Legend:
- **includes** (dotted arrow)
- **inherits** (solid arrow)

Categories:
- **FileIO** (blue)
- **Indexing** (orange)
- **Assembly** (green)
- **Alignment** (purple)
- **Annotation** (red)

BioAlphabet: defines the valid alphabet for different type of biological sequences

HMM: performs I/O for hidden Markov Models (HMM)

BioSequence: performs I/O for supported file formats, check validity and correct if necessary

SequenceIndex: constructs suffix array or BWT from sequence, also handles index I/O

CM: performs I/O for covariant models (CM)

ProfileHMM: the Pfam model

ORFHMM: the ORF model

SeqProfile: In addition to the consensus sequence, further stores the residue frequency for each position

GraphNode: definition of nodes in AssemblyGraph

GraphEdge: definition of edges in AssemblyGraph

PfamQuantify: quantify Pfam models in profile HMM

GeneCalling: quantify Pfam models in profile HMM

RfamQuantify: quantify Rfam families in CM

AssemblyGraph: use constructed sequence index to build assembly graph

GraphEssential: defines essential graph storage and operations such as add/remove nodes/edges

SequenceQuantify: quantify individual biological sequences

HMMAlign: Aligns HMM with BioSequences

GraphAnalysis: Analyze graph completeness and topological statistics

CMAlign: Aligns CM with BioSequences

SeqAlign: Aligns BioSequences

GraphPrune: simplifies graph topology

GraphTraversal: traverses the graph and output contigs

Scaffolding: refines the output contigs. Note that it operates on a set of sequences but does not include AssemblyGraph.