
| **Field** | **Type** | **Description** |
| “cand” | PhasedGenotypeMatrix | Parental candidate population |
| “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 |

Minimum required fields for BreedingProgram.bval (dict)

|  |  |  |
| --- | --- | --- |
| **Field** | **Type** | **Description** |
| “cand” | BreedingValueMatrix | Breeding values for parental candidate population |
| “cand\_true” | BreedingValueMatrix | True breeding values for parental candidate population |
| “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** |
| “cand” | GenomicModel | Genomic model for parental candidate population |
| “main” | GenomicModel | Genomic model for main population |
| “queue” | List of GenomicModel | Genomic models for queue populations |
| “true” | GenomicModel | True genomic model for trait(s) |
| … | GenomicModel | Genomic models for special populations |

**General breeding simulation algorithm:**

0. Initialize breeding populations operator (initop) – population burnin

Loop:

1. Parental selection operator (pselop)

2. Mating operator (mateop)

3. Evaluation operator (evalop)

4. Integration operator (intgop)

5. Calibration operator (calibrop)

6. Survivor selection operator (sselop)

End loop