AMAS_JGLAHE

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Chapter 1

AMAS

Alignment manipulation and summary statistics

If you are using this program, please cite `this publication`:

```
Borowiec, M.L. 2016. AMAS: a fast tool for alignment manipulation and computing of summary statistics. PeerJ
      4:e1660.
```

1.1 This fork: AMAS_JGLAHE

Fork of the main repo which:

- Adds a `metapartition` command -> collates discontinuous metapartitions within a superalignment and concatenates them into a new superalignment of contiguous metapartitons.
- Reduces restrictions on input partition file formatting -> accepts partition files for RAxML(-NG) and IQ-TREE2 (best_scheme, best_scheme.nex and best_model.nex).

1.2 Installation

Use `AMAS.py` in the `amas` directory as a stand-alone program or clone it if you have `git installed` on your system.

If your system doesn't have a Python version 3.4 or newer (`AMAS` will work under Python 3.0 but you may noy be able to use it with multiple cores), you will need to `download and install it`. On Linux-like systems (including Ubuntu) you can install it from the command line using

It may be possible to use this version as a module, but only through manual configuration.

1.3 Command line interface

AMAS can be run from the command line. Here is the general usage (you can view this in your command line with `python3 AMAS.py -h`):

```
usage: AMAS <command> [<args>]

The AMAS commands are:
  concat            Concatenate input alignments.
  convert           Convert to other file format.
  replicate         Create replicate data sets for phylogenetic jackknife.
  split             Split alignment according to a partitions file.
  metapartitions    Runs `split' and concatenates the output.
  summary           Write alignment summary.
  remove            Remove taxa from alignment.
  translate         Translate DNA alignment into protein alignment.
  trim              Remove columns from alignment.

Use AMAS <command> -h for help with arguments of the command of interest

positional arguments:
  command     Subcommand to run

optional arguments:
  -h, --help  show this help message and exit
```

To show help for individual commands, use `AMAS.py <command> -h` or `AMAS.py <command> --help`.

1.3.1 Examples

For every `AMAS.py` run on the command line you need to specify action with `concat`, `convert`, `replicate`, `split`, or `summary` for the input to be processed. Additionally, you need to provide three arguments required for all commands. The order in which the arguments are given does not matter:

1) input file name(s) with `-i` (or in long version: `--in-files`),

2) format with `-f` (`--in-format`),

3) and data type with `-d` (`--data-type`).

The options available for the format are `fasta`, `phylip`, `nexus` (sequential), `phylip-int`, and `nexus-int` (interleaved). Data types are `aa` for protein alignments and `dna` for nucleotide alignments.

For example:

```
python3 AMAS.py concat -i gene1.nex gene2.nex -f nexus -d dna
```

If you have many files that you want to input in one run, you can use multiple cores of your computer to process them in parallel. The `summary` command supports `-c` or `--cores` with which you can specify the number of cores to be used:

```
python3 AMAS.py summary -f phylip -d dna -i *phy -c 12
```

In the above, we specified 12 cores. Note that this won't improve computing time if you're working with only one or very few files. The parallel processing is only used for the file parsing step and calculating alignment summaries.

In addition to overall alignment summaries, you can also print statistics calculated on a sequence (taxon) by sequence basis. Use `-s` or `--by-taxon` flag to turn it on. AMAS in this mode will print out one file with overall alignment summaries and a file with taxon summaries for each input alignment.

IMPORTANT! AMAS is fast and powerful, but be careful: it assumes you know what you are doing and will not prevent you overwriting a file. It will, however, print out a warning if this has happened. AMAS was also written to work with aligned data and some of the output generated from unaligned sequences won't make sense. Because of computing efficiency AMAS by default does not check if input sequences are aligned. You can turn this option on with `-e` or `--check-align`.

1.3.1.1 Concatenating alignments

For example, if you want to concatenate all DNA phylip files in a directory and all of them have the `.phy` extension, you can run:
```
python3 AMAS.py concat -f phylip -d dna -i *phy
```

By default the output will be written to two files: `partitions.txt`, containing partitions from which your new alignment was constructed, and `concatenated.out` with the alignment itself in the fasta format. You can change the default names for these files with `-p` (`--concat-part`) and `-t` (`--concat-out`), respectively, followed by the desired name. The output format is specified by `-u` (`--out-format`) and can also be any of the following: `fasta`, `phylip`, `nexus` (sequential), `phylip-int`, or `nexus-int` (interleaved).

Below is a command specifying the concatenated file output format as nexus with `-u nexus`:
```
python3 AMAS.py concat -f fasta -d aa -i *fas -u nexus
```

Alignments to be concatenated need not have identical sets of taxa before processing: the concatenated alignment will be populated with missing data where a given locus is missing a taxon. However, if every file to be concatenated includes only unique names (for example species name plus sequence name: `D_melanogaster_NW↩ _001845408.1` in one alignment, `D_melanogaster_NW_001848855.1` in other alignment etc.), you will first need to trim those names so that sequences from one taxon have equivalents in all files.
In addition to the name, you can also specify the format of the partitions output file. By default, the format is the following:
```
AA = 1-605
AK = 606-1200
28S = 1201-1800
```

RAxML:
```
python3 AMAS.py concat -f phylip -d dna -i *phy --part-format raxml
DNA, AA = 1-605
DNA, AK = 606-1200
DNA, 28S = 1201-1800
```

Nexus:
```
python3 AMAS.py concat -f phylip -d dna -i *phy --part-format nexus
#NEXUS
Begin sets;
    charset AA = 1-605;
    charset AK = 606-1200;
    charset 28S = 1201-1800;
End;
```

Partitions can also be written by codon positions using the `-n` or `--codons` flag, either for alignments containing first and second or all three positions. In the above example, supplying `-n 123` would result in:
```
AA_pos1 = 1-605\3
AA_pos2 = 2-605\3
AA_pos3 = 3-605\3
AK_pos1 = 606-1200\3
AK_pos2 = 607-1200\3
AK_pos3 = 608-1200\3
28S_pos1 = 1201-1800\3
28S_pos2 = 1202-1800\3
28S_pos3 = 1203-1800\3
```

1.3.1.2 Getting alignment statistics

This is an example of how you can summarize two protein fasta alignments by running:
```
python3 AMAS.py summary -f fasta -d aa -i my_aln.fasta my_aln2.fasta
```

By default `AMAS` will write a file with the summary of the alignment in `summary.txt`. You can change the name of this file with `-o` or `--summary-out`. You can also summarize a single or multiple sequence alignments at once.

The statistics calculated include the number of taxa, alignment length, total number of matrix cells, overall number of undetermined characters, percent of missing data, AT and GC contents (for DNA alignments), number and proportion of variable sites, number and proportion of parsimony informative sites, and counts of all characters present in the relevant alphabet.

1.3.1.3 Converting among formats

To convert all nucleotide fasta files with a `.fas` extension in a directory to nexus alignments, you could use:

```
python3 AMAS.py convert -d dna -f fasta -i *fas -u nexus
```

In the above, the required options are combined with `convert` command to convert the input files and `-u nexus` which indicates the output format.

`AMAS` will not overwrite over input here but will create new files instead, automatically appending appropriate extensions to the input file's name: `-out.fas`, `-out.phy`, `-out.int-phy`, `-out.nex`, or `-out.int-nex`.

1.3.1.4 Splitting alignment by partitions (updated for AMAS_JGLAHE)

If you have a partition file, you can split a concatenated alignment and write a file for each partition:

```
python3 AMAS.py split -f nexus -d dna -i concat.nex -l partitions.txt -u nexus
```

In the above one input file `concat.nex` was provided for splitting with `split` and partitions file `partitions.txt` with `-l` (same as `--split-by`). For splitting you should only use one input and one partition file at a time. This is an example partition file:

```
AApos1&2  =  1-604\3, 2-605\3
AApos3  =  3-606\3
28SAutapoInDels=7583, 7584, 7587, 7593
```

If this was the `partitions.txt` file from the example command above, `AMAS` would write three output files called `concat_AApos1&2.nex`, `concat_AApos3.nex`, and `concat_28SautapoInDels.nex`.

Option -j|–remove-empty

Sometimes after splitting you will have alignments with taxa that have only gaps `-` or missing data `?`. If you want to these to not be included in the output , add `-j` or `--remove-empty` to the command line.

Partition parsing

`split` and `metapartitions` parse partition files with `AMAS.FileParser.partition_parse()`. This method has been updated in the AMAS_JGLAHE fork to recognize common configurations of RAxML(-NG) and IQ-TREE2 partitions files using the regex:

```
matches = re.finditer(
            r"""^[ \t]*                                    # start of line w/ zero-or-more (just)
      whitespaces/tabs
                (
                 (?P<nexus>charset[ ]+)                    # case 1: (IQ-TREE 2)best_scheme.nex partition
      directive; partition name
                 |
                 (?P<raxml>[A-Za-z0-9_+.\{\}\/-]+,[ \t]+) # case 2: RAxML/RAxML-NG model(+other pars);
      partition name
                )?
                (?P<partition_name>[A-Za-z0-9_&.-]+)       # partition name;
      alt(?P<partition_name>[A-Za-z0-9_&.\(\)\[\]-]+)
                [ ]*=[ ]*                                  # whitespace-padded (or unpadded) '=': (IQ-TREE
      2)best_scheme.nex compatabiliy
                (?P<numbers>[\\0-9, -]+)                   # position ranges w/ stride (multiple intervals;
      from original regex)
                (?P<nexus_term>[ ]*[;])?                   # whitespace-prepended (or unprepended) ';'
      (nexus terminator)
            """,
            self.in_file_lines,
            re.MULTILINE | re.VERBOSE
        )
```

This generally handles RAxML(-NG) and IQ-TREE2 partition files correctly, with the following caveats:

- It doesn't recognize filenames after '=', so you can't a partition file that maps to multiple alignments, e.g.
```
#nexus
begin sets;
    charset part1 = aln1.phy: 1-100\3 201-300;
    charset part2 = aln1.phy: 101-200;
    charset part3 = aln2.phy: *;
    charpartition mine = HKY:part1, GTR+G:part2, WAG+I+G:part3;
end
```
- The capture groups `<raxml>` and `<partition_name>` aim to be comprehensive, but note that unmatched edge-cases will fail silently. This includes model specification based on the full 'MULTISTATE' `datatype`, as well as partition names containing metacharacter other than `&`, `.`, and `-` (see next point).
- Literal-metacharacter matching is now refined by capture group with explicit character class declarations. Metacharacters may be unavoidable when specifying complex models, but users should be aware that certain metacharacter pattern in *partition names* could lead to unexpected results, depending on the environment. `split` and `metapartitions` use unsanitized partition names as the (sub)alignment filenames, potentially leading to shell execution of filenames as command sequences in the context of a pipeline or wrapper script. For this reason, and because this script doesn't support the full 'MULTISTATE' datatype, the characters `$`, `(`, `)`, `*`, `` ` ` ``, `?`, `!`, `<` and `>` are excluded from the regex entirely.

1.3.1.5 Convert a superalignment of fragmented partitions into one with contiguous partitions

The `metapartitions` command splits the input superalignment based on its partition file, collating these (typically fragmented) partitions into separate alignment files, operating essentially the same as `split`. It then then concatenates these alignments into a new superalignment of contiguous partitons that is equivalent to the original with respect to partition data content, facilitating analyses of a metapartitioned alignment with utilities that cannot parse discontinuous partition definitions.

Note the term 'metapartitions' as used here refers specifically to optimzed partitions generated through an optimization process (usually merging according to model-fit) of the initial partitions, typically performed with `PartitionFinder` or a `deriviative implementation`. This usually results in a smaller number of larger partitions with discontinuous ranges, although partitions with discontinuous ranges aren't necessarily metapartitions by this definition, and this command could equally well be called 'defragmentation' based on the operations it performs.

The following is a contrived example (for brevity) demonstrating how the `metapartions` command can be implemented on a superalignment of fragmented (though not necessarily meta-) partitions:
```
./AMAS.py metapartitions -i concat.fas -f fasta -d dna --no-san --no-mpan -l partitions.txt -t
      concat.out.fas -p defrag_partitions.txt -y raxml --prepend Nuc_defrag
```

The above command takes the input superalignment `concat.fas` of `dna` data in `fasta` format and splits it based on `partitions.txt`, writing the collated partitions to subalignment files named after the corresponding partiton names, where the `--no-san` flag prevents the label 'concat_' (from the input superalignment filename) from being prepended to these filenames; subalignment files are then concatenated into the new superalignment `concat.out.fas`, writing its contiguous partitions to the file `defrag_partitions.txt` in the RAxML(-NG) format based on `-y raxml`, with `--prepend Nuc_defrag` prepending the label 'Nuc_defrag_' to each of these partition names.

Figure: `concat.fas` (left), is converted into `concat.out.fas` (right) with the `metapartitions` command; visualized in `Aliview` v1.28

The `concat.fas` partition file `partitions.txt` is shown below. This includes loosely conforming examples of the three partition formatting types recognized by AMAS (the AMAS-default, RAxML(-NG)and IQ-TREE2-Nexus), which serves to demonstrate the tolerances the updated parser's regex. Note that the lack of '=' in IQ-TREE2-↩ Nexus model specifications (as used in .best_scheme.nex and .best_model.nex files) means these lines are safely ignored.
```
charset     partition_A_pos1 =      7 - 21\3
  charset s& = 8  -21\3
    charset partition_A_pos3 = 9-   21\3
Q.insect, parti&tion_B_pos1 = 40-    45\3
PROTGTR{rates.txt}+FU{freqs.txt},   partition_B-pos2 = 41   -45\3
```

```
GTR{0.5/2.0/1.0/1.2/0.1/1.0}+Rn{r1/r2/r3}{w1/w2/w3}, partition_B.pos3   =„  42-45\3
    GTR+G4,    partition_C =  , , „38 39            37,
9.20b, partitio_D_pos1 = 1-6\3 22 - 36\3
       partition_D_pos2= 2-6\3 23 -36\3
p1_3_a                 = 3-6\3             24 -      36\3
  charpartition mymodels =
    9.20b: partition_D_pos1;
end;
```

The concat.out.fas partition file defrag_partitions.txt is shown below. Note that all commands using -y raxml currently output partition files with either 'DNA' (with -d dna) or 'WAG' (with -d aa) for their model specifications, as per the original repo.

```
DNA, Nuc_defrag_p01 = 1-5
DNA, Nuc_defrag_p02 = 6-10
DNA, Nuc_defrag_p03 = 11-15
DNA, Nuc_defrag_p04 = 16-17
DNA, Nuc_defrag_p05 = 18-19
DNA, Nuc_defrag_p06 = 20-21
DNA, Nuc_defrag_p07 = 22-24
DNA, Nuc_defrag_p08 = 25-31
DNA, Nuc_defrag_p09 = 32-38
DNA, Nuc_defrag_p10 = 39-45
```

The command from the above example should generate 12 files: the new superalignment and its partition file defrag_partitions.txt, as well the 10 -meta.fas alignments collated by the inital split operation:

```
|- concat.out.fas
|- defrag_partitions.txt
|- p1_3_a-meta.fas
|- parti&tion_B_pos1-meta.fas
|- partitio_D_pos1-meta.fas
|- partition_A_pos1-meta.fas
|- partition_A_pos3-meta.fas
|- partition_B.pos3-meta.fas
|- partition_B-pos2-meta.fas
|- partition_C-meta.fas
|- partition_D_pos2-meta.fas
|- s&-meta.fas
```

You can try running this with the AMAS_JGLAHE fork yourself using concat.fas, checking the result against concat.out.fas and defrag_partitions.txt.

1.3.1.6 Translating a DNA alignment into aligned protein sequences

You can translate a nucleotide alignment to amino acids with AMAS using one of the NCBI translation tables. For example, to correctly translate an insect mitochondrial gene alignment that begins at a second codon position:

```
python3 AMAS.py translate -f nexus -d dna -i concat.nex --code 5 --reading-frame 2 --out-format phylip
```

--code and --reading-frame are the same as -b and -k and are both set to 1 (the standard genetic code and the first character of the alignment corresponds to the first codon position) by default. When translating, AMAS will contract gaps - and missing ?, such that --- becomes - in the translated alignment. A warning will be printed if stop codons are found and these are indicated as asterisks * in the output. See AMAS.py translate -h for more info.

1.3.1.7 Creating replicate data sets

With AMAS you can create concatenated alignments from a proportion of randomly chosen alignments that can be used for, for example, a phylogenetic jackknife analysis. Say you have 1000 phylip files, each containing a single aligned locus, and you want to create 200 replicate phylip alignments, each built from 100 loci randomly chosen from all the input files. You can do this by specifying replicate command and following it with -r or --rep-aln followed by the number of replicates (in this case 200) and number of alignments (100). Remember to supply the output format with -u if you want it to be other than fasta:

```
python3 AMAS.py replicate -r 200 100 -d dna -f phylip -i *phy -u phylip
```

1.3.1.8 Removing taxa/sequences from alignment

It is possible to remove taxa from alignments:
```
python3 AMAS.py remove -x species1 species2 -d dna -f nexus -i *nex -u nexus-int -g no_species12_
```

The above will process all `nexus` files in the directory and remove taxa called `species1` and `species2`. The argument `-x` (the same as `--taxa-to-remove`) is followed by the names of sequences to be removed. Note that `AMAS` converts spaces into underscores and strips any quotes present in input sequence names before processing, so you may need to modify your names to remove accordingly. The argument `-g` (the same as `--out-prefix`) specifies a prefix to be added to output file names. The default prefix is 'reduced_'. You may want to realign your files after taxon removal.

1.3.1.9 Checking if input is aligned

By specifying optional argument `-e` (`--check-align`), you can make `AMAS` check if your input files contain only aligned sequences. This option is disabled by default because it can substantially increase computation times in files with many taxa. Enabling this option also provides an additional check against misspecified input file format.

1.4 AMAS as a Python module

Using `AMAS` inside your Python pipeline gives you much more flexibility in how the input and output are being processed. All the major functions of the command line interface can recreated using `AMAS` as a module. Following installation from `pip` use:
```
pydoc amas.AMAS
```

To access detailed documentation for the classes and functions available.

You can import `AMAS` to your script with:
```
from amas import AMAS
```

The class used to manipulate alignments in `AMAS` is `MetaAlignment`. This class has to be instantiated with the same, named arguments as on the command line: `in_files`, `data_type`, `in_format`. You also need to supply the number of cores to be used with `cores`. MetaAlignment holds one or multiple alignments and its `in_files` option must be a list, even if only one file is being read.
```
meta_aln = AMAS.MetaAlignment(in_files=["gene1.phy"], data_type="dna",in_format="phylip", cores=1)
```

Creating MetaAlignment with multiple files is easy:
```
multi_meta_aln = AMAS.MetaAlignment(in_files=["gene1.phy", "gene1.phy"], data_type="dna",
      in_format="phylip", cores=2)
```

Now you can call the various methods on your alignments. `.get_summaries()` method will compute summaries for your alignments and produce headers for them as atuple with first element being the header and the second element a list of lists with the statistics:
```
summaries = meta_aln.get_summaries()
```

The header is different for nucleotide and amino acid data. You may choose to skip it and print only the second element of the tuple, that is a list of summary statistics:
```
= summaries[1]
```

`.get_parsed_alignments()` returns a list of dictionaries where each dictionary is an alignment and where taxa are the keys and sequences are the values. This allows you to, for example, print only taxa names in each alignment or do other manipulation of the sequence data:
```
# get parsed dictionaties
aln_dicts = multi_meta_aln.get_parsed_alignments()

# print only taxa names in the alignments:
for alignment in aln_dicts:
    for taxon_name in alignment.keys():
        print(taxon_name)
```

Similar to the above example, it is also easy to get translated amino acid alignment as a list of dictionaries (one per input alignment):

```
# get parsed dictionaties
aln_dicts = multi_meta_aln.get_translated(2, 1) # 2: vertebrate mitochondrial genetic code and 1: reading
      frame starting at first character
```

To split alignment use `.get_partitioned("your_partitions_file")` on a `MetaAlignment` with a single input file. `.get_partitioned()` returns a list of dictionaries of dictionaries, with `{ partition_name : { taxon : sequence } }` structure for each partition:

```
partitions = meta_aln.get_partitioned("partitions.txt")
```

`AMAS` uses `.get_partitions("your_partitions_file")` to parse the partition file:

```
parsed_parts = meta_aln.get_partitions("partitions.txt")
print(parsed_parts)
```

`.get_replicate(no_replicates, no_loci)` gives a list of parsed alignments (dictionaries), each a replicate constructed from the specified number of loci:

```
replicate_sets = multi_meta_aln.get_replicate(2, 2)
```

To concatenate multiple alignments first parse them with `.get_parsed_alignments()`, then pass to `.get↩ _concatenated(your_parsed_alignments)`. This will return a tuple where the first element is the `{ taxon : sequence }` dictionary of concatenated alignment and the second element is the partitions dict with `{ name : range }`.

```
parsed_alns = multi_meta_aln.get_parsed_alignments()
concat_tuple = multi_meta_aln.get_concatenated(parsed_alns)
concatenated_alignments = concat_tuple[0]
concatenated_partitions = concat_tuple[1]
```

Removing taxa from alignments is very easy:

```
spp_to_remove = ["taxon1", "taxon2", "taxon3"]
reduced_alns = multi_meta_aln.remove_taxa(spp_to_remove)
```

To print to file or convert among file formats use one of the `.print_format(parsed_alignment)` methods called with a parsed dictionary as an argument. These methods include `.print_fasta()`, `.print_↩ nexus()`, `.print_nexus_int()`, `print_phylip()`, and `.print_phylip_int()`. They return an apporpriately formatted string.

```
for alignment in concatenated_alignments:
    nex_int_string = meta_aln.print_nexus_int(alignment)
    print(nex_int_string)
```

Chapter 2

Namespace Index

2.1 Namespace List

Here is a list of all namespaces with brief descriptions:

Chapter 3

Hierarchical Index

3.1 Class Hierarchy

This inheritance list is sorted roughly, but not completely, alphabetically:

Chapter 4

Class Index

4.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

Chapter 5

File Index

5.1 File List

Here is a list of all files with brief descriptions:

Chapter 6

Namespace Documentation

6.1 amas Namespace Reference

Namespaces

- namespace AMAS

Variables

- str __author__ = 'Marek Borowiec'
- str __email__ = 'petiolus@gmail.com'
- str __version__ = '1.02'
- __all__ = dir()

6.1.1 Variable Documentation

6.1.1.1 __all__

```
amas.__all__ = dir()  [private]
```

Definition at line 6 of file __init__.py.

6.1.1.2 __author__

```
str amas.__author__ = 'Marek Borowiec'  [private]
```

Definition at line 3 of file __init__.py.

6.1.1.3 __email__

```
str amas.__email__ = 'petiolus@gmail.com'  [private]
```

Definition at line 4 of file __init__.py.

6.1.1.4 __version__

```
str amas.__version__ = '1.02'  [private]
```

Definition at line 5 of file __init__.py.

6.2 amas.AMAS Namespace Reference

Classes

- class Alignment
- class AminoAcidAlignment
- class DNAAlignment
- class FileHandler
- class FileParser
- class MetaAlignment
- class ParsedArgs

Functions

- proportion (x)
- main ()
- run ()

6.2.1 Detailed Description

```
This stand-alone program allows manipulations of multiple sequence
alignments. It supports sequential FASTA, PHYLIP, NEXUS, and interleaved PHYLIP
and NEXUS formats for DNA and aino acid sequences. It can print summary statistics,
convert among formats, and concatenate alignments.

Current statistics include the number of taxa, alignment length, total number
of matrix cells, overall number of undetermined characters, percent of missing
data, AT and GC contents (for DNA alignments), number and proportion of
variable sites, number and proportion of parsimony informative sites,
and counts of all characters present in the relevant (nucleotide or amino acid) alphabet.
```

6.2.2 Function Documentation

6.2.2.1 main()

```
amas.AMAS.main ( )
```

Definition at line 2363 of file AMAS.py.

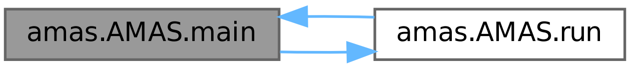
```
02363 def main():
02364 
02365     # initialize parsed arguments and meta alignment objects
02366     kwargs = run()
02367     meta_aln = MetaAlignment(**kwargs)
02368 
02369     if meta_aln.command == "summary":
02370         meta_aln.write_summaries(kwargs["summary_out"])
02371 
02372     if meta_aln.by_taxon_summary:
02373         print("Printing taxon summaries")
```

```
            meta_aln.write_taxa_summaries()

        if meta_aln.command == "convert":
            meta_aln.write_out("convert", kwargs["out_format"])

        if meta_aln.command == "concat":
            meta_aln.write_out("concat", kwargs["out_format"])
            meta_aln.write_partitions(kwargs["concat_part"], kwargs["part_format"], kwargs["data_type"],
      kwargs["codons"])

        if meta_aln.command == "replicate":
            meta_aln.write_out("replicate", kwargs["out_format"])

        if meta_aln.command == "split":
            meta_aln.write_out("split", kwargs["out_format"])

        if meta_aln.command == "metapartitions":
            # `metapartitions` is essentially `split` + `concat`. Currently you can't set an out_format:
            # it's automatically set to match the in_format because the intermediate `split` outputs
      become
            # the 'new' in_files for the `concat` operation, and then calling either:
            #  -> AminoAcidAlignment(Alignment.__init__(self, in_file, in_format, data_type))
            #  -> DNAAlignment(Alignment.__init__(self, in_file, in_format, data_type))
            # through MetaAlignment.get_alignment_object(alignment, self.in_format, self.data_type)
            meta_aln.write_out("metapartitions", kwargs["in_format"])
            meta_aln.write_partitions(kwargs["concat_part"], kwargs["part_format"], kwargs["data_type"],
      "none")

        if meta_aln.command == "remove":
            meta_aln.write_out("remove", kwargs["out_format"])

        if meta_aln.command == "translate":
            meta_aln.write_out("translate", kwargs["out_format"])

        if meta_aln.command == "trim":
            meta_aln.write_out("trim", kwargs["out_format"])

            # meta_aln.write_out("translate", kwargs["out_format"])

```

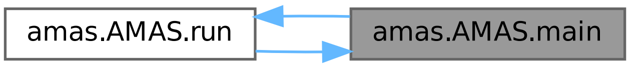
References amas.AMAS.run().

Referenced by amas.AMAS.run().

Here is the call graph for this function:



Here is the caller graph for this function:



6.2.2.2 proportion()

```
amas.AMAS.proportion (
              x )
```

Definition at line 43 of file AMAS.py.

```
def proportion(x):
    # needed to prevent input of invalid floats in trim mode
    x = float(x)
    if x < 0.0 or x > 1.0:
        raise argparse.ArgumentTypeError("%r not in range [0.0, 1.0]" % (x,))
    return x

```

6.2.2.3 run()

```
amas.AMAS.run ( )
```

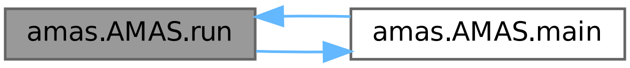
Definition at line 2410 of file AMAS.py.

```
def run():

    # initialize parsed arguments
    config = ParsedArgs()
    # get arguments
    config_dict = config.get_args_dict()
    return config_dict

```

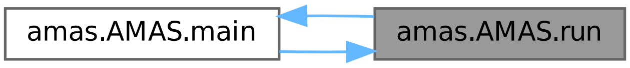
References amas.AMAS.main().

Referenced by amas.AMAS.main().

Here is the call graph for this function:



Here is the caller graph for this function:

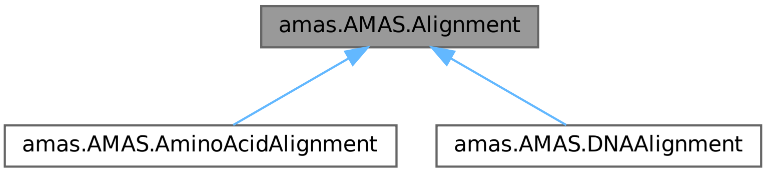


Chapter 7

Class Documentation

7.1 amas.AMAS.Alignment Class Reference

Inheritance diagram for amas.AMAS.Alignment:



Public Member Functions

- __init__ (self, in_file, in_format, data_type)
- __str__ (self)
- get_aln_input (self)
- get_parsed_aln (self)
- summarize_alignment (self)
- summarize_alignment_by_taxa (self)
- get_char_summary (self)
- get_taxon_char_summary (self)
- append_count (self, char_dict)
- matrix_creator (self)
- get_column (self, i)
- all_same (self, site)
- get_sites_no_missing_ambiguous (self)
- get_site_no_missing_ambiguous (self, column)
- replace_missing (self, column)
- get_trim_selection (self, trim_fraction, parsimony_check)
- get_variable (self)
- get_parsimony_informative (self)

- get_prop_variable (self)
- get_prop_parsimony (self)
- get_name (self)
- get_taxa_no (self)
- get_alignment_length (self)
- get_matrix_cells (self)
- get_missing (self)
- get_missing_percent (self)
- get_missing_from_parsed (self)
- get_missing_from_seq (self, seq)
- get_missing_percent_from_seq (self, seq)
- get_counts (self)
- get_counts_from_parsed (self)
- get_counts_from_seq (self, seq)
- check_data_type (self)

Public Attributes

- in_file
- in_format
- data_type
- parsed_aln
- length
- matrix
- no_missing_ambiguous
- variable_sites
- prop_variable
- parsimony_informative
- prop_parsimony
- missing_records
- missing
- check

Static Public Attributes

- all_matrix_cells

7.1.1 Detailed Description

```
Base class: Gets in parsed sequences as input and summarizes their stats.
Based on the data type, the subclasses AminoAcidAlignment & DNAAlignment define the attributes:
`alphabet`, `missing_ambiguous_chars`, `missing_chars`, `non_alphabet`
```

Definition at line 805 of file AMAS.py.

7.1.2 Constructor & Destructor Documentation

7.1.2.1 __init__()

```
amas.AMAS.Alignment.__init__ (
                self,
                in_file,
                in_format,
                data_type )
```

Definition at line 811 of file AMAS.py.

```
    def __init__(self, in_file, in_format, data_type):
        # initialize alignment class with parsed records and alignment name as arguments,
        # create empty lists for list of sequences, sites without
        # ambiguous or missing characters, and initialize variable for the number
        # of parsimony informative sites
        self.in_file = in_file
        self.in_format = in_format
        self.data_type = data_type

        self.parsed_aln = self.get_parsed_aln()

```

7.1.3 Member Function Documentation

7.1.3.1 __str__()

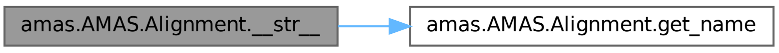
```
amas.AMAS.Alignment.__str__ (
                self )
```

Definition at line 822 of file AMAS.py.

```
    def __str__(self):
        #  purpose of override? (originally returned method object)
        return self.get_name()

```

References amas.AMAS.Alignment.get_name().

Here is the call graph for this function:



7.1.3.2 all_same()

```
amas.AMAS.Alignment.all_same (
                self,
                site )
```

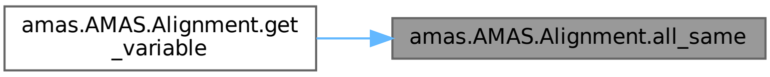
Definition at line 937 of file AMAS.py.

```
    def all_same(self, site):
        # check if all elements of a site are the same
        return not site or site.count(site[0]) == len(site)
```

```
00940
```

Referenced by amas.AMAS.Alignment.get_variable().

Here is the caller graph for this function:


amas.AMAS.Alignment.get_variable
amas.AMAS.Alignment.all_same

7.1.3.3 append_count()

```
amas.AMAS.Alignment.append_count (
                self,
                char_dict )
```

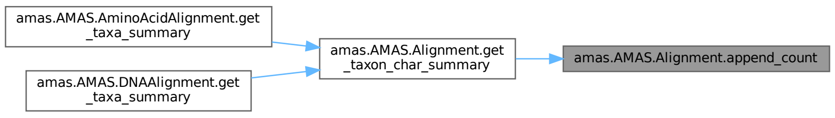
Definition at line 919 of file AMAS.py.

```
00919     def append_count(self, char_dict):
00920         count_list = []
00921         for char in self.alphabet:
00922             if char in char_dict.keys():
00923                 count_list.append(char_dict[char])
00924             else:
00925                 count_list.append(0)
00926         return count_list
00927
```

References amas.AMAS.AminoAcidAlignment.alphabet, and amas.AMAS.DNAAlignment.alphabet.

Referenced by amas.AMAS.Alignment.get_taxon_char_summary().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.append_count

7.1.3.4 check_data_type()

```
amas.AMAS.Alignment.check_data_type (
                self )
```

Definition at line 1074 of file AMAS.py.

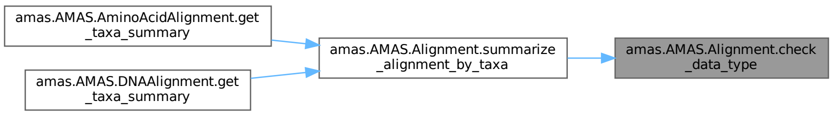
```
01074     def check_data_type(self):
01075         # check if the data type is correct; only one seq to save on computation
01076         seq = next(iter(self.parsed_aln.values()))
01077         self.check = any(char in self.non_alphabet for char in seq)
01078         if self.check is True:
```

```
            print(
                "WARNING: found non-" + self.data_type + " characters. "
                "Are you sure you specified the right data type?"
            )


```

References amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get _taxa_summary
amas.AMAS.DNAAlignment.get _taxa_summary
amas.AMAS.Alignment.summarize _alignment_by_taxa
amas.AMAS.Alignment.check _data_type

7.1.3.5 get_alignment_length()

amas.AMAS.Alignment.get_alignment_length (
    self)

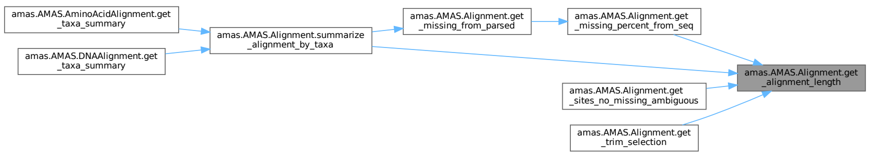
Definition at line 1011 of file AMAS.py.

```
    def get_alignment_length(self):
        # get alignment length by just checking the first seq length
        # this assumes that all sequences are of equal length
        return len(next(iter(self.parsed_aln.values())))

```

References amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.Alignment.get_missing_percent_from_seq(), amas.AMAS.Alignment.get_sites_no_missing_ambiguous() amas.AMAS.Alignment.get_trim_selection(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get _taxa_summary
amas.AMAS.DNAAlignment.get _taxa_summary
amas.AMAS.Alignment.summarize _alignment_by_taxa
amas.AMAS.Alignment.get _missing_from_parsed
amas.AMAS.Alignment.get _missing_percent_from_seq
amas.AMAS.Alignment.get _alignment_length
amas.AMAS.Alignment.get _sites_no_missing_ambiguous
amas.AMAS.Alignment.get _trim_selection

7.1.3.6 get_aln_input()

```
amas.AMAS.Alignment.get_aln_input (
              self )
```

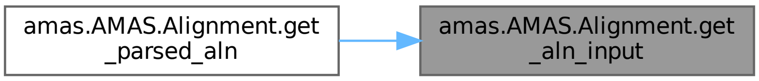
Definition at line 826 of file AMAS.py.

```
00826     def get_aln_input(self):
00827         # open and parse input file
00828         aln_input = FileParser(self.in_file)
00829         return aln_input
00830
```

References amas.AMAS.FileHandler.in_file, amas.AMAS.FileParser.in_file, and amas.AMAS.Alignment.in_file.

Referenced by amas.AMAS.Alignment.get_parsed_aln().

Here is the caller graph for this function:


amas.AMAS.Alignment.get _parsed_aln
amas.AMAS.Alignment.get _aln_input

7.1.3.7 get_char_summary()

```
amas.AMAS.Alignment.get_char_summary (
              self )
```

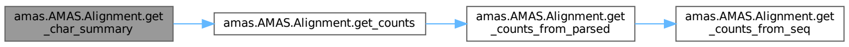
Definition at line 899 of file AMAS.py.

```
00899     def get_char_summary(self):
00900         # get summary of frequencies for all characters
00901         characters = []
00902         counts = []
00903         add_to_chars = characters.append
00904         add_to_counts = counts.append
00905         char_count_dicts = self.get_counts()
00906         for char in self.alphabet:
00907             add_to_chars(char)
00908             if char in char_count_dicts.keys():
00909                 add_to_counts(str(char_count_dicts[char]))
00910             else:
00911                 add_to_counts("0")
00912         return characters, counts
00913
```

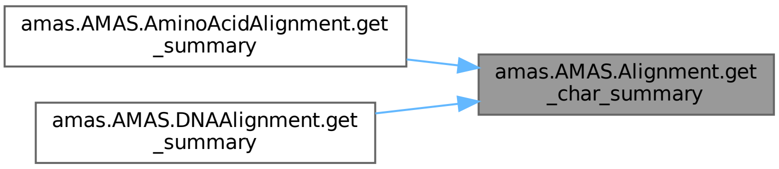
References amas.AMAS.AminoAcidAlignment.alphabet, amas.AMAS.DNAAlignment.alphabet, and amas.AMAS.Alignment.get_counts().

Referenced by amas.AMAS.AminoAcidAlignment.get_summary(), and amas.AMAS.DNAAlignment.get_summary().

Here is the call graph for this function:


amas.AMAS.Alignment.get _char_summary
amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get _counts_from_parsed
amas.AMAS.Alignment.get _counts_from_seq

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_summary
amas.AMAS.DNAAlignment.get_summary
amas.AMAS.Alignment.get_char_summary

7.1.3.8 get_column()

```
amas.AMAS.Alignment.get_column (
                self,
                i )
```

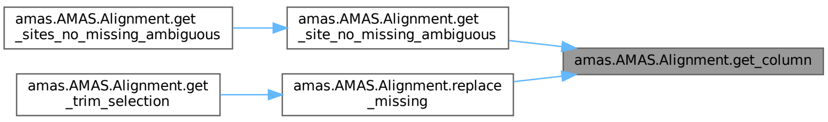
Definition at line 933 of file AMAS.py.

```
    def get_column(self, i):
        # get site from the character matrix
        return [row[i] for row in self.matrix]
```

References amas.AMAS.Alignment.matrix.

Referenced by amas.AMAS.Alignment.get_site_no_missing_ambiguous(), and amas.AMAS.Alignment.replace_missing().

Here is the caller graph for this function:


amas.AMAS.Alignment.get_sites_no_missing_ambiguous
amas.AMAS.Alignment.get_site_no_missing_ambiguous
amas.AMAS.Alignment.get_trim_selection
amas.AMAS.Alignment.replace_missing
amas.AMAS.Alignment.get_column

7.1.3.9 get_counts()

```
amas.AMAS.Alignment.get_counts (
                self )
```

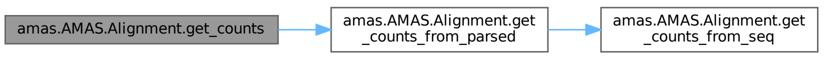
Definition at line 1052 of file AMAS.py.

```
    def get_counts(self):
        # get counts of each character in the used alphabet for all sequences
        counters = [Counter(chars) for taxon, chars in self.get_counts_from_parsed()]
        all_counts = sum(counters, Counter())
        counts_dict = dict(all_counts)
        return counts_dict
```

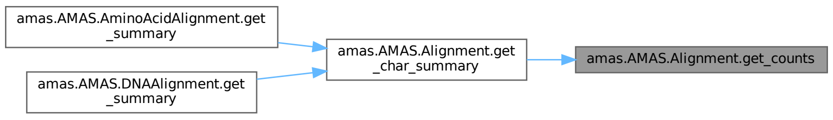
References amas.AMAS.Alignment.get_counts_from_parsed().

Referenced by amas.AMAS.Alignment.get_char_summary().

Here is the call graph for this function:


amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get _counts_from_parsed
amas.AMAS.Alignment.get _counts_from_seq

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get _summary
amas.AMAS.DNAAlignment.get _summary
amas.AMAS.Alignment.get _char_summary
amas.AMAS.Alignment.get_counts

7.1.3.10 get_counts_from_parsed()

```
amas.AMAS.Alignment.get_counts_from_parsed (
                self )
```

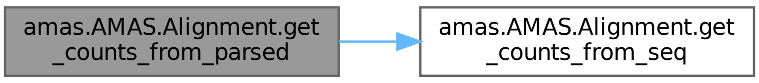
Definition at line 1059 of file AMAS.py.

```
    def get_counts_from_parsed(self):
        # get counts of all characters from parsed alignment
        # return a list of tuples with taxon name and counts
        return sorted(
            [
                (taxon, self.get_counts_from_seq(seq))
                for taxon, seq in self.parsed_aln.items()
            ]
        )

```

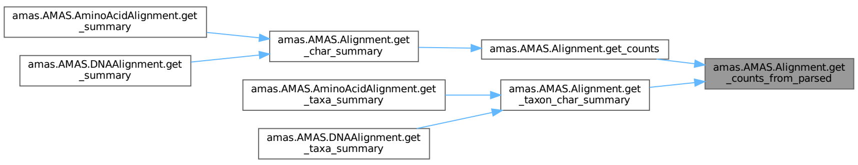
References amas.AMAS.Alignment.get_counts_from_seq(), and amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.Alignment.get_counts(), and amas.AMAS.Alignment.get_taxon_char_summary().

Here is the call graph for this function:


amas.AMAS.Alignment.get _counts_from_parsed
amas.AMAS.Alignment.get _counts_from_seq

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_summary
amas.AMAS.DNAAlignment.get_summary
amas.AMAS.Alignment.get_char_summary
amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.get_counts_from_parsed

7.1.3.11 get_counts_from_seq()

```
amas.AMAS.Alignment.get_counts_from_seq (
                self,
                seq )
```

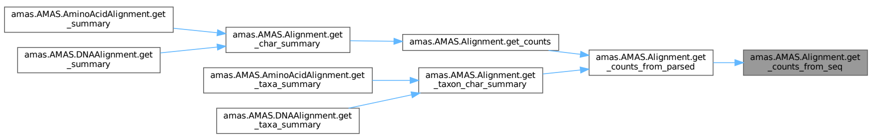
Definition at line 1069 of file AMAS.py.

```
def get_counts_from_seq(self, seq):
    # get all alphabet chars count for individual sequence
    char_counts = {char : seq.count(char) for char in self.alphabet}
    return char_counts
```

References amas.AMAS.AminoAcidAlignment.alphabet, and amas.AMAS.DNAAlignment.alphabet.

Referenced by amas.AMAS.Alignment.get_counts_from_parsed().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_summary
amas.AMAS.DNAAlignment.get_summary
amas.AMAS.Alignment.get_char_summary
amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq

7.1.3.12 get_matrix_cells()

```
amas.AMAS.Alignment.get_matrix_cells (
                self )
```

Definition at line 1016 of file AMAS.py.

```
def get_matrix_cells(self):
```

7.1.3.13 get_missing()

```
amas.AMAS.Alignment.get_missing (
                self )
```

Definition at line 1021 of file AMAS.py.

```
def get_missing(self):
    # count missing characters from the list of missing for all sequences
    self.missing = sum(count for taxon, count, percent in self.missing_records)
    return self.missing
```

7.1.3.14 get_missing_from_parsed()

```
amas.AMAS.Alignment.get_missing_from_parsed (
                self )
```

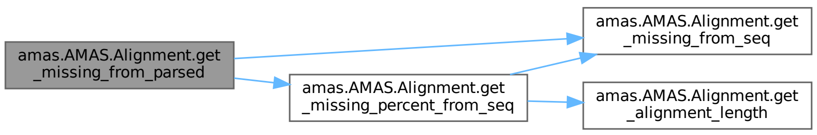
Definition at line 1031 of file AMAS.py.

```
    def get_missing_from_parsed(self):
        # get missing count and percent from parsed alignment
        # return a list of tuples with taxon name, count, and percent missing
        self.missing_records = sorted(
            [
                (taxon, self.get_missing_from_seq(seq), self.get_missing_percent_from_seq(seq))
                for taxon, seq in self.parsed_aln.items()
            ]
        )
        return self.missing_records

```

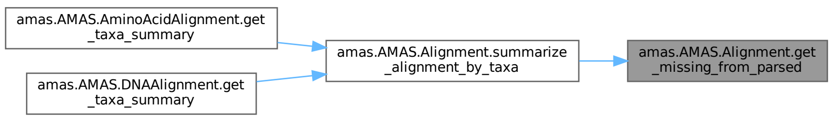
References amas.AMAS.Alignment.get_missing_from_seq(), amas.AMAS.Alignment.get_missing_percent_from_seq(), amas.AMAS.Alignment.missing_records, and amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the call graph for this function:


amas.AMAS.Alignment.get_missing_from_parsed
amas.AMAS.Alignment.get_missing_from_seq
amas.AMAS.Alignment.get_missing_percent_from_seq
amas.AMAS.Alignment.get_alignment_length

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.Alignment.get_missing_from_parsed

7.1.3.15 get_missing_from_seq()

```
amas.AMAS.Alignment.get_missing_from_seq (
                self,
                seq )
```

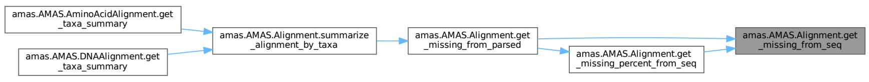
Definition at line 1042 of file AMAS.py.

```
    def get_missing_from_seq(self, seq):
        # count missing characters for individual sequence
        missing_count = sum(seq.count(char) for char in self.missing_chars)
        return missing_count

```

References amas.AMAS.AminoAcidAlignment.missing_chars, and amas.AMAS.DNAAlignment.missing_chars.

Referenced by amas.AMAS.Alignment.get_missing_from_parsed(), and amas.AMAS.Alignment.get_missing_percent_from_seq().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get _taxa_summary
amas.AMAS.DNAAlignment.get _taxa_summary
amas.AMAS.Alignment.summarize _alignment_by_taxa
amas.AMAS.Alignment.get _missing_from_parsed
amas.AMAS.Alignment.get _missing_percent_from_seq
amas.AMAS.Alignment.get _missing_from_seq

7.1.3.16 get_missing_percent()

```
amas.AMAS.Alignment.get_missing_percent (
                self )
```

Definition at line 1026 of file AMAS.py.

```
01026     def get_missing_percent(self):
01027         # get missing percent
01028         missing_percent = round((self.missing / self.all_matrix_cells * 100), 3)
01029         return missing_percent
01030
```

References amas.AMAS.Alignment.all_matrix_cells, and amas.AMAS.Alignment.missing.

7.1.3.17 get_missing_percent_from_seq()

```
amas.AMAS.Alignment.get_missing_percent_from_seq (
                self,
                seq )
```

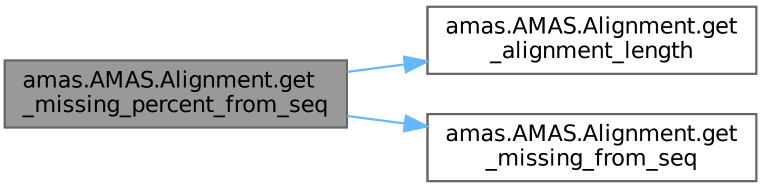
Definition at line 1047 of file AMAS.py.

```
01047     def get_missing_percent_from_seq(self, seq):
01048         # get missing percent from individual sequence
01049         missing_seq_percent = round((self.get_missing_from_seq(seq) / self.get_alignment_length() *
      100), 3)
01050         return missing_seq_percent
01051
```

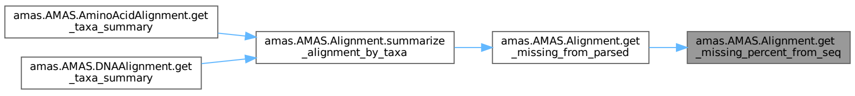
References amas.AMAS.Alignment.get_alignment_length(), and amas.AMAS.Alignment.get_missing_from_seq().

Referenced by amas.AMAS.Alignment.get_missing_from_parsed().

Here is the call graph for this function:


amas.AMAS.Alignment.get _missing_percent_from_seq
amas.AMAS.Alignment.get _alignment_length
amas.AMAS.Alignment.get _missing_from_seq

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.Alignment.get_missing_from_parsed
amas.AMAS.Alignment.get_missing_percent_from_seq

7.1.3.18 get_name()

```
amas.AMAS.Alignment.get_name (
                self )
```

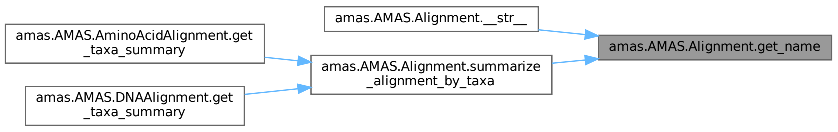
Definition at line 1002 of file AMAS.py.

```
    def get_name(self):
        # get input file name
        in_filename = path.basename(self.in_file)
        return in_filename

```

References amas.AMAS.FileHandler.in_file, amas.AMAS.FileParser.in_file, and amas.AMAS.Alignment.in_file.

Referenced by amas.AMAS.Alignment.__str__(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the caller graph for this function:


amas.AMAS.Alignment.__str__
amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.Alignment.get_name

7.1.3.19 get_parsed_aln()

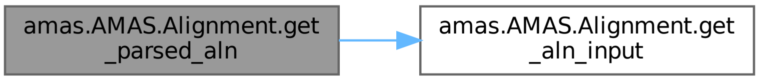
```
amas.AMAS.Alignment.get_parsed_aln (
                self )
```

Definition at line 831 of file AMAS.py.

```
    def get_parsed_aln(self):
        # parse according to the given format
        aln_input = self.get_aln_input()
        if self.in_format == "fasta":
            parsed_aln = aln_input.fasta_parse()
        elif self.in_format == "phylip":
            parsed_aln = aln_input.phylip_parse()
        elif self.in_format == "phylip-int":
            parsed_aln = aln_input.phylip_interleaved_parse()
        elif self.in_format == "nexus":
            parsed_aln = aln_input.nexus_parse()
        elif self.in_format == "nexus-int":
            parsed_aln = aln_input.nexus_interleaved_parse()

        return parsed_aln

```

References amas.AMAS.Alignment.get_aln_input(), amas.AMAS.Alignment.in_format, and amas.AMAS.MetaAlignment.in_format.

Here is the call graph for this function:


amas.AMAS.Alignment.get_parsed_aln
amas.AMAS.Alignment.get_aln_input

7.1.3.20 get_parsimony_informative()

```
amas.AMAS.Alignment.get_parsimony_informative (
                self )
```

Definition at line 978 of file AMAS.py.

```
    def get_parsimony_informative(self):
        # if the count for a unique character in a site is at least two,
        # and there are at least two such characters in a site without missing
        # or ambiguous characters, consider it parsimony informative
        parsimony_informative = 0
        for site in self.no_missing_ambiguous:
            unique_chars = set(site)
            pattern = [base for base in unique_chars if site.count(base) >= 2]
            no_patterns = len(pattern)

            if no_patterns >= 2:
                parsimony_informative += 1
        return parsimony_informative

```

References amas.AMAS.Alignment.no_missing_ambiguous.

7.1.3.21 get_prop_parsimony()

```
amas.AMAS.Alignment.get_prop_parsimony (
                self )
```

Definition at line 997 of file AMAS.py.

```
    def get_prop_parsimony(self):
        # get proportion of parsimony informative sites to all sites
        prop_parsimony = self.parsimony_informative / int(self.length)
        return round(prop_parsimony, 3)

```

References amas.AMAS.Alignment.length, and amas.AMAS.Alignment.parsimony_informative.

7.1.3.22 get_prop_variable()

```
amas.AMAS.Alignment.get_prop_variable (
                self )
```

Definition at line 992 of file AMAS.py.

```
    def get_prop_variable(self):
        # get proportion of variable sites to all sites
        prop_variable = self.variable_sites / int(self.length)
        return round(prop_variable, 3)

```

References amas.AMAS.Alignment.length, and amas.AMAS.Alignment.variable_sites.

7.1.3.23 get_site_no_missing_ambiguous()

```
amas.AMAS.Alignment.get_site_no_missing_ambiguous (
                self,
                column )
```

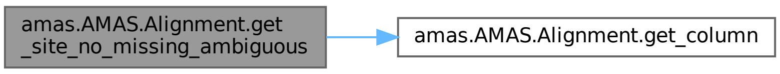
Definition at line 946 of file AMAS.py.

```
    def get_site_no_missing_ambiguous(self, column):
        site = self.get_column(column)
        return [char for char in site if char not in self.missing_ambiguous_chars]

```

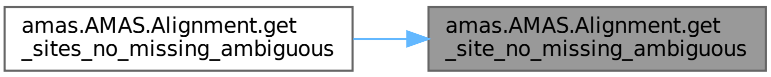
References amas.AMAS.Alignment.get_column(), amas.AMAS.AminoAcidAlignment.missing_ambiguous_chars, and amas.AMAS.DNAAlignment.missing_ambiguous_chars.

Referenced by amas.AMAS.Alignment.get_sites_no_missing_ambiguous().

Here is the call graph for this function:


amas.AMAS.Alignment.get_site_no_missing_ambiguous
amas.AMAS.Alignment.get_column

Here is the caller graph for this function:


amas.AMAS.Alignment.get_sites_no_missing_ambiguous
amas.AMAS.Alignment.get_site_no_missing_ambiguous

7.1.3.24 get_sites_no_missing_ambiguous()

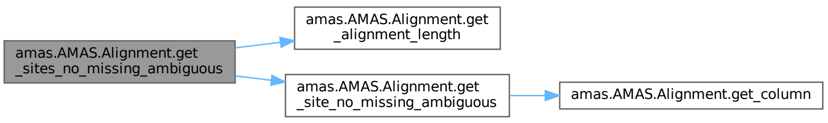
```
amas.AMAS.Alignment.get_sites_no_missing_ambiguous (
                self )
```

Definition at line 941 of file AMAS.py.

```
    def get_sites_no_missing_ambiguous(self):
        # get each site without missing or ambiguous characters
        no_missing_ambiguous_sites = [self.get_site_no_missing_ambiguous(column) for column in
  range(self.get_alignment_length())]
        return no_missing_ambiguous_sites

```

References amas.AMAS.Alignment.get_alignment_length(), and amas.AMAS.Alignment.get_site_no_missing_ambiguous().

Here is the call graph for this function:


amas.AMAS.Alignment.get_sites_no_missing_ambiguous
amas.AMAS.Alignment.get_alignment_length
amas.AMAS.Alignment.get_site_no_missing_ambiguous
amas.AMAS.Alignment.get_column

7.1.3.25 get_taxa_no()

```
amas.AMAS.Alignment.get_taxa_no (
                self )
```

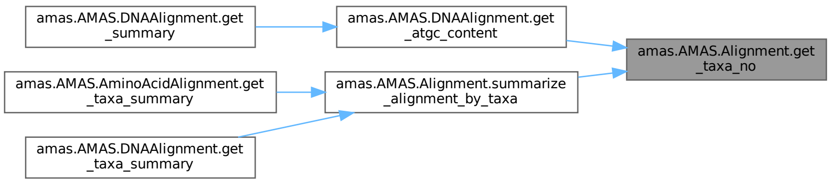
Definition at line 1007 of file AMAS.py.

```
    def get_taxa_no(self):
        # get number of taxa
        return len(self.parsed_aln.values())

```

References amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.DNAAlignment.get_atgc_content(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the caller graph for this function:


amas.AMAS.DNAAlignment.get_summary
amas.AMAS.DNAAlignment.get_atgc_content
amas.AMAS.Alignment.get_taxa_no
amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.DNAAlignment.get_taxa_summary

7.1.3.26 get_taxon_char_summary()

```
amas.AMAS.Alignment.get_taxon_char_summary (
                self )
```

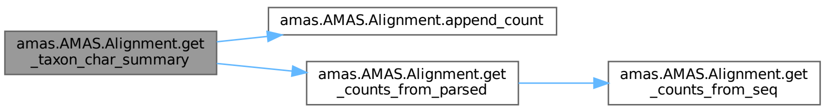
Definition at line 914 of file AMAS.py.

```
    def get_taxon_char_summary(self):
        # get summary of frequencies for all characters
        records = (self.append_count(char_dict) for taxon, char_dict in self.get_counts_from_parsed())
        return records

```

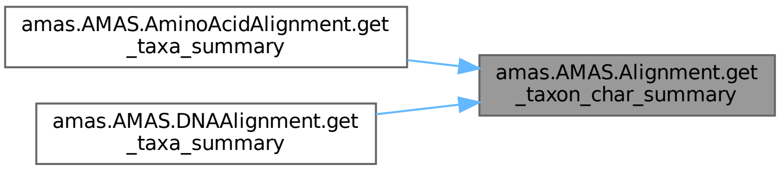
References amas.AMAS.Alignment.append_count(), and amas.AMAS.Alignment.get_counts_from_parsed().

Referenced by amas.AMAS.AminoAcidAlignment.get_taxa_summary(), and amas.AMAS.DNAAlignment.get_taxa_summary().

Here is the call graph for this function:


amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.append_count
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.Alignment.get_taxon_char_summary

7.1.3.27 get_trim_selection()

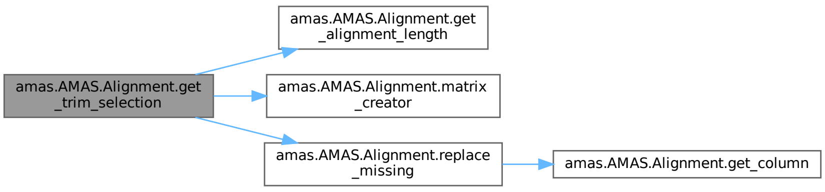
```
amas.AMAS.Alignment.get_trim_selection (
                self,
                trim_fraction,
                parsimony_check )
```

Definition at line 953 of file AMAS.py.

```
    def get_trim_selection(self, trim_fraction, parsimony_check):
        # this checks each column of alignment for minimum occupancy
        self.matrix = self.matrix_creator()
        trim_vector = []
        for column in range(self.get_alignment_length()):
            site = self.replace_missing(column)
            occ = (len(site) - site.count("-")) / len(site)
            if parsimony_check:
                unique_chars = set(site)
                try:
                    unique_chars.remove("-")
                except KeyError:
                    pass # this occurs if we have no missing data
                pattern = [base for base in unique_chars if site.count(base) >= 2]
                trim_vector.append(len(pattern) >= 2 and occ >= trim_fraction)
            else:
                trim_vector.append(occ >= trim_fraction)
        return trim_vector

```

References amas.AMAS.Alignment.get_alignment_length(), amas.AMAS.Alignment.matrix, amas.AMAS.Alignment.matrix_creator(), and amas.AMAS.Alignment.replace_missing().

Here is the call graph for this function:


amas.AMAS.Alignment.get_trim_selection
amas.AMAS.Alignment.get_alignment_length
amas.AMAS.Alignment.matrix_creator
amas.AMAS.Alignment.replace_missing
amas.AMAS.Alignment.get_column

7.1.3.28 get_variable()

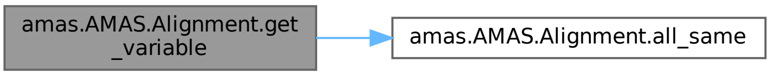
```
amas.AMAS.Alignment.get_variable (
              self )
```

Definition at line 972 of file AMAS.py.

```
    def get_variable(self):
        # if all elements of a site without missing or ambiguous characters
        # are not the same, consider it variable
        variable = len([site for site in self.no_missing_ambiguous if not self.all_same(site)])
        return variable

```

References amas.AMAS.Alignment.all_same(), and amas.AMAS.Alignment.no_missing_ambiguous.

Here is the call graph for this function:


amas.AMAS.Alignment.get_variable
amas.AMAS.Alignment.all_same

7.1.3.29 matrix_creator()

```
amas.AMAS.Alignment.matrix_creator (
              self )
```

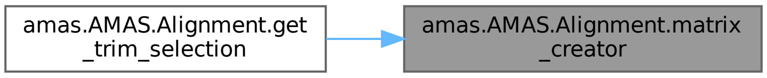
Definition at line 928 of file AMAS.py.

```
    def matrix_creator(self):
        # decompose character matrix into a two-dimensional list
        matrix = [list(sequence) for sequence in self.parsed_aln.values()]
        return matrix

```

References amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.Alignment.get_trim_selection().

Here is the caller graph for this function:


amas.AMAS.Alignment.get_trim_selection
amas.AMAS.Alignment.matrix_creator

7.1.3.30 replace_missing()

```
amas.AMAS.Alignment.replace_missing (
              self,
              column )
```

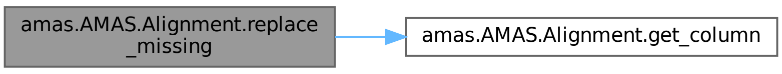
Definition at line 950 of file AMAS.py.

```
    def replace_missing(self, column):
        return ["-" if x in self.missing_chars else x for x in self.get_column(column)]

```

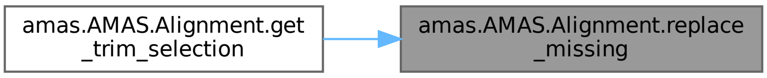
References amas.AMAS.Alignment.get_column(), amas.AMAS.AminoAcidAlignment.missing_chars, and amas.AMAS.DNAAlignment.missing_chars.

Referenced by amas.AMAS.Alignment.get_trim_selection().

Here is the call graph for this function:


amas.AMAS.Alignment.replace_missing
amas.AMAS.Alignment.get_column

Here is the caller graph for this function:


amas.AMAS.Alignment.get_trim_selection
amas.AMAS.Alignment.replace_missing

7.1.3.31 summarize_alignment()

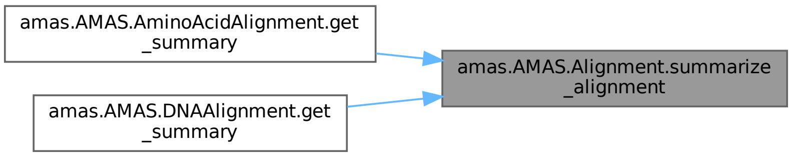
```
amas.AMAS.Alignment.summarize_alignment (
              self )
```

Definition at line 847 of file AMAS.py.

```
    def summarize_alignment(self):
        # call methods to create sequences list, matrix, sites without ambiguous or
        # missing characters; get and summarize alignment statistics
        summary = []
        self.length = str(self.get_alignment_length())
        self.matrix = self.matrix_creator()
        self.no_missing_ambiguous = self.get_sites_no_missing_ambiguous()
        self.variable_sites = self.get_variable()
        self.prop_variable = self.get_prop_variable()
        self.parsimony_informative = self.get_parsimony_informative()
        self.prop_parsimony = self.get_prop_parsimony()
        self.missing_records = self.get_missing_from_parsed()
        name = str(self.get_name())
        taxa_no = str(self.get_taxa_no())
        cells = str(self.get_matrix_cells())
        missing = str(self.get_missing())
        missing_percent = str(self.get_missing_percent())
        self.check_data_type()
        summary = [
            name,
            taxa_no,
            self.length,
            cells,
            missing,
            missing_percent,
            str(self.variable_sites),
            str(self.prop_variable),
            str(self.parsimony_informative),
            str(self.prop_parsimony)
        ]
        return summary

```

Referenced by amas.AMAS.AminoAcidAlignment.get_summary(), and amas.AMAS.DNAAlignment.get_summary().

Here is the caller graph for this function:


amas.AMAS.AminoAcidAlignment.get
_summary
amas.AMAS.DNAAlignment.get
_summary
amas.AMAS.Alignment.summarize
_alignment

7.1.3.32 summarize_alignment_by_taxa()

```
amas.AMAS.Alignment.summarize_alignment_by_taxa (
                self )
```

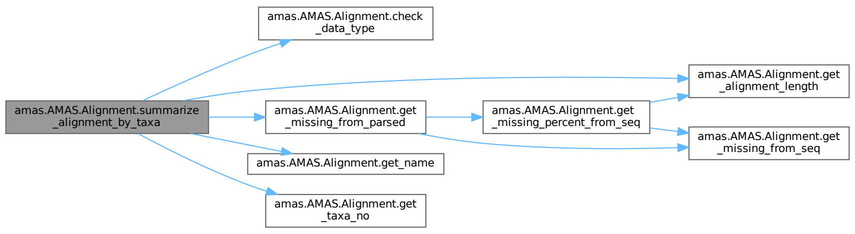
Definition at line 879 of file AMAS.py.

```
    def summarize_alignment_by_taxa(self):
        # get summary for all taxa/sequences in alignment
        per_taxon_summary = []
        taxa_no = self.get_taxa_no()
        self.missing_records = self.get_missing_from_parsed()
        self.length = self.get_alignment_length()
        lengths = (self.length for i in range(taxa_no))
        name = self.get_name()
        names = (name for i in range(taxa_no))
        taxa_names = (
            taxon.replace(" ", "_").replace(".", "_").replace("'", "")
            for taxon, missing_count, missing_percent in self.missing_records
        )
        missing = (missing_count for taxon, missing_count, missing_percent in self.missing_records)
        missing_percent = (missing_percent for taxon, missing_count, missing_percent in
self.missing_records)
        self.check_data_type()
        per_taxon_summary = (names, taxa_names, lengths, missing, missing_percent)
        zipped = list(zip(*per_taxon_summary))
        return zipped

```

References amas.AMAS.Alignment.check_data_type(), amas.AMAS.Alignment.get_alignment_length(), amas.AMAS.Alignment.get_missing_from_parsed(), amas.AMAS.Alignment.get_name(), amas.AMAS.Alignment.get_taxa_no(), amas.AMAS.Alignment.length, and amas.AMAS.Alignment.missing_records.

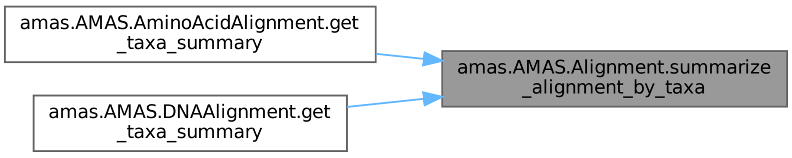
Referenced by amas.AMAS.AminoAcidAlignment.get_taxa_summary(), and amas.AMAS.DNAAlignment.get_taxa_summary().

Here is the call graph for this function:



amas.AMAS.Alignment.summarize _alignment_by_taxa
amas.AMAS.Alignment.check _data_type
amas.AMAS.Alignment.get _missing_from_parsed
amas.AMAS.Alignment.get_name
amas.AMAS.Alignment.get _taxa_no
amas.AMAS.Alignment.get _missing_percent_from_seq
amas.AMAS.Alignment.get _alignment_length
amas.AMAS.Alignment.get _missing_from_seq

Here is the caller graph for this function:



amas.AMAS.AminoAcidAlignment.get _taxa_summary
amas.AMAS.DNAAlignment.get _taxa_summary
amas.AMAS.Alignment.summarize _alignment_by_taxa

7.1.4 Member Data Documentation

7.1.4.1 all_matrix_cells

`amas.AMAS.Alignment.all_matrix_cells [static]`

Definition at line 1018 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_missing_percent().

7.1.4.2 check

`amas.AMAS.Alignment.check`

Definition at line 1077 of file AMAS.py.

7.1.4.3 data_type

`amas.AMAS.Alignment.data_type`

Definition at line 818 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_object(), amas.AMAS.MetaAlignment.get_summaries(), amas.AMAS.MetaAlignment.get_taxon_summaries(), amas.AMAS.MetaAlignment.print_nexus(), amas.AMAS.MetaAlignment.print_nexus_int(), and amas.AMAS.MetaAlignment.write_out().

7.1.4.4 in_file

```
amas.AMAS.Alignment.in_file
```

Definition at line 816 of file AMAS.py.

Referenced by amas.AMAS.FileHandler.__exit__(), amas.AMAS.Alignment.get_aln_input(), and amas.AMAS.Alignment.get_name().

7.1.4.5 in_format

```
amas.AMAS.Alignment.in_format
```

Definition at line 817 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_object(), amas.AMAS.Alignment.get_parsed_aln(), and amas.AMAS.MetaAlignment.write_out().

7.1.4.6 length

```
amas.AMAS.Alignment.length
```

Definition at line 851 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_prop_parsimony(), amas.AMAS.Alignment.get_prop_variable(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

7.1.4.7 matrix

```
amas.AMAS.Alignment.matrix
```

Definition at line 852 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_column(), and amas.AMAS.Alignment.get_trim_selection().

7.1.4.8 missing

```
amas.AMAS.Alignment.missing
```

Definition at line 1023 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_missing_percent().

7.1.4.9 missing_records

```
amas.AMAS.Alignment.missing_records
```

Definition at line 858 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_missing_from_parsed(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

7.1.4.10 no_missing_ambiguous

```
amas.AMAS.Alignment.no_missing_ambiguous
```

Definition at line 853 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_parsimony_informative(), and amas.AMAS.Alignment.get_variable().

7.1.4.11 parsed_aln

```
amas.AMAS.Alignment.parsed_aln
```

Definition at line 820 of file AMAS.py.

Referenced by amas.AMAS.Alignment.check_data_type(), amas.AMAS.Alignment.get_alignment_length(), amas.AMAS.DNAAlignment.get_atgc_from_parsed(), amas.AMAS.Alignment.get_counts_from_parsed(), amas.AMAS.Alignment.get_missing_from_parsed(), amas.AMAS.Alignment.get_taxa_no(), and amas.AMAS.Alignment.matrix_creator().

7.1.4.12 parsimony_informative

```
amas.AMAS.Alignment.parsimony_informative
```

Definition at line 856 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_prop_parsimony().

7.1.4.13 prop_parsimony

```
amas.AMAS.Alignment.prop_parsimony
```

Definition at line 857 of file AMAS.py.

7.1.4.14 prop_variable

```
amas.AMAS.Alignment.prop_variable
```

Definition at line 855 of file AMAS.py.

7.1.4.15 variable_sites

```
amas.AMAS.Alignment.variable_sites
```

Definition at line 854 of file AMAS.py.

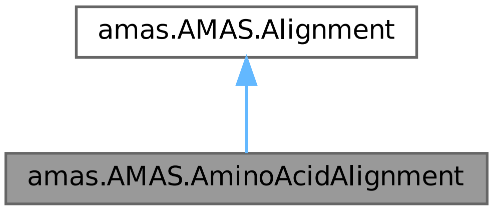
Referenced by amas.AMAS.Alignment.get_prop_variable().

The documentation for this class was generated from the following file:

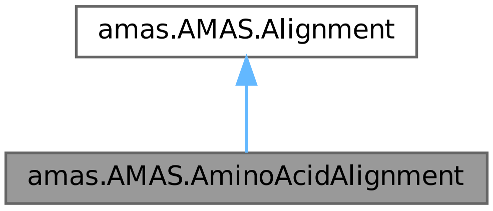
- amas/AMAS.py

7.2 amas.AMAS.AminoAcidAlignment Class Reference

Inheritance diagram for amas.AMAS.AminoAcidAlignment:



Collaboration diagram for amas.AMAS.AminoAcidAlignment:



Public Member Functions

- get_summary (self)
- get_taxa_summary (self)

Static Public Attributes

- list alphabet = ["A", "C", "D", "E", "F", "G", "H", "I", "K", "L", "M", "N", "P", "Q", "R", "S", "T", "V", "W", "Y", "B", "J", "Z", "X", ".", "*", "-", "?"]
- list missing_ambiguous_chars = ["B", "J", "Z", "X", ".", "*", "-", "?"]
- list missing_chars = ["X", ".", "*", "-", "?"]
- list non_alphabet = ["O"]

7.2.1 Detailed Description

```
Alphabets specific to amino acid alignments
```

Definition at line 1085 of file AMAS.py.

7.2.2 Member Function Documentation

7.2.2.1 get_summary()

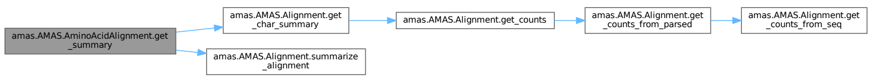
```
amas.AMAS.AminoAcidAlignment.get_summary (
                self )
```

Definition at line 1093 of file AMAS.py.

```
01093     def get_summary(self):
01094         # get alignment summary specific to amino acids
01095         data = self.summarize_alignment()
01096         new_data = data + list(self.get_char_summary()[1])
01097         return new_data
01098
```

References amas.AMAS.Alignment.get_char_summary(), and amas.AMAS.Alignment.summarize_alignment().

Here is the call graph for this function:


amas.AMAS.AminoAcidAlignment.get_summary
amas.AMAS.Alignment.get_char_summary
amas.AMAS.Alignment.summarize_alignment
amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq

7.2.2.2 get_taxa_summary()

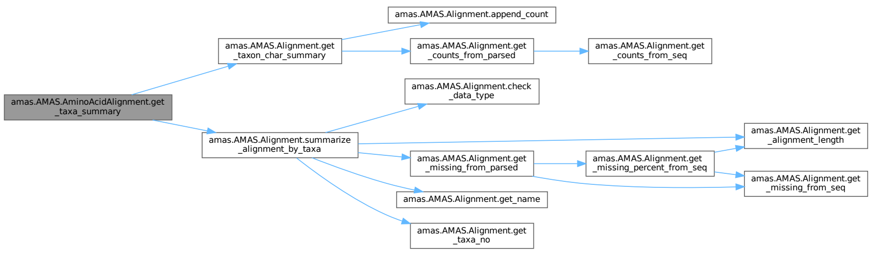
```
amas.AMAS.AminoAcidAlignment.get_taxa_summary (
                self )
```

Definition at line 1099 of file AMAS.py.

```
01099     def get_taxa_summary(self):
01100         # get per-taxon/sequence alignment summary specific to amino acids
01101         data = self.summarize_alignment_by_taxa()
01102         aa_summary = (data, self.get_taxon_char_summary())
01103         zipped_list = list(zip(*aa_summary))
01104         new_data = [list(data_tupl) + chars for data_tupl, chars in zipped_list]
01105         return new_data
01106
```

References amas.AMAS.Alignment.get_taxon_char_summary(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the call graph for this function:


amas.AMAS.AminoAcidAlignment.get_taxa_summary
amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.Alignment.append_count
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq
amas.AMAS.Alignment.check_data_type
amas.AMAS.Alignment.get_missing_from_parsed
amas.AMAS.Alignment.get_missing_percent_from_seq
amas.AMAS.Alignment.get_alignment_length
amas.AMAS.Alignment.get_missing_from_seq
amas.AMAS.Alignment.get_name
amas.AMAS.Alignment.get_taxa_no

7.2.3 Member Data Documentation

7.2.3.1 alphabet

```
list amas.AMAS.AminoAcidAlignment.alphabet = ["A", "C", "D", "E", "F", "G", "H", "I", "K",
"L", "M", "N", "P", "Q", "R", "S", "T", "V", "W", "Y", "B", "J", "Z", "X", ".", "*", "-", "?"]
[static]
```

Definition at line 1088 of file AMAS.py.

Referenced by amas.AMAS.Alignment.append_count(), amas.AMAS.Alignment.get_char_summary(), and amas.AMAS.Alignment.get_counts_from_seq().

7.2.3.2 missing_ambiguous_chars

```
list amas.AMAS.AminoAcidAlignment.missing_ambiguous_chars = ["B", "J", "Z", "X", ".", "*",
"-", "?"]  [static]
```

Definition at line 1089 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_site_no_missing_ambiguous().

7.2.3.3 missing_chars

```
list amas.AMAS.AminoAcidAlignment.missing_chars = ["X", ".", "*", "-", "?"]  [static]
```

Definition at line 1090 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_missing_from_seq(), and amas.AMAS.Alignment.replace_missing().

7.2.3.4 non_alphabet

```
list amas.AMAS.AminoAcidAlignment.non_alphabet = ["O"]  [static]
```

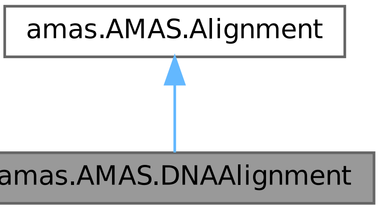
Definition at line 1091 of file AMAS.py.

The documentation for this class was generated from the following file:

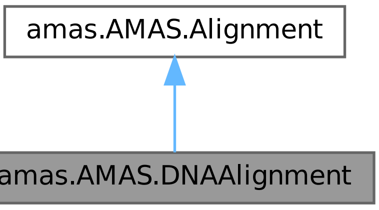
- amas/AMAS.py

7.3 amas.AMAS.DNAAlignment Class Reference

Inheritance diagram for amas.AMAS.DNAAlignment:



Collaboration diagram for amas.AMAS.DNAAlignment:



Public Member Functions

- get_summary (self)
- get_taxa_summary (self)
- get_atgc_content (self)
- get_list_from_atgc (self)
- get_atgc_from_parsed (self)
- get_atgc_from_seq (self, seq)

Static Public Attributes

- list alphabet = ["A", "C", "G", "T", "K", "M", "R", "Y", "S", "W", "B", "V", "H", "D", "X", "N", "O", "-", "?"]
- list missing_ambiguous_chars = ["K", "M", "R", "Y", "S", "W", "B", "V", "H", "D", "X", "N", "O", "-", "?"]
- list missing_chars = ["X", "N", "O", "-", "?"]
- list non_alphabet = ["E", "F", "I", "L", "P", "Q", "J", "Z", ".", "∗"]

7.3.1 Detailed Description

```
Alphabets specific to DNA alignments
```

Definition at line 1107 of file AMAS.py.

7.3.2 Member Function Documentation

7.3.2.1 get_atgc_content()

```
amas.AMAS.DNAAlignment.get_atgc_content (
                self )
```

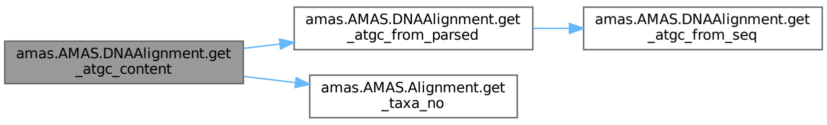
Definition at line 1129 of file AMAS.py.

```
    def get_atgc_content(self):
        # get AC and GC contents for all sequences
        # AT content is the first element of AT, GC content tuple
        # returned by get_atgc_from_seq()
        atgc_records = self.get_atgc_from_parsed()
        at_content = round(sum(atgc[0] for taxon, atgc in atgc_records) / self.get_taxa_no(), 3)
        gc_content = round(1 - float(at_content), 3)

        atgc_content = [str(at_content), str(gc_content)]
        return atgc_content

```

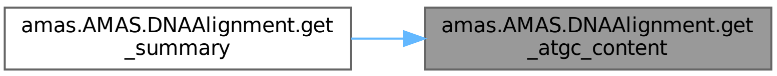
References amas.AMAS.DNAAlignment.get_atgc_from_parsed(), and amas.AMAS.Alignment.get_taxa_no().

Referenced by amas.AMAS.DNAAlignment.get_summary().

Here is the call graph for this function:


amas.AMAS.DNAAlignment.get_atgc_content
amas.AMAS.DNAAlignment.get_atgc_from_parsed
amas.AMAS.DNAAlignment.get_atgc_from_seq
amas.AMAS.Alignment.get_taxa_no

Here is the caller graph for this function:


amas.AMAS.DNAAlignment.get_summary
amas.AMAS.DNAAlignment.get_atgc_content

7.3.2.2 get_atgc_from_parsed()

```
amas.AMAS.DNAAlignment.get_atgc_from_parsed (
                self )
```

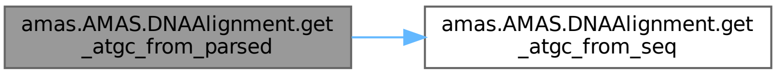
Definition at line 1144 of file AMAS.py.

```
    def get_atgc_from_parsed(self):
        # get AT and GC contents from parsed alignment dictionary
        # return a list of tuples with taxon name, AT content, and GC content
        return sorted([(taxon, self.get_atgc_from_seq(seq)) for taxon, seq in
      self.parsed_aln.items()])

```

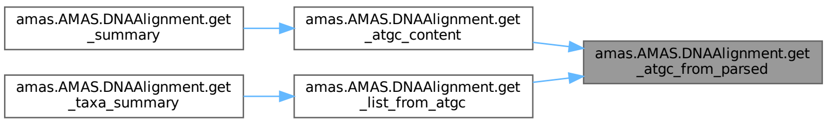
References amas.AMAS.DNAAlignment.get_atgc_from_seq(), and amas.AMAS.Alignment.parsed_aln.

Referenced by amas.AMAS.DNAAlignment.get_atgc_content(), and amas.AMAS.DNAAlignment.get_list_from_atgc().

Here is the call graph for this function:



Here is the caller graph for this function:


amas.AMAS.DNAAlignment.get
_summary
amas.AMAS.DNAAlignment.get
_atgc_content
amas.AMAS.DNAAlignment.get
_taxa_summary
amas.AMAS.DNAAlignment.get
_list_from_atgc
amas.AMAS.DNAAlignment.get
_atgc_from_parsed

7.3.2.3 get_atgc_from_seq()

```
amas.AMAS.DNAAlignment.get_atgc_from_seq (
                self,
                seq )
```

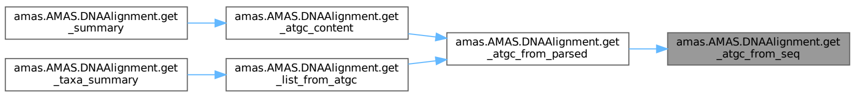
Definition at line 1149 of file AMAS.py.

```
    def get_atgc_from_seq(self, seq):
        # get AT and GC contents from individual sequences

        at_count = seq.count("A") + seq.count("T") + seq.count("W")
        gc_count = seq.count("G") + seq.count("C") + seq.count("S")

        try:
            at_content = round(at_count / (at_count + gc_count), 3)
            gc_content = round(1 - float(at_content), 3)

        except ZeroDivisionError:
            at_content = 0
            gc_content = 0

        return at_content, gc_content
```

```
01164
```

Referenced by amas.AMAS.DNAAlignment.get_atgc_from_parsed().

Here is the caller graph for this function:


amas.AMAS.DNAAlignment.get_summary
amas.AMAS.DNAAlignment.get_atgc_content
amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_list_from_atgc
amas.AMAS.DNAAlignment.get_atgc_from_parsed
amas.AMAS.DNAAlignment.get_atgc_from_seq

7.3.2.4 get_list_from_atgc()

```
amas.AMAS.DNAAlignment.get_list_from_atgc (
                self )
```

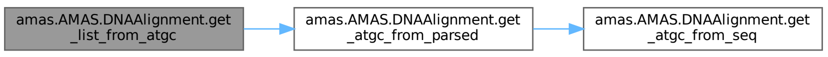
Definition at line 1140 of file AMAS.py.

```
01140     def get_list_from_atgc(self):
01141         records = (atgc for taxon, atgc in self.get_atgc_from_parsed())
01142         return records
01143
```

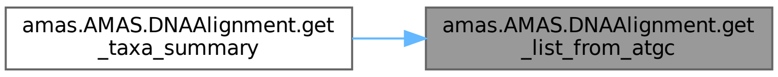
References amas.AMAS.DNAAlignment.get_atgc_from_parsed().

Referenced by amas.AMAS.DNAAlignment.get_taxa_summary().

Here is the call graph for this function:


amas.AMAS.DNAAlignment.get_list_from_atgc
amas.AMAS.DNAAlignment.get_atgc_from_parsed
amas.AMAS.DNAAlignment.get_atgc_from_seq

Here is the caller graph for this function:


amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_list_from_atgc

7.3.2.5 get_summary()

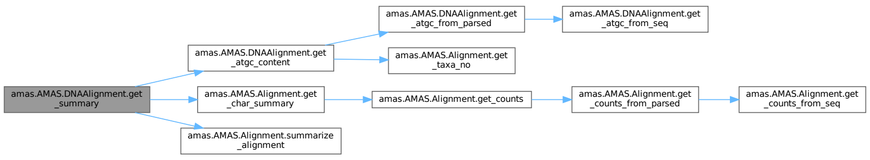
```
amas.AMAS.DNAAlignment.get_summary (
              self )
```

Definition at line 1115 of file AMAS.py.

```
01115     def get_summary(self):
01116         # get alignment summarry specific to nucleotide
01117         data = self.summarize_alignment()
01118         new_data = data + self.get_atgc_content() + list(self.get_char_summary()[1])
01119         return new_data
01120
```

References amas.AMAS.DNAAlignment.get_atgc_content(), amas.AMAS.Alignment.get_char_summary(), and amas.AMAS.Alignment.summarize_alignment().

Here is the call graph for this function:


amas.AMAS.DNAAlignment.get_summary
amas.AMAS.DNAAlignment.get_atgc_content
amas.AMAS.DNAAlignment.get_atgc_from_parsed
amas.AMAS.DNAAlignment.get_atgc_from_seq
amas.AMAS.Alignment.get_taxa_no
amas.AMAS.Alignment.get_char_summary
amas.AMAS.Alignment.get_counts
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq
amas.AMAS.Alignment.summarize_alignment

7.3.2.6 get_taxa_summary()

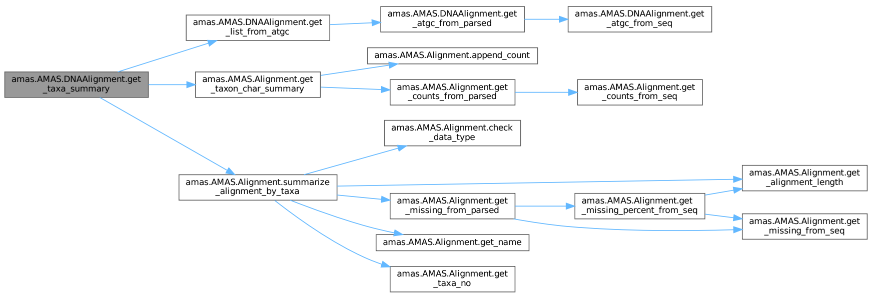
```
amas.AMAS.DNAAlignment.get_taxa_summary (
              self )
```

Definition at line 1121 of file AMAS.py.

```
01121     def get_taxa_summary(self):
01122         # get per-taxon/sequence alignment summary specific to nucleotides
01123         data = self.summarize_alignment_by_taxa()
01124         dna_summary = (data, self.get_list_from_atgc(), self.get_taxon_char_summary())
01125         zipped_list = list(zip(*dna_summary))
01126         new_data = [list(data_tupl) + list(atgc) + chars for data_tupl, atgc, chars in zipped_list]
01127         return new_data
01128
```

References amas.AMAS.DNAAlignment.get_list_from_atgc(), amas.AMAS.Alignment.get_taxon_char_summary(), and amas.AMAS.Alignment.summarize_alignment_by_taxa().

Here is the call graph for this function:


amas.AMAS.DNAAlignment.get_taxa_summary
amas.AMAS.DNAAlignment.get_list_from_atgc
amas.AMAS.DNAAlignment.get_atgc_from_parsed
amas.AMAS.DNAAlignment.get_atgc_from_seq
amas.AMAS.Alignment.append_count
amas.AMAS.Alignment.get_taxon_char_summary
amas.AMAS.Alignment.get_counts_from_parsed
amas.AMAS.Alignment.get_counts_from_seq
amas.AMAS.Alignment.check_data_type
amas.AMAS.Alignment.summarize_alignment_by_taxa
amas.AMAS.Alignment.get_alignment_length
amas.AMAS.Alignment.get_missing_from_parsed
amas.AMAS.Alignment.get_missing_percent_from_seq
amas.AMAS.Alignment.get_missing_from_seq
amas.AMAS.Alignment.get_name
amas.AMAS.Alignment.get_taxa_no

7.3.3 Member Data Documentation

7.3.3.1 alphabet

```
list amas.AMAS.DNAAlignment.alphabet = ["A", "C", "G", "T", "K", "M", "R", "Y", "S", "W", "B",
"V", "H", "D", "X", "N", "O", "-", "?"]  [static]
```

Definition at line 1110 of file AMAS.py.

Referenced by amas.AMAS.Alignment.append_count(), amas.AMAS.Alignment.get_char_summary(), and amas.AMAS.Alignment.get_counts_from_seq().

7.3.3.2 missing_ambiguous_chars

```
list amas.AMAS.DNAAlignment.missing_ambiguous_chars = ["K", "M", "R", "Y", "S", "W", "B", "V",
"H", "D", "X", "N", "O", "-", "?"]  [static]
```

Definition at line 1111 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_site_no_missing_ambiguous().

7.3.3.3 missing_chars

```
list amas.AMAS.DNAAlignment.missing_chars = ["X", "N", "O", "-", "?"]  [static]
```

Definition at line 1112 of file AMAS.py.

Referenced by amas.AMAS.Alignment.get_missing_from_seq(), and amas.AMAS.Alignment.replace_missing().

7.3.3.4 non_alphabet

```
list amas.AMAS.DNAAlignment.non_alphabet = ["E", "F", "I", "L", "P", "Q", "J", "Z", ".", "*"]
[static]
```

Definition at line 1113 of file AMAS.py.

The documentation for this class was generated from the following file:

- amas/AMAS.py

7.4 amas.AMAS.FileHandler Class Reference

Public Member Functions

- __init__ (self, file_name)
- __enter__ (self)
- __exit__ (self, ∗args)
- get_file_name (self)

Public Attributes

- file_name
- in_file

7.4.1 Detailed Description

```
Define file handle that closes when out of scope
```

Definition at line 518 of file AMAS.py.

7.4.2 Constructor & Destructor Documentation

7.4.2.1 __init__()

```
amas.AMAS.FileHandler.__init__ (
              self,
              file_name )
```

Definition at line 521 of file AMAS.py.

```
    def __init__(self, file_name):
        self.file_name = file_name

```

7.4.3 Member Function Documentation

7.4.3.1 __enter__()

```
amas.AMAS.FileHandler.__enter__ (
              self )
```

Definition at line 524 of file AMAS.py.

```
    def __enter__(self):
        try:
            self.in_file = open(self.file_name, "r", encoding="utf-8")
        except FileNotFoundError:
            print("ERROR: File '" + self.file_name + "' not found.")
            sys.exit()
        return self.in_file

```

7.4.3.2 __exit__()

```
amas.AMAS.FileHandler.__exit__ (
              self,
            * args )
```

Definition at line 532 of file AMAS.py.

```
    def __exit__(self, *args):
        self.in_file.close()

```

References amas.AMAS.FileHandler.in_file, amas.AMAS.FileParser.in_file, and amas.AMAS.Alignment.in_file.

7.4.3.3 get_file_name()

```
amas.AMAS.FileHandler.get_file_name (
              self )
```

Definition at line 535 of file AMAS.py.

```
    def get_file_name(self):
        return self.file_name

```

References amas.AMAS.FileHandler.file_name.

7.4.4 Member Data Documentation

7.4.4.1 file_name

```
amas.AMAS.FileHandler.file_name
```

Definition at line 522 of file AMAS.py.

Referenced by amas.AMAS.FileHandler.get_file_name().

7.4.4.2 in_file

```
amas.AMAS.FileHandler.in_file
```

Definition at line 526 of file AMAS.py.

Referenced by amas.AMAS.FileHandler.__exit__(), amas.AMAS.Alignment.get_aln_input(), and amas.AMAS.Alignment.get_name().

The documentation for this class was generated from the following file:

- amas/AMAS.py

7.5 amas.AMAS.FileParser Class Reference

Public Member Functions

- __init__ (self, in_file)
- fasta_parse (self)
- phylip_parse (self)
- phylip_interleaved_parse (self)
- nexus_parse (self)
- nexus_interleaved_parse (self)
- translate_ambiguous (self, seq)
- partitions_parse (self)

Public Attributes

- in_file
- in_file_lines

Static Public Attributes

- tax_chars_matches
- name_matches
- seq_matches
- tax_match = match.group(2)
- chars_match = match.group(3)
- list taxa = [ ]
- list sequences = [ ]
- dict records = {}
- int counter = 0
- name_match = match.group(2).replace("\n", "")
- seq_match = match.group(3).replace("\n", "").upper()
- matches
- str seq_match = "".join(seq_match.split())
- str sequence = ""

7.5.1 Detailed Description

```
Parse file contents and return sequences and sequence names
```

Definition at line 538 of file AMAS.py.

7.5.2 Constructor & Destructor Documentation

7.5.2.1 __init__()

```
amas.AMAS.FileParser.__init__ (
                self,
                in_file )
```

Definition at line 541 of file AMAS.py.

```
    def __init__(self, in_file):
        self.in_file = in_file
        with FileHandler(in_file) as handle:
            self.in_file_lines = handle.read().rstrip("\r\n")

```

7.5.3 Member Function Documentation

7.5.3.1 fasta_parse()

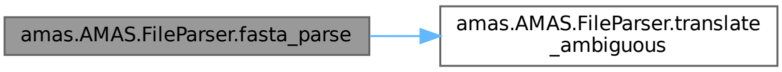
```
amas.AMAS.FileParser.fasta_parse (
                self )
```

Definition at line 546 of file AMAS.py.

```
00546     def fasta_parse(self):
00547         # use regex to parse names and sequences in sequential fasta files
00548         matches = re.finditer(
00549             r"^>(.*[^$])([^>]*)",
00550             self.in_file_lines, re.MULTILINE
00551         )
00552         records = {}
00553 
00554         for match in matches:
00555             name_match = match.group(1).replace("\n", "")
00556             seq_match = match.group(2).replace("\n", "").upper()
00557             seq_match = self.translate_ambiguous(seq_match)
00558             records[name_match] = seq_match
00559 
00560         return records
00561 
```

References amas.AMAS.FileParser.in_file_lines, and amas.AMAS.FileParser.translate_ambiguous().

Here is the call graph for this function:


amas.AMAS.FileParser.fasta_parse
amas.AMAS.FileParser.translate_ambiguous

7.5.3.2 nexus_interleaved_parse()

```
amas.AMAS.FileParser.nexus_interleaved_parse (
                self )
```

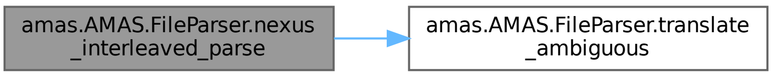
Definition at line 671 of file AMAS.py.

```
00671     def nexus_interleaved_parse(self):
00672         # use regex to parse names and sequences in sequential nexus files
00673         # find the matrix block
00674         matches = re.finditer(
00675             r"(\s+)?(MATRIX\n|matrix\n|MATRIX\r\n|matrix\r\n)(.*?;)",
00676             self.in_file_lines, re.DOTALL
00677         )
00678         # initiate lists for taxa names and sequence strings on separate lines
00679         taxa = []
00680         sequences = []
00681         # initiate a dictionary for the name:sequence records
00682         records = {}
00683 
00684         for match in matches:
00685             matrix_match = match.group(3)
00686             # get names and sequences from the matrix block
00687             seq_matches = re.finditer(
00688                 r"^(\s+)?[’]?(\S+\s\S+|\S+)[’]?\s+([A-Za-z*?.{}-]+)($|\s+\[[0-9]+\]$)",
00689                 matrix_match, re.MULTILINE
00690             )
00691 
00692             for match in seq_matches:
00693                 name_match = match.group(2)
00694                 if name_match not in taxa:
```

```
00695                     taxa.append(name_match)
00696                 seq_match = match.group(3)
00697 
00698                 sequences.append(seq_match)
00699 
00700         # initiate a counter to keep track of sequences strung together
00701         # from separate lines
00702         counter = 0
00703 
00704         for taxon_no in range(len(taxa)):
00705 
00706             full_length_sequence = "".join([sequences[index] for index in
      range(counter,len(sequences),len(taxa))])
00707             records[taxa[taxon_no]] = self.translate_ambiguous(full_length_sequence).replace("\n",
      "").upper()
00708             counter += 1
00709 
00710         return records
00711 
```

References amas.AMAS.FileParser.in_file_lines, and amas.AMAS.FileParser.translate_ambiguous().

Here is the call graph for this function:


amas.AMAS.FileParser.nexus_interleaved_parse
amas.AMAS.FileParser.translate_ambiguous

7.5.3.3 nexus_parse()

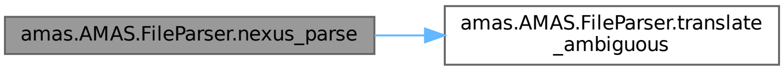
```
amas.AMAS.FileParser.nexus_parse (
                self )
```

Definition at line 645 of file AMAS.py.

```
00645     def nexus_parse(self):
00646         # use regex to parse names and sequences in sequential nexus files
00647         # find the matrix block
00648         matches = re.finditer(
00649             r"(\s+)?(MATRIX\n|matrix\n|MATRIX\r\n|matrix\r\n)(.*?;)",
00650             self.in_file_lines, re.DOTALL
00651         )
00652 
00653         records = {}
00654         # get names and sequences from the matrix block
00655 
00656         for match in matches:
00657             matrix_match = match.group(3)
00658             seq_matches = re.finditer(
00659                 r"^(\s+)?['']?(\S+\s\S+|\S+)['']?\s+([A-Za-z*?.{}-]+)($|\s+\[[0-9]+\]$)",
00660                 matrix_match, re.MULTILINE
00661             )
00662 
00663             for match in seq_matches:
00664                 name_match = match.group(2).replace("\n", "")
00665                 seq_match = match.group(3).replace("\n", "").upper()
00666                 seq_match = self.translate_ambiguous(seq_match)
00667                 records[name_match] = seq_match
00668 
00669         return records
00670 
```

References amas.AMAS.FileParser.in_file_lines, and amas.AMAS.FileParser.translate_ambiguous().

Here is the call graph for this function:


amas.AMAS.FileParser.nexus_parse
amas.AMAS.FileParser.translate _ambiguous

7.5.3.4 partitions_parse()

```
amas.AMAS.FileParser.partitions_parse (
                self )
```

Definition at line 731 of file AMAS.py.

```
00731     def partitions_parse(self):
00732         # parse partitions file using regex
00733         # original: `matches = re.finditer(r"^(\s+)?([^ =]+)[ =]+([\\0-9, -]+)", self.in_file_lines,
      re.MULTILINE)`
00734         # new version: more permissive -> handles PartionFinder/RAxML/(IQ-TREE 2)best_scheme.nex
      format partition files
00735         matches = re.finditer(
00736             r"""^[ \t]*                                # start line w/ 0+ whitespaces/tabs
00737                 (
00738                  (?P<nexus>charset[ ]+)                # <1>: best_scheme.nex partition directive
00739                  |
00740                  (?P<raxml>[A-Za-z0-9_+.\{\}\/-]+,[ \t]+)   # <2>: RAxML(-NG) model(+pars)
00741                 )?
00742                 (?P<partition_name>[A-Za-z0-9_&.-]+)       # partition name
00743                 [ ]*=[ ]*                              # whitespace-(un)padded '='
00744                 (?P<numbers>[\\0-9, -]+)               # position ranges w/stride (multiple
      intervals)
00745                 (?P<nexus_term>[ ]*[;])?               # whitespace-(un)prepended ';' (nexus
      terminator)
00746             """,
00747             self.in_file_lines,
00748             re.MULTILINE | re.VERBOSE
00749         )
00750 
00751         # initiate list to store dictionaries with lists
00752         # of slice positions as values
00753         partitions = []
00754         add_to_partitions = partitions.append
00755 
00756         for match in matches:
00757             # initiate dictionary of partition name as key
00758             dict_of_dicts = {}
00759             # and list of dictionaries with slice positions
00760             list_of_dicts = []
00761             add_to_list_of_dicts = list_of_dicts.append
00762             # get parition name and numbers from parsed partition strings
00763             partition_name = match.group('partition_name')
00764             numbers = match.group('numbers')
00765             # remove any whitespace padding '-' (to be consistent with partition-writing format)
00766             numbers = re.sub(r"[ ]*-[ ]*", "-", numbers)
00767             # find all numbers that will be used to parse positions
00768             positions = re.findall(r"([^ ,]+)", numbers)
00769 
00770             for position in positions:
00771                 # create dictionary for slicing input sequence
00772                 # conditioning on whether positions are represented
00773                 # by range, range with stride, or single number
00774                 pos_dict = {}
00775 
00776                 if "-" in position:
00777                     m = re.search(r"([0-9]+)-([0-9]+)", position)
00778                     pos_dict["start"] = int(m.group(1)) - 1
00779                     pos_dict["stop"] = int(m.group(2))
00780                 else:
00781                     pos_dict["start"] = int(position) - 1
00782                     pos_dict["stop"] = int(position)
00783 
00784                 if "\\" in position:
```

```
                    # Note: the value of `N' in `...\N' isn't read: the script simply assumes `N' is
consistent with the number of
                    # increments per interval when the alignment is parsed with a stride of 3
(designating each cpos).
                    # E.g. For the partition file:
                    #       ...'1-N\2'
                    #       ...'2-N\2'
                    #       ...'(N+1)-M\2'
                    #       ...'(N+2)-M\2'
                    # 3'cpos are ignored due to the absence of intervals `3-N...', `(N+3)-M...', not
because the associated stride values are'\2'
                    pos_dict["stride"] = 3
                elif "\\" not in position:
                    pos_dict["stride"] = 1

                add_to_list_of_dicts(pos_dict)

            dict_of_dicts[partition_name] = list_of_dicts
            add_to_partitions(dict_of_dicts)

        return partitions


```

References amas.AMAS.FileParser.in_file_lines.

7.5.3.5 phylip_interleaved_parse()

```
amas.AMAS.FileParser.phylip_interleaved_parse (
                self )
```

Definition at line 579 of file AMAS.py.

```
    def phylip_interleaved_parse(self):
```

7.5.3.6 phylip_parse()

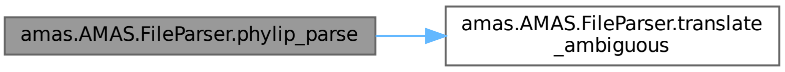
```
amas.AMAS.FileParser.phylip_parse (
                self )
```

Definition at line 562 of file AMAS.py.

```
    def phylip_parse(self):
        # use regex to parse names and sequences in sequential phylip files
        matches = re.finditer(
            r"^(\s+)?(\S+)\s+([A-Za-z*?.{}-]+)",
            self.in_file_lines, re.MULTILINE
        )

        records = {}

        for match in matches:
            name_match = match.group(2).replace("\n", "")
            seq_match = match.group(3).replace("\n", "").upper()
            seq_match = self.translate_ambiguous(seq_match)
            records[name_match] = seq_match

        return records

```

References amas.AMAS.FileParser.in_file_lines, and amas.AMAS.FileParser.translate_ambiguous().

Here is the call graph for this function:


amas.AMAS.FileParser.phylip_parse
amas.AMAS.FileParser.translate
_ambiguous

7.5.3.7 translate_ambiguous()

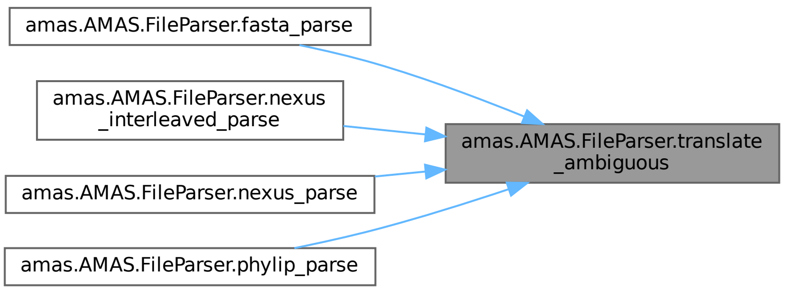
```
amas.AMAS.FileParser.translate_ambiguous (
                self,
                seq )
```

Definition at line 712 of file AMAS.py.

```
    def translate_ambiguous(self, seq):
        # translate ambiguous characters from curly bracket format
        # to single letter format
        # also remove spaces from sequences
        seq = seq.replace("{GT}", "K")
        seq = seq.replace("{AC}", "M")
        seq = seq.replace("{AG}", "R")
        seq = seq.replace("{CT}", "Y")
        seq = seq.replace("{CG}", "S")
        seq = seq.replace("{AT}", "W")
        seq = seq.replace("{CGT}", "B")
        seq = seq.replace("{ACG}", "V")
        seq = seq.replace("{ACT}", "H")
        seq = seq.replace("{AGT}", "D")
        seq = seq.replace("{GATC}", "N")
        seq = seq.replace(" ", "")

        return seq

```

Referenced by amas.AMAS.FileParser.fasta_parse(), amas.AMAS.FileParser.nexus_interleaved_parse(), amas.AMAS.FileParser.nexus_parse(), and amas.AMAS.FileParser.phylip_parse().

Here is the caller graph for this function:


amas.AMAS.FileParser.fasta_parse
amas.AMAS.FileParser.nexus _interleaved_parse
amas.AMAS.FileParser.nexus_parse
amas.AMAS.FileParser.phylip_parse
amas.AMAS.FileParser.translate _ambiguous

7.5.4 Member Data Documentation

7.5.4.1 chars_match

```
amas.AMAS.FileParser.chars_match = match.group(3)  [static]
```

Definition at line 596 of file AMAS.py.

7.5.4.2 counter

```
int amas.AMAS.FileParser.counter = 0  [static]
```

Definition at line 605 of file AMAS.py.

7.5.4.3 in_file

```
amas.AMAS.FileParser.in_file
```

Definition at line 542 of file AMAS.py.

Referenced by amas.AMAS.FileHandler.__exit__(), amas.AMAS.Alignment.get_aln_input(), and amas.AMAS.Alignment.get_name().

7.5.4.4 in_file_lines

```
amas.AMAS.FileParser.in_file_lines
```

Definition at line 544 of file AMAS.py.

Referenced by amas.AMAS.FileParser.fasta_parse(), amas.AMAS.FileParser.nexus_interleaved_parse(), amas.AMAS.FileParser.nexus_parse(), amas.AMAS.FileParser.partitions_parse(), and amas.AMAS.FileParser.phylip_parse().

7.5.4.5 matches

```
amas.AMAS.FileParser.matches  [static]
```

Initial value:

```
=  re.finditer(
                    r"(^(\s+)?(\S+)( ){2,}|^\s+)([ A-Za-z*?.{}-]+)",
                    self.in_file_lines, re.MULTILINE
               )
```

Definition at line 619 of file AMAS.py.

7.5.4.6 name_match

```
amas.AMAS.FileParser.name_match = match.group(2).replace("\n", "")  [static]
```

Definition at line 608 of file AMAS.py.

7.5.4.7 name_matches

```
amas.AMAS.FileParser.name_matches  [static]
```

Initial value:

```
=  re.finditer(
               r"^(\s+)?(\S+)[ \t]+[A-Za-z*?.{}-]+",
               self.in_file_lines, re.MULTILINE
          )
```

Definition at line 585 of file AMAS.py.

7.5.4.8 records

```
dict amas.AMAS.FileParser.records = {}  [static]
```

Definition at line 602 of file AMAS.py.

7.5.4.9 seq_match [1/2]

```
amas.AMAS.FileParser.seq_match = match.group(3).replace("\n", "").upper()  [static]
```

Definition at line 612 of file AMAS.py.

7.5.4.10 seq_match [2/2]

```
str amas.AMAS.FileParser.seq_match = "".join(seq_match.split())  [static]
```

Definition at line 631 of file AMAS.py.

7.5.4.11 seq_matches

```
amas.AMAS.FileParser.seq_matches  [static]
```

Initial value:

```
=  re.finditer(
            r"(^(\s+)?\S+[ \t]+|^)([A-Za-z*?.{}-]+)$",
            self.in_file_lines, re.MULTILINE
        )
```

Definition at line 589 of file AMAS.py.

7.5.4.12 sequence

```
str amas.AMAS.FileParser.sequence = ""  [static]
```

Definition at line 636 of file AMAS.py.

7.5.4.13 sequences

```
list amas.AMAS.FileParser.sequences = []  [static]
```

Definition at line 600 of file AMAS.py.

7.5.4.14 tax_chars_matches

```
amas.AMAS.FileParser.tax_chars_matches  [static]
```

Initial value:

```
=  re.finditer(
            r"^(\s+)?([0-9]+)[ \t]+([0-9]+)",
            self.in_file_lines, re.MULTILINE
        )
```

Definition at line 581 of file AMAS.py.

7.5.4.15 tax_match

```
amas.AMAS.FileParser.tax_match = match.group(2)  [static]
```

Definition at line 595 of file AMAS.py.

7.5.4.16 taxa

```
list amas.AMAS.FileParser.taxa = [ ]  [static]
```

Definition at line 599 of file AMAS.py.

The documentation for this class was generated from the following file:

- amas/AMAS.py

7.6 amas.AMAS.MetaAlignment Class Reference

Public Member Functions

- __init__ (self, **kwargs)
- translate_dna_to_aa (self, seq, translation_table, frame)
- translate_dict (self, source_dict)
- get_translated (self, translation_table, reading_frame)
- trim_dict (self, alignment)
- get_trimmed (self, trim_fraction, parsimony_check)
- remove_unknown_chars (self, seq)
- remove_empty_sequences (self, split_alignment)
- get_partitions (self, partitions_file)
- get_alignment_object (self, alignment)
- get_alignment_objects (self)
- get_parsed_alignments (self)
- get_partitioned (self, partitions_file)
- get_summaries (self)
- summarize_alignments (self, alignment)
- get_taxon_summaries (self)
- summarize_alignments_taxa (self, alignment)
- write_summaries (self, file_name)
- write_taxa_summaries (self)
- get_replicate (self, no_replicates, no_loci)
- get_concatenated (self, alignments)
- remove_from_alignment (self, alignment, species_to_remove_set, index)
- remove_taxa (self, species_to_remove_set)
- print_fasta (self, source_dict)
- print_phylip (self, source_dict)
- print_phylip_int (self, source_dict)
- print_nexus (self, source_dict)
- print_nexus_int (self, source_dict)
- natural_sort (self, a_list)
- print_unspecified_partitions (self, data_type, codons)
- print_nexus_partitions (self, data_type, codons)

- print_iqtree_nexus_partitions (self, data_type, codons)
- print_raxml_partitions (self, data_type, codons)
- replace_string_in_file (self, file_name, old_string, new_string)
- write_partitions (self, file_name, part_format, data_type, codons)
- get_extension (self, file_format)
- get_metapartition_extension (self, file_format)
- file_overwrite_error (self, file_name)
- write_formatted_file (self, file_format, file_name, alignment)
- get_alignment_name (self, i, extension)
- get_alignment_name_no_ext (self, i)
- write_concat (self, file_format)
- write_convert (self, index, alignment, file_format, extension)
- write_replicate (self, index, alignment, file_format, extension)
- write_split (self, item, file_format, extension)
- write_reduced (self, file_format, extension)
- write_translated (self, index, alignment, file_format, extension)
- write_trimmed (self, index, alignment, file_format, extension)
- write_metapartitions (self, file_format)
- write_out (self, action, file_format)

Public Attributes

- in_files
- in_format
- data_type
- command
- concat_out
- using_metapartitions
- check_align
- cores
- by_taxon_summary
- no_sup_aln_name
- no_mpan
- codons
- no_replicates
- no_loci
- split
- remove_empty
- prepend_label
- species_to_remove
- species_to_remove_set
- reduced_file_prefix
- check_taxa
- reading_frame
- genetic_code
- trim_fraction
- trim_out
- parsimony_check
- alignment_objects
- parsed_alignments
- codes_list
- gencode_NCBI_1
- gencode_NCBI_2
- gencode_NCBI_3

- gencode_NCBI_4
- gencode_NCBI_5
- gencode_NCBI_6
- gencode_NCBI_9
- gencode_NCBI_10
- gencode_NCBI_11
- gencode_NCBI_12
- gencode_NCBI_13
- gencode_NCBI_14
- gencode_NCBI_16
- gencode_NCBI_21
- gencode_NCBI_22
- gencode_NCBI_23
- gencode_NCBI_24
- gencode_NCBI_25
- gencode_NCBI_26
- codes

7.6.1 Detailed Description

```
Class of multiple sequence alignments
```

Definition at line 1165 of file AMAS.py.

7.6.2 Constructor & Destructor Documentation

7.6.2.1 __init__()

```
amas.AMAS.MetaAlignment.__init__ (
                self,
              ** kwargs )
```

Definition at line 1168 of file AMAS.py.

```
    def __init__(self, **kwargs):
        # set defaults and get values from kwargs
        self.in_files = kwargs.get("in_files")
        self.in_format = kwargs.get("in_format")
        self.data_type = kwargs.get("data_type")
        self.command = kwargs.get("command")
        self.concat_out = kwargs.get("concat_out", "concatenated.out")
        self.using_metapartitions = False
        self.check_align = kwargs.get("check_align", False)
        self.cores = kwargs.get("cores")
        self.by_taxon_summary = kwargs.get("by_taxon_summary")
        self.no_sup_aln_name = False
        self.no_mpan = False

        if self.command == "concat":
            self.codons = kwargs.get("codons", "none")
            if self.data_type == "aa" and self.codons != "none":
                print("ERROR: when option -d|--data-type is set to 'aa', option -n|--codons must be
      set to 'none'.")
                sys.exit(1)

        if self.command == "replicate":
            self.no_replicates = kwargs.get("replicate_args")[0]
            self.no_loci = kwargs.get("replicate_args")[1]

        if self.command == "split":
            self.split = kwargs.get("split_by")
            self.remove_empty = kwargs.get("remove_empty", False)
            self.no_sup_aln_name = kwargs.get("no_sup_aln_name", False)

        if self.command == "metapartitions":
            self.using_metapartitions = True
            self.split = kwargs.get("split_by")
            self.remove_empty = kwargs.get("remove_empty", False)
            self.no_sup_aln_name = kwargs.get("no_sup_aln_name", False)
            self.no_mpan = kwargs.get("no_mpan", False)
            self.prepend_label = kwargs.get("prepend_label")
            if self.prepend_label is not None and isinstance(self.prepend_label, str):
                self.prepend_label = self.prepend_label + "_"
            else:
                self.prepend_label = ""

        if self.command == "remove":
            self.species_to_remove = kwargs.get("taxa_to_remove")
            self.species_to_remove_set = set(self.species_to_remove)
            self.reduced_file_prefix = kwargs.get("out_prefix")
            self.check_taxa = kwargs.get("check_taxa", False)

        if self.command == "translate":
            self.reading_frame = kwargs.get("reading_frame")
            self.genetic_code = kwargs.get("genetic_code")

        if self.command == "trim":
            self.trim_fraction = kwargs.get("trim_fraction")
            self.trim_out = kwargs.get("trim_out")
            self.parsimony_check = kwargs.get("parsimony_check", False)

        self.alignment_objects = self.get_alignment_objects()
        self.parsed_alignments = self.get_parsed_alignments()

        # The code list:
        self.codes_list = """
         1. The Standard Code
         2. The Vertebrate Mitochondrial Code
         3. The Yeast Mitochondrial Code
         4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma
      Code
         5. The Invertebrate Mitochondrial Code
         6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
         9. The Echinoderm and Flatworm Mitochondrial Code
        10. The Euplotid Nuclear Code
        11. The Bacterial, Archaeal and Plant Plastid Code
        12. The Alternative Yeast Nuclear Code
        13. The Ascidian Mitochondrial Code
        14. The Alternative Flatworm Mitochondrial Code
        16. Chlorophycean Mitochondrial Code
        21. Trematode Mitochondrial Code
        22. Scenedesmus obliquus Mitochondrial Code
        23. Thraustochytrium Mitochondrial Code
        24. Pterobranchia Mitochondrial Code
        25. Candidate Division SR1 and Gracilibacteria Code
        26. Pachysolen tannophilus Nuclear Code
        """

        # 1: The Standard Code
        self.gencode_NCBI_1 = {
        "TTT" : "F", # Phe
        "TCT" : "S", # Ser
        "TAT" : "Y", # Tyr
        "TGT" : "C", # Cys
        "TTC" : "F", # Phe
        "TCC" : "S", # Ser
        "TAC" : "Y", # Tyr
        "TGC" : "C", # Cys
        "TTA" : "L", # Leu
        "TCA" : "S", # Ser
        "TAA" : "*", # Ter
        "TGA" : "*", # Ter
        "TTG" : "L", # Leu i
        "TCG" : "S", # Ser
        "TAG" : "*", # Ter
        "TGG" : "W", # Trp
        "CTT" : "L", # Leu
        "CCT" : "P", # Pro
        "CAT" : "H", # His
        "CGT" : "R", # Arg
        "CTC" : "L", # Leu
        "CCC" : "P", # Pro
        "CAC" : "H", # His
        "CGC" : "R", # Arg
        "CTA" : "L", # Leu
        "CCA" : "P", # Pro
        "CAA" : "Q", # Gln
        "CGA" : "R", # Arg
        "CTG" : "L", # Leu i
        "CCG" : "P", # Pro
        "CAG" : "Q", # Gln
        "CGG" : "R", # Arg
        "ATT" : "I", # Ile
        "ACT" : "T", # Thr
        "AAT" : "N", # Asn
        "AGT" : "S", # Ser
        "ATC" : "I", # Ile
        "ACC" : "T", # Thr
        "AAC" : "N", # Asn
        "AGC" : "S", # Ser
        "ATA" : "I", # Ile
        "ACA" : "T", # Thr
        "AAA" : "K", # Lys
        "AGA" : "R", # Arg
        "ATG" : "M", # Met i
        "ACG" : "T", # Thr
        "AAG" : "K", # Lys
        "AGG" : "R", # Arg
        "GTT" : "V", # Val
        "GCT" : "A", # Ala
        "GAT" : "D", # Asp
        "GGT" : "G", # Gly
        "GTC" : "V", # Val
        "GCC" : "A", # Ala
        "GAC" : "D", # Asp
        "GGC" : "G", # Gly
        "GTA" : "V", # Val
        "GCA" : "A", # Ala
        "GAA" : "E", # Glu
        "GGA" : "G", # Gly
        "GTG" : "V", # Val
        "GCG" : "A", # Ala
        "GAG" : "E", # Glu
        "GGG" : "G", # Gly
        "---" : "-", # Gap
        "???" : "?", # Unk
        "NNN" : "X", # Unk
        }

        # 2: The Vertebrate Mitochondrial Code
        self.gencode_NCBI_2 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_2["AGA"] = "*" # Ter
        self.gencode_NCBI_2["AGG"] = "*" # Ter
        self.gencode_NCBI_2["ATA"] = "M" # Met
        self.gencode_NCBI_2["TGA"] = "W" # Trp

        # 3: The Yeast Mitochondrial Code
        self.gencode_NCBI_3 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_3["ATA"] = "M" # Met
        self.gencode_NCBI_3["CTT"] = "T" # Thr
        self.gencode_NCBI_3["CTC"] = "T" # Thr
        self.gencode_NCBI_3["CTA"] = "T" # Thr
        self.gencode_NCBI_3["CTG"] = "T" # Thr
        self.gencode_NCBI_3["TGA"] = "W" # Trp

        del self.gencode_NCBI_3["CGA"]
        del self.gencode_NCBI_3["CGC"]

        # 4: The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma
 Code
        self.gencode_NCBI_4 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_4["TGA"] = "W" # Trp

        # 5: The Invertebrate Mitochondrial Code
        self.gencode_NCBI_5 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_5["AGA"] = "S" # Ser
        self.gencode_NCBI_5["AGG"] = "S" # Ser
        self.gencode_NCBI_5["ATA"] = "M" # Met
        self.gencode_NCBI_5["TGA"] = "W" # Trp

        # 6: The Ciliate, Dasycladacean and Hexamita Nuclear Code
        self.gencode_NCBI_6 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_6["TAA"] = "Q" # Gln
        self.gencode_NCBI_6["TAG"] = "Q" # Gln

        # 9: The Echinoderm and Flatworm Mitochondrial Code
        self.gencode_NCBI_9 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_9["AAA"] = "N" # Asn
        self.gencode_NCBI_9["AGA"] = "S" # Ser
        self.gencode_NCBI_9["AGG"] = "S" # Ser
        self.gencode_NCBI_9["TGA"] = "W" # Trp

        # 10: The Euplotid Nuclear Code
        self.gencode_NCBI_10 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_10["TGA"] = "C" # Cys

        # 11: The Bacterial, Archaeal and Plant Plastid Code
        self.gencode_NCBI_11 = self.gencode_NCBI_1.copy()

        # 12: The Alternative Yeast Nuclear Code
        self.gencode_NCBI_12 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_12["CTG"] = "S" # Ser

        # 13: The Ascidian Mitochondrial Code
        self.gencode_NCBI_13 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_13["AGA"] = "G" # Gly
        self.gencode_NCBI_13["AGG"] = "G" # Gly
        self.gencode_NCBI_13["ATA"] = "M" # Met
        self.gencode_NCBI_13["TGA"] = "W" # Trp

        # 14: The Alternative Flatworm Mitochondrial Code
        self.gencode_NCBI_14 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_14["AAA"] = "N" # Asn
        self.gencode_NCBI_14["AGA"] = "S" # Ser
        self.gencode_NCBI_14["AGG"] = "S" # Ser
        self.gencode_NCBI_14["TAA"] = "Y" # Tyr
        self.gencode_NCBI_14["TGA"] = "W" # Trp

        # 16: Chlorophycean Mitochondrial Code
        self.gencode_NCBI_16 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_16["TAG"] = "L" # Leu

        # 21: Trematode Mitochondrial Code
        self.gencode_NCBI_21 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_21["TGA"] = "W" # Trp
        self.gencode_NCBI_21["ATA"] = "M" # Met
        self.gencode_NCBI_21["AGA"] = "S" # Ser
        self.gencode_NCBI_21["AGG"] = "S" # Ser
        self.gencode_NCBI_21["AAA"] = "N" # Asn

        # 22: Scenedesmus obliquus Mitochondrial Code
        self.gencode_NCBI_22 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_22["TCA"] = "*" # Ter
        self.gencode_NCBI_22["TAG"] = "L" # Leu

        # 23: Thraustochytrium Mitochondrial Code
        self.gencode_NCBI_23 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_23["TTA"] = "*" # Ter

        # 24: Pterobranchia Mitochondrial Code
        self.gencode_NCBI_24 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_24["AGA"] = "S" # Ser
        self.gencode_NCBI_24["AGG"] = "K" # Lys
        self.gencode_NCBI_24["TGA"] = "W" # Trp

        # 25: Candidate Division SR1 and Gracilibacteria Code
        self.gencode_NCBI_25 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_25["TGA"] = "G" # Gly

        # 26: Pachysolen tannophilus Nuclear Code
        self.gencode_NCBI_26 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_26["CTG"] = "A" # Ala

        self.codes = {
        1 : self.gencode_NCBI_1,
        2 : self.gencode_NCBI_2,
        3 : self.gencode_NCBI_3,
        4 : self.gencode_NCBI_4,
        5 : self.gencode_NCBI_5,
        6 : self.gencode_NCBI_6,
        9 : self.gencode_NCBI_9,
        10 : self.gencode_NCBI_10,
        11 : self.gencode_NCBI_11,
        12 : self.gencode_NCBI_12,
        13 : self.gencode_NCBI_13,
        14 : self.gencode_NCBI_14,
        16 : self.gencode_NCBI_16,
        21 : self.gencode_NCBI_21,
        22 : self.gencode_NCBI_22,
        23 : self.gencode_NCBI_23,
        24 : self.gencode_NCBI_24,
        25 : self.gencode_NCBI_25,
        26 : self.gencode_NCBI_26
        }

```

7.6.3 Member Function Documentation

7.6.3.1 file_overwrite_error()

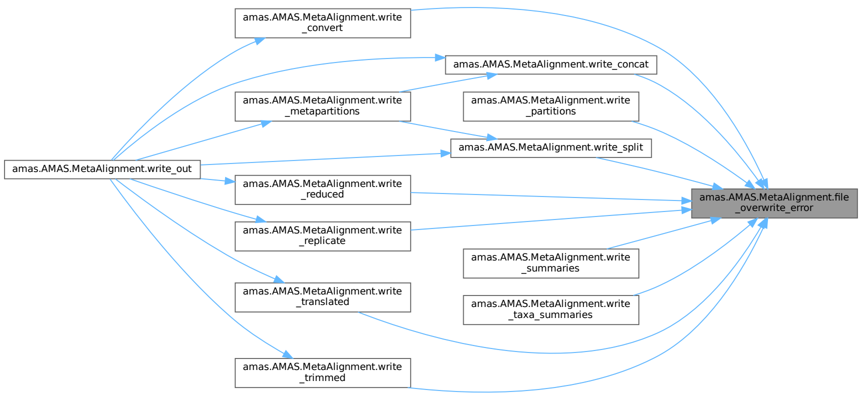
```
amas.AMAS.MetaAlignment.file_overwrite_error (
              self,
              file_name )
```

Definition at line 2159 of file AMAS.py.

```
02159     def file_overwrite_error(self, file_name):
02160         # print warning when overwriting a file
02161         if path.exists(file_name):
02162             print("WARNING: You are overwriting '" + file_name + "'")
02163
```

Referenced by amas.AMAS.MetaAlignment.write_concat(), amas.AMAS.MetaAlignment.write_convert(), amas.AMAS.MetaAlignment.write_partitions(), amas.AMAS.MetaAlignment.write_reduced(), amas.AMAS.MetaAlignment.write_replicate(), amas.AMAS.MetaAlignment.write_split(), amas.AMAS.MetaAlignment.write_summaries(), amas.AMAS.MetaAlignment.write_taxa_summaries(), amas.AMAS.MetaAlignment.write_translated(), and amas.AMAS.MetaAlignment.write_trimmed().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.write_summaries
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_taxa_summaries
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.file_overwrite_error

7.6.3.2 get_alignment_name()

```
amas.AMAS.MetaAlignment.get_alignment_name (
              self,
              i,
              extension )
```

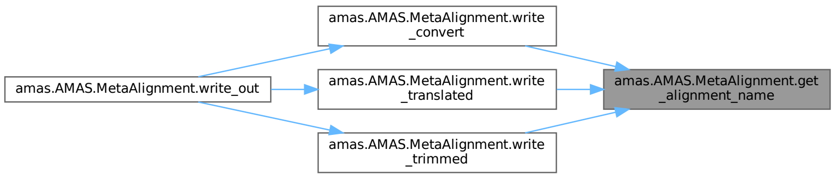
Definition at line 2178 of file AMAS.py.

```
02178     def get_alignment_name(self, i, extension):
02179         # get file name
02180         file_name = self.alignment_objects[i].get_name() + extension
02181
02182         return file_name
02183
```

References amas.AMAS.MetaAlignment.alignment_objects.

Referenced by amas.AMAS.MetaAlignment.write_convert(), amas.AMAS.MetaAlignment.write_translated(), and amas.AMAS.MetaAlignment.write_trimmed().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.get_alignment_name

7.6.3.3 get_alignment_name_no_ext()

```
amas.AMAS.MetaAlignment.get_alignment_name_no_ext (
                self,
                i )
```

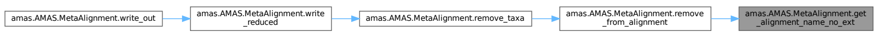
Definition at line 2184 of file AMAS.py.

```
02184     def get_alignment_name_no_ext(self, i):
02185         # get file name without extension
02186         file_name = self.alignment_objects[i].get_name()
02187 
02188         return file_name
02189 
```

References amas.AMAS.MetaAlignment.alignment_objects.

Referenced by amas.AMAS.MetaAlignment.remove_from_alignment().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.remove_taxa
amas.AMAS.MetaAlignment.remove_from_alignment
amas.AMAS.MetaAlignment.get_alignment_name_no_ext

7.6.3.4 get_alignment_object()

```
amas.AMAS.MetaAlignment.get_alignment_object (
                self,
                alignment )
```

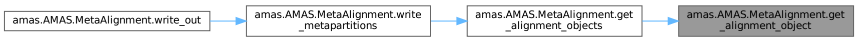
Definition at line 1523 of file AMAS.py.

```
01523     def get_alignment_object(self, alignment):
01524         # parse according to the given alphabet;
01525         # Note:(‘alignment‘) <=> `in_file‘ outside MetaAlignment, e.g.
01526         #
      AminoAcidAlignment(Alignment<-.get_parsed_aln<-.get_aln_input)<-FileParser.__init__(in_file)<-FileHandler(...open(self.
01527         if self.data_type == "aa":
01528             aln = AminoAcidAlignment(alignment, self.in_format, self.data_type)
01529         elif self.data_type == "dna":
01530             aln = DNAAlignment(alignment, self.in_format, self.data_type)
01531         return aln
01532 
```

References amas.AMAS.Alignment.data_type, amas.AMAS.MetaAlignment.data_type, amas.AMAS.Alignment.in_format, and amas.AMAS.MetaAlignment.in_format.

Referenced by amas.AMAS.MetaAlignment.get_alignment_objects().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_alignment_objects
amas.AMAS.MetaAlignment.get_alignment_object

7.6.3.5 get_alignment_objects()

```
amas.AMAS.MetaAlignment.get_alignment_objects (
                self )
```

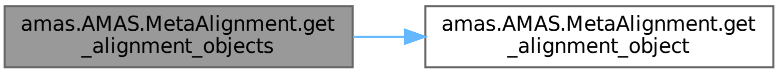
Definition at line 1533 of file AMAS.py.

```
    def get_alignment_objects(self):
        # get alignment objects on which statistics can be computed
        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            alignments = [self.get_alignment_object(alignment) for alignment in self.in_files]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            alignments = pool.map(self.get_alignment_object, self.in_files)
        return alignments

```

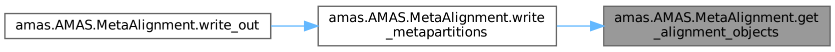
References amas.AMAS.MetaAlignment.cores, amas.AMAS.MetaAlignment.get_alignment_object(), and amas.AMAS.MetaAlignment.in_files.

Referenced by amas.AMAS.MetaAlignment.write_metapartitions().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_alignment_objects
amas.AMAS.MetaAlignment.get_alignment_object

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_alignment_objects

7.6.3.6 get_concatenated()

```
amas.AMAS.MetaAlignment.get_concatenated (
                self,
                alignments )
```

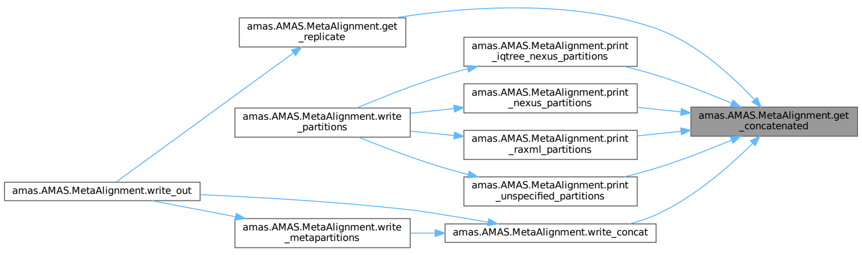
Definition at line 1746 of file AMAS.py.

```
    def get_concatenated(self, alignments):
        # concatenate muntiple input alignments
        # create empty dictionary of lists
        concatenated = defaultdict(list)

        # first create list of taxa in all alignments
        # you need this to insert empty seqs in
        # the concatenated alignment
        all_taxa = []
        for alignment in alignments:
            for taxon in alignment.keys():
                if taxon not in all_taxa:
                    all_taxa.append(taxon)

        # start counters to keep track of partitions
        partition_counter = 1
        position_counter = 1
        # get dict for alignment name and partition
        partitions = {}
        digits_to_pad = len(str(len(alignments)))

        for alignment in alignments:
            # get alignment length from a random taxon
            partition_length = len(alignment[list(alignment.keys())[0]])
            # get base name of each alignment for use when writing partitions file
            # NOTE: the base name here is whatever comes before fist period in the file name
            alignment_name = self.alignment_objects[partition_counter - 1].get_name().split('.')[0]

            if self.using_metapartitions:
                #  Implementation of `--no-mpan`, i.e. 'no metapartition alignment name'.
                #  `prepend_label` either assigned to `<str>_` via option `--prepend <str>`
                #  or empty ("") -> see def MetaAlignment.__init__()
                if self.no_mpan:
                    # omit original alignment names from the printed partition file
                    partition_name = self.prepend_label + "p" +
      str(partition_counter).zfill(digits_to_pad)
                else:
                    # keep original alignment names in the printed partition file
                    partition_name = self.prepend_label + "p" +
      str(partition_counter).zfill(digits_to_pad) + "_" + alignment_name
            else:
                partition_name = "p" + str(partition_counter) + "_" + alignment_name

            start = position_counter
            position_counter += partition_length
            end = position_counter - 1
            partitions[partition_name] = str(start) + "-" + str(end)
            partition_counter += 1

            # get empty sequence if there is missing taxon
            # getting length from first element of list of keys
            # created from the original dict for this alignment
            empty_seq = '?' * partition_length

            for taxon in all_taxa:

                if taxon not in alignment.keys():
                    concatenated[taxon].append(empty_seq)
                else:
                    concatenated[taxon].append(alignment[taxon])

        concatenated = {taxon:''.join(seqs) for taxon, seqs in concatenated.items()}

        return concatenated, partitions

```

References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.MetaAlignment.no_mpan, amas.AMAS.MetaAlignment.prepend_label, amas.AMAS.MetaAlignment.split, and amas.AMAS.MetaAlignment.using_metapartitions.

Referenced by amas.AMAS.MetaAlignment.get_replicate(), amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions(), amas.AMAS.MetaAlignment.print_nexus_partitions(), amas.AMAS.MetaAlignment.print_raxml_partitions(), amas.AMAS.MetaAlignment.print_unspecified_partitions(), and amas.AMAS.MetaAlignment.write_concat().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.get_replicate
amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions
amas.AMAS.MetaAlignment.print_nexus_partitions
amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.print_raxml_partitions
amas.AMAS.MetaAlignment.print_unspecified_partitions
amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_concat

7.6.3.7 get_extension()

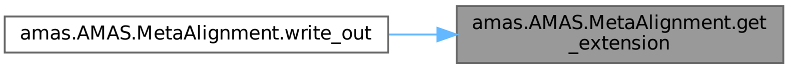
```
amas.AMAS.MetaAlignment.get_extension (
                self,
                file_format )
```

Definition at line 2129 of file AMAS.py.

```
    def get_extension(self, file_format):
        # get proper extension string
        if file_format == "phylip":
            extension = "-out.phy"
        elif file_format == "phylip-int":
            extension = "-out.int-phy"
        elif file_format == "fasta":
            extension = "-out.fas"
        elif file_format == "nexus":
            extension = "-out.nex"
        elif file_format == "nexus-int":
            extension = "-out.int-nex"

        return extension

```

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_extension

7.6.3.8 get_metapartition_extension()

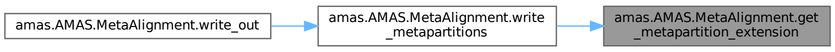
```
amas.AMAS.MetaAlignment.get_metapartition_extension (
                self,
                file_format )
```

Definition at line 2144 of file AMAS.py.

```
    def get_metapartition_extension(self, file_format):
        # get proper metapartition_extension string
        if file_format == "phylip":
            metapartition_extension = "-meta.phy"
        elif file_format == "phylip-int":
            metapartition_extension = "-meta.int-phy"
        elif file_format == "fasta":
            metapartition_extension = "-meta.fas"
        elif file_format == "nexus":
            metapartition_extension = "-meta.nex"
        elif file_format == "nexus-int":
            metapartition_extension = "-meta.int-nex"

        return metapartition_extension

```

Referenced by amas.AMAS.MetaAlignment.write_metapartitions().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_metapartition_extension

7.6.3.9 get_parsed_alignments()

amas.AMAS.MetaAlignment.get_parsed_alignments (
self)

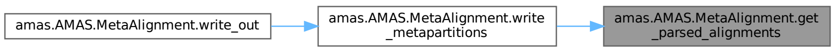
Definition at line 1543 of file AMAS.py.

```
    def get_parsed_alignments(self):
        # get parsed dictionaries with taxa and sequences
        parsed_alignments = []
        add_to_parsed_alignments = parsed_alignments.append
        for alignment in self.alignment_objects:
            parsed = alignment.parsed_aln
            add_to_parsed_alignments(parsed)
            # checking if every seq has the same length or if parsed is not empty; exit if false
            if self.check_align:
                equal = all(
                    x == [len(list(parsed.values())[i]) for i in
      range(0,len(list(parsed.values())))][0]
                    for x in [len(list(parsed.values())[i]) for i in
      range(0,len(list(parsed.values())))]
                )
                if equal is False:
                    print("ERROR: Sequences in input are of varying lengths. Be sure to align them
      first.")
                    sys.exit()

            if not parsed.keys() or not any(parsed.values()):
                print(
                    "ERROR: Parsed sequences of " + alignment.in_file + " are empty. "
                    "Are you sure you specified the right input format and/or that input is a valid
      alignment?"
                )
                sys.exit()

        return parsed_alignments

```

References amas.AMAS.MetaAlignment.alignment_objects, and amas.AMAS.MetaAlignment.check_align.

Referenced by amas.AMAS.MetaAlignment.write_metapartitions().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_parsed_alignments

7.6.3.10 get_partitioned()

```
amas.AMAS.MetaAlignment.get_partitioned (
                self,
                partitions_file )
```

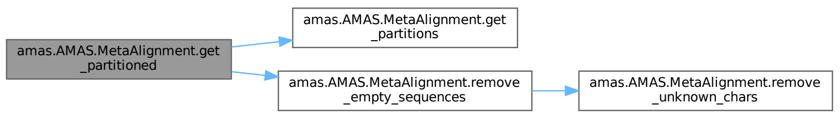
Definition at line 1569 of file AMAS.py.

```
01569     def get_partitioned(self, partitions_file):
01570         # partition alignment according to a partitions file
01571         partitions = self.get_partitions(partitions_file)
01572         alignment = self.parsed_alignments[0]
01573 
01574         # initiate list of newly partitioned alignments
01575         list_of_parts = []
01576         add_to_list_of_parts = list_of_parts.append
01577         for partition in partitions:
01578             # loop over all parsed partitions, adding taxa and sliced sequences
01579             for name, elements in partition.items():
01580                 new_dict = {}
01581 
01582                 for taxon, seq in alignment.items():
01583                     new_seq = ""
01584 
01585                     for dictionary in elements:
01586                         new_seq = new_seq +
      seq[dictionary["start"]:dictionary["stop"]:dictionary["stride"]]
01587                         new_dict[taxon] = new_seq
01588 
01589                 if self.remove_empty:
01590                     # check if remove empty sequences
01591                     no_empty_dict = self.remove_empty_sequences(new_dict)
01592                     add_to_list_of_parts({name : no_empty_dict})
01593                 else:
01594                     # add partition name : dict of taxa and sequences to the list
01595                     add_to_list_of_parts({name : new_dict})
01596 
01597         return list_of_parts
01598 
```

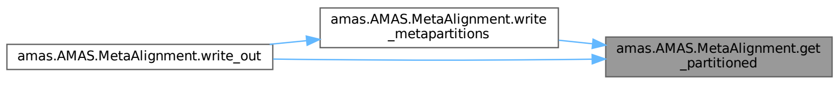
References amas.AMAS.MetaAlignment.get_partitions(), amas.AMAS.MetaAlignment.parsed_alignments, amas.AMAS.MetaAlignment.remove_empty, and amas.AMAS.MetaAlignment.remove_empty_sequences().

Referenced by amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_partitioned
amas.AMAS.MetaAlignment.get_partitions
amas.AMAS.MetaAlignment.remove_empty_sequences
amas.AMAS.MetaAlignment.remove_unknown_chars

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_partitioned

7.6.3.11 get_partitions()

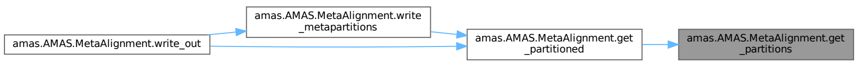
```
amas.AMAS.MetaAlignment.get_partitions (
                self,
                partitions_file )
```

Definition at line 1516 of file AMAS.py.

```
    def get_partitions(self, partitions_file):
        # parse and get partitions from partitions file
        partitions = FileParser(partitions_file)
        parsed_partitions = partitions.partitions_parse()

        return parsed_partitions

```

Referenced by amas.AMAS.MetaAlignment.get_partitioned().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_partitioned
amas.AMAS.MetaAlignment.get_partitions

7.6.3.12 get_replicate()

```
amas.AMAS.MetaAlignment.get_replicate (
                self,
                no_replicates,
                no_loci )
```

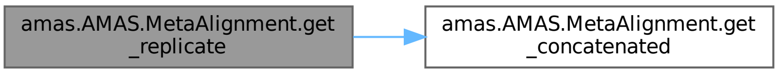
Definition at line 1726 of file AMAS.py.

```
    def get_replicate(self, no_replicates, no_loci):
        # construct replicate data sets for phylogenetic jackknife
        replicates = []
        add_to_replicates = replicates.append
        counter = 1
        for replicate in range(no_replicates):

            try:
                random_alignments = sample(self.parsed_alignments, no_loci)
            except ValueError:
                print("ERROR: You specified more loci per replicate than there are in your input.")
                sys.exit()

            random_alignments = sample(self.parsed_alignments, no_loci)
            concat_replicate = self.get_concatenated(random_alignments)[0]
            add_to_replicates(concat_replicate)
            counter += 1

        return replicates

```

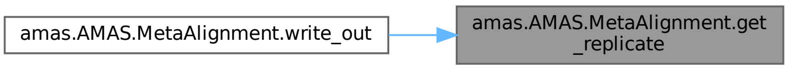
References amas.AMAS.MetaAlignment.get_concatenated(), and amas.AMAS.MetaAlignment.parsed_alignments.

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_replicate
amas.AMAS.MetaAlignment.get_concatenated

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get _replicate

7.6.3.13 get_summaries()

```
amas.AMAS.MetaAlignment.get_summaries (
                self )
```

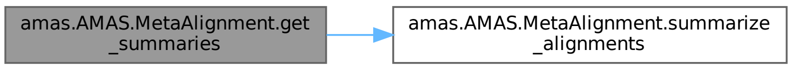
Definition at line 1599 of file AMAS.py.

```
    def get_summaries(self):
        # get summaries for all alignment objects

        # define different headers for aa and dna alignments
        aa_header = [
            "Alignment_name",
            "No_of_taxa",
            "Alignment_length",
            "Total_matrix_cells",
            "Undetermined_characters",
            "Missing_percent",
            "No_variable_sites",
            "Proportion_variable_sites",
            "Parsimony_informative_sites",
            "Proportion_parsimony_informative"
        ]

        dna_header = [
            "Alignment_name",
            "No_of_taxa",
            "Alignment_length",
            "Total_matrix_cells",
            "Undetermined_characters",
            "Missing_percent",
            "No_variable_sites",
            "Proportion_variable_sites",
            "Parsimony_informative_sites",
            "Proportion_parsimony_informative",
            "AT_content",
            "GC_content"
        ]

        alignments = self.alignment_objects
        parsed_alignments = self.parsed_alignments
        freq_header = [char for char in alignments[0].alphabet]

        if self.data_type == "aa":
            header = aa_header + freq_header
        elif self.data_type == "dna":
            header = dna_header + freq_header

        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            summaries = [alignment.get_summary() for alignment in alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            summaries = pool.map(self.summarize_alignments, alignments)
        return header, summaries

```

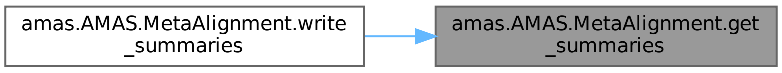
References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.MetaAlignment.cores, amas.AMAS.Alignment.data_type, amas.AMAS.MetaAlignment.data_type, amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.summarize_alignments().

Referenced by amas.AMAS.MetaAlignment.write_summaries().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_summaries
amas.AMAS.MetaAlignment.summarize_alignments

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_summaries
amas.AMAS.MetaAlignment.get_summaries

7.6.3.14 get_taxon_summaries()

```
amas.AMAS.MetaAlignment.get_taxon_summaries (
                self )
```

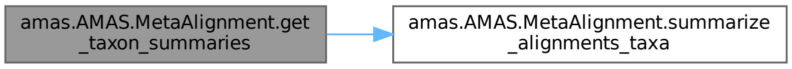
Definition at line 1653 of file AMAS.py.

```
    def get_taxon_summaries(self):
        # get per-sequence summaries for all alignment objects

        # define different headers for aa and dna alignments
        aa_header = [
            "Alignment_name",
            "Taxon_name",
            "Sequence_length",
            "Undetermined_characters",
            "Missing_percent"
        ]

        dna_header = [
            "Alignment_name",
            "Taxon_name",
            "Sequence_length",
            "Undetermined_characters",
            "Missing_percent",
            "AT_content",
            "GC_content"
        ]

        alignments = self.alignment_objects
        parsed_alignments = self.parsed_alignments
        freq_header = alignments[0].alphabet

        if self.data_type == "aa":
            header = aa_header + freq_header
        elif self.data_type == "dna":
            header = dna_header + freq_header

        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            summaries = [alignment.get_taxa_summary() for alignment in alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            summaries = pool.map(self.summarize_alignments_taxa, alignments)

        return header, summaries
```

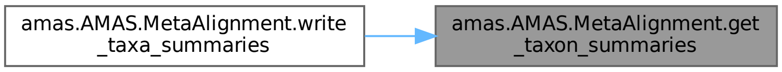
References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.MetaAlignment.cores, amas.AMAS.Alignment.data_type, amas.AMAS.MetaAlignment.data_type, amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.summarize_alignments_taxa().

Referenced by amas.AMAS.MetaAlignment.write_taxa_summaries().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_taxon_summaries
amas.AMAS.MetaAlignment.summarize_alignments_taxa

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_taxa_summaries
amas.AMAS.MetaAlignment.get_taxon_summaries

7.6.3.15 get_translated()

```
amas.AMAS.MetaAlignment.get_translated (
              self,
              translation_table,
              reading_frame )
```

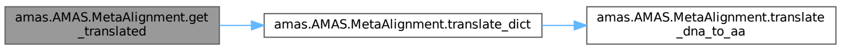
Definition at line 1478 of file AMAS.py.

```
    def get_translated(self, translation_table, reading_frame):
        if int(self.cores) == 1:
            translated_alignments = [self.translate_dict(alignment) for alignment in
      self.parsed_alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            translated_alignments = pool.map(self.translate_dict, self.parsed_alignments)

        return translated_alignments

```

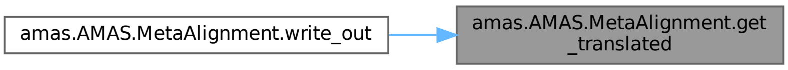
References amas.AMAS.MetaAlignment.cores, amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.translate_dict().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_translated
amas.AMAS.MetaAlignment.translate_dict
amas.AMAS.MetaAlignment.translate_dna_to_aa

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_translated

7.6.3.16 get_trimmed()

```
amas.AMAS.MetaAlignment.get_trimmed (
                self,
                trim_fraction,
                parsimony_check )
```

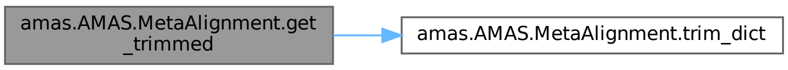
Definition at line 1495 of file AMAS.py.

```
    def get_trimmed(self, trim_fraction, parsimony_check):
        if int(self.cores) == 1:
            trimmed_alignments = [self.trim_dict(alignment) for alignment in self.alignment_objects]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            trimmed_alignments = pool.map(self.trim_dict, self.alignment_objects)

        return trimmed_alignments

```

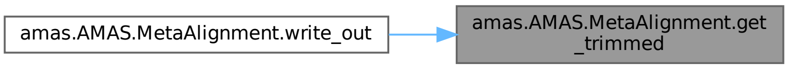
References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.MetaAlignment.cores, and amas.AMAS.MetaAlignment.trim_dict().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.get_trimmed
amas.AMAS.MetaAlignment.trim_dict

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_trimmed

7.6.3.17 natural_sort()

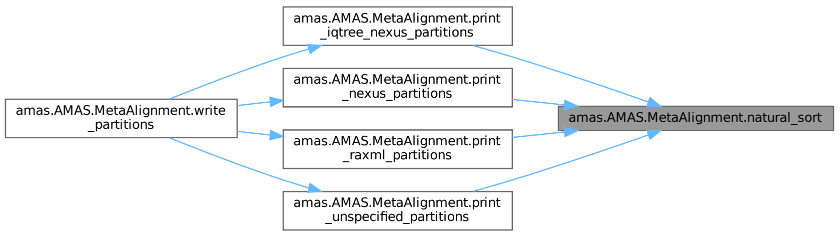
```
amas.AMAS.MetaAlignment.natural_sort (
                self,
                a_list )
```

Definition at line 1962 of file AMAS.py.

```
    def natural_sort(self, a_list):
        # create a function that does 'human sort' on a list
        convert = lambda text: int(text) if text.isdigit() else text.lower()
        alphanum_key = lambda key: [convert(c) for c in re.split('([0-9]+)', key)]
        return sorted(a_list, key = alphanum_key)
```

Referenced by amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions(), amas.AMAS.MetaAlignment.print_nexus_partitions(), amas.AMAS.MetaAlignment.print_raxml_partitions(), and amas.AMAS.MetaAlignment.print_unspecified_partitions().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions
amas.AMAS.MetaAlignment.print_nexus_partitions
amas.AMAS.MetaAlignment.print_raxml_partitions
amas.AMAS.MetaAlignment.print_unspecified_partitions
amas.AMAS.MetaAlignment.natural_sort

7.6.3.18 print_fasta()

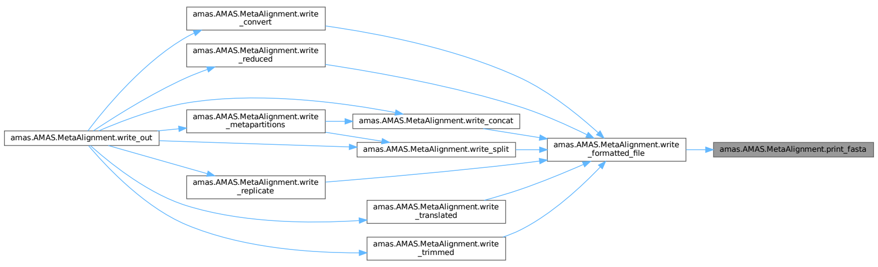
```
amas.AMAS.MetaAlignment.print_fasta (
                self,
                source_dict )
```

Definition at line 1835 of file AMAS.py.

```
    def print_fasta(self, source_dict):
        # print fasta-formatted string from a dictionary
        fasta_string = ""
        # each sequence line will have 80 characters
        n = 80

        for taxon, seq in sorted(source_dict.items()):
            # split dictionary values to a list of string, each n chars long
            seq = [seq[i:i+n] for i in range(0, len(seq), n)]
            # in case there are unwanted spaces in taxon names
            taxon = taxon.replace(" ", "_").strip("'")
            fasta_string += ">" + taxon + "\n"
            for element in seq:
                fasta_string += element + "\n"

        return fasta_string
```

Referenced by amas.AMAS.MetaAlignment.write_formatted_file().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write _convert
amas.AMAS.MetaAlignment.write _reduced
amas.AMAS.MetaAlignment.write _metapartitions
amas.AMAS.MetaAlignment.write _replicate
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write _translated
amas.AMAS.MetaAlignment.write _trimmed
amas.AMAS.MetaAlignment.write _formatted_file
amas.AMAS.MetaAlignment.print_fasta

7.6.3.19 print_iqtree_nexus_partitions()

```
amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions (
                self,
                data_type,
                codons )
```

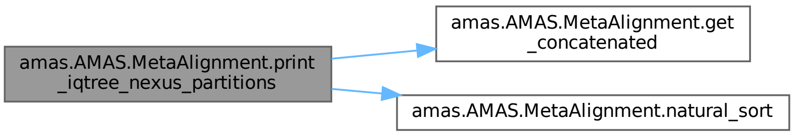
Definition at line 2029 of file AMAS.py.

```
02029     def print_iqtree_nexus_partitions(self, data_type, codons):
02030         # print partitions for concatenated alignment
02031         part_string = ""
02032         part_dict = self.get_concatenated(self.parsed_alignments)[1]
02033         part_list = self.natural_sort(part_dict.keys())
02034         # write beginning of nexus sets
02035         part_string += "#nexus\n"
02036         part_string += "begin sets;\n"
02037 
02038         if data_type == "dna":
02039             if codons == "none":
02040                 for key in part_list:
02041                     part_string += "  charset " + key + " = " + str(part_dict[key]) + ";\n"
02042             elif codons == "12":
02043                 for key in part_list:
02044                     start, end = str(part_dict[key]).split("-")
02045                     part_string += "  charset " + key + "_pos1" + " = " + start + " - " + end + "\\2"
      + ";\n"
02046                     part_string += "  charset " + key + "_pos2" + " = " + str(int(start) + 1) + " - "
      + end + "\\2" + ";\n"
02047             elif codons == "123":
02048                 for key in part_list:
02049                     start, end = str(part_dict[key]).split("-")
02050                     part_string += "  charset " + key + "_pos1" + " = " + start + " - " + end + "\\3"
      + ";\n"
02051                     part_string += "  charset " + key + "_pos2" + " = " + str(int(start) + 1) + " - "
      + end + "\\3" + ";\n"
02052                     part_string += "  charset " + key + "_pos3" + " = " + str(int(start) + 2) + " - "
      + end + "\\3" + ";\n"
02053             part_string += "end;\n"
02054 
02055         elif data_type == "aa":
02056             for key in part_list:
02057                 part_string += "  charset " + key + " = " + str(part_dict[key]) + ";\n"
02058             part_string += "end;\n"
02059 
02060         return part_string
02061 
```

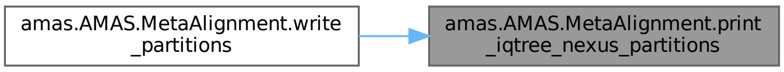
References amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.natural_sort(), amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.split.

Referenced by amas.AMAS.MetaAlignment.write_partitions().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.print
_iqtree_nexus_partitions
amas.AMAS.MetaAlignment.get
_concatenated
amas.AMAS.MetaAlignment.natural_sort

Here is the caller graph for this function:



7.6.3.20 print_nexus()

```
amas.AMAS.MetaAlignment.print_nexus (
                self,
                source_dict )
```

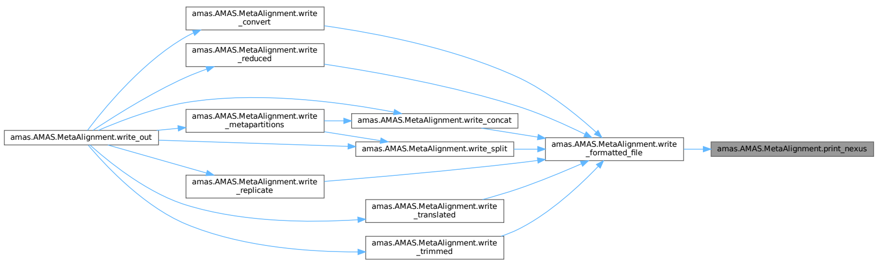
Definition at line 1899 of file AMAS.py.

```
    def print_nexus(self, source_dict):
        # print nexus-formatted string from a dictionary
        if self.data_type == "aa" or self.command == "translate":
            data_type = "PROTEIN"
        elif self.data_type == "dna":
            data_type = "DNA"

        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        nexus_string = (
            "#NEXUS\n\nBEGIN DATA;\n\tDIMENSIONS  NTAX=" + str(no_taxa) + " NCHAR=" + str(seq_length)
            + ";\n\tFORMAT DATATYPE=" + data_type + "  GAP = - MISSING = ?;\n\tMATRIX\n"
        )

        for taxon, seq in sorted(source_dict.items()):
            taxon = taxon.replace(" ", "_").strip("'")
            nexus_string += "\t" + taxon.ljust(pad_longest_name, ' ') + seq + "\n"
        nexus_string += "\n;\n\nEND;"

        return nexus_string

```

References amas.AMAS.MetaAlignment.command, amas.AMAS.Alignment.data_type, and amas.AMAS.MetaAlignment.data_type.

Referenced by amas.AMAS.MetaAlignment.write_formatted_file().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_nexus

7.6.3.21 print_nexus_int()

```
amas.AMAS.MetaAlignment.print_nexus_int (
                self,
                source_dict )
```

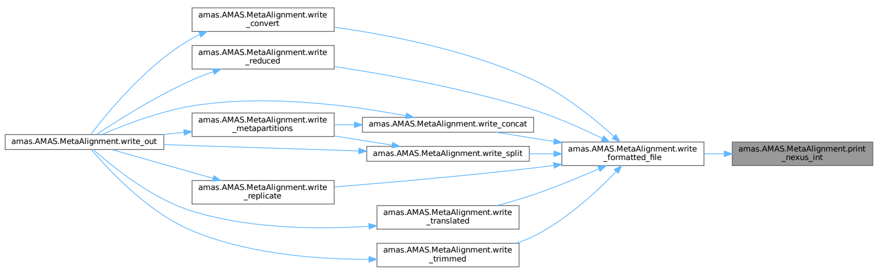
Definition at line 1923 of file AMAS.py.

```
01923     def print_nexus_int(self, source_dict):
01924         # print nexus interleaved-formatted string from a dictionary
01925         if self.data_type == "aa":
01926             data_type = "PROTEIN"
01927         elif self.data_type == "dna":
01928             data_type = "DNA"
01929 
01930         taxa_list = list(source_dict.keys())
01931         no_taxa = len(taxa_list)
01932         pad_longest_name = len(max(taxa_list, key=len)) + 3
01933         seq_length = len(next(iter(source_dict.values())))
01934         header = str(len(source_dict)) + " " + str(seq_length)
01935         # this will be a list of tuples to hold taxa names and sequences
01936         seq_matrix = []
01937         nexus_int_string = (
01938             "#NEXUS\n\nBEGIN DATA;\n\tDIMENSIONS  NTAX=" + str(no_taxa) + " NCHAR=" + str(seq_length)
01939             + ";\n\tFORMAT   INTERLEAVE" + "   DATATYPE=" + data_type + "  GAP = - MISSING =
      ?;\n\tMATRIX\n"
01940         )
01941         # each sequence line will have 500 characters
01942         n = 500
01943 
01944         # recreate sequence matrix
01945         add_to_matrix = seq_matrix.append
01946         for taxon, seq in sorted(source_dict.items()):
01947             add_to_matrix((taxon, [seq[i:i+n] for i in range(0, len(seq), n)]))
01948 
01949         first_seq = seq_matrix[0][1]
01950         for index, item in enumerate(first_seq):
01951             for taxon, sequence in seq_matrix:
01952                 if index == 0:
01953                     nexus_int_string += taxon.ljust(pad_longest_name, ' ') + sequence[index] + "\n"
01954                 else:
01955                     nexus_int_string += sequence[index] + "\n"
01956             nexus_int_string += "\n"
01957 
01958         nexus_int_string += "\n;\n\nEND;"
01959 
01960         return nexus_int_string
01961 
```

References amas.AMAS.Alignment.data_type, and amas.AMAS.MetaAlignment.data_type.

Referenced by amas.AMAS.MetaAlignment.write_formatted_file().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_nexus_int

7.6.3.22 print_nexus_partitions()

```
amas.AMAS.MetaAlignment.print_nexus_partitions (
                self,
                data_type,
                codons )
```

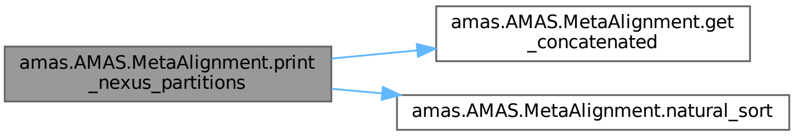
Definition at line 1996 of file AMAS.py.

```
    def print_nexus_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())
        # write beginning of nexus sets
        part_string += "#NEXUS\n\n"
        part_string += "BEGIN SETS;\n"

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += "\tcharset " + key + " = " + str(part_dict[key]) + ";\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "\tcharset " + key + "_pos1" + " = " + start + "-" + end + "\\2" + ";\n"
                    part_string += "\tcharset " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\2" + ";\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "\tcharset " + key + "_pos1" + " = " + start + "-" + end + "\\3" + ";\n"
                    part_string += "\tcharset " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" + ";\n"
                    part_string += "\tcharset " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" + ";\n"
            part_string += "END;"

        elif data_type == "aa":
            for key in part_list:
                part_string += "\tcharset " + key + " = " + str(part_dict[key]) + ";\n"
            part_string += "END;"

        return part_string

```

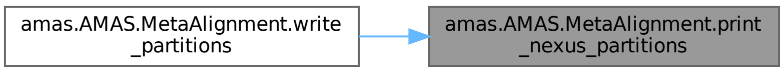
References amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.natural_sort(), amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.split.

Referenced by amas.AMAS.MetaAlignment.write_partitions().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.print
_nexus_partitions
amas.AMAS.MetaAlignment.get
_concatenated
amas.AMAS.MetaAlignment.natural_sort

Here is the caller graph for this function:



7.6.3.23 print_phylip()

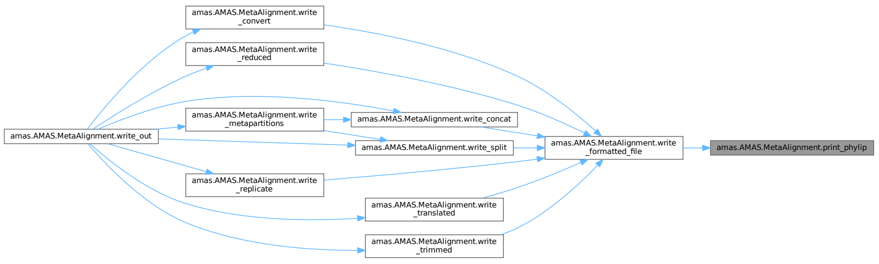
```
amas.AMAS.MetaAlignment.print_phylip (
                self,
                source_dict )
```

Definition at line 1852 of file AMAS.py.

```
    def print_phylip(self, source_dict):
        # print phylip-formatted string from a dictionary
        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        # figure out the max length of a taxon for nice padding of sequences
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        # get sequence length from a random value
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        phylip_string = header + "\n"
        for taxon, seq in sorted(source_dict.items()):
            taxon = taxon.replace(" ", "_").strip("'")
            # left-justify taxon names relative to sequences
            phylip_string += taxon.ljust(pad_longest_name, ' ') + seq + "\n"

        return phylip_string

```

Referenced by amas.AMAS.MetaAlignment.write_formatted_file().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write
_convert
amas.AMAS.MetaAlignment.write
_reduced
amas.AMAS.MetaAlignment.write
_metapartitions
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write
_replicate
amas.AMAS.MetaAlignment.write
_translated
amas.AMAS.MetaAlignment.write
_trimmed
amas.AMAS.MetaAlignment.write
_formatted_file
amas.AMAS.MetaAlignment.print_phylip

7.6.3.24 print_phylip_int()

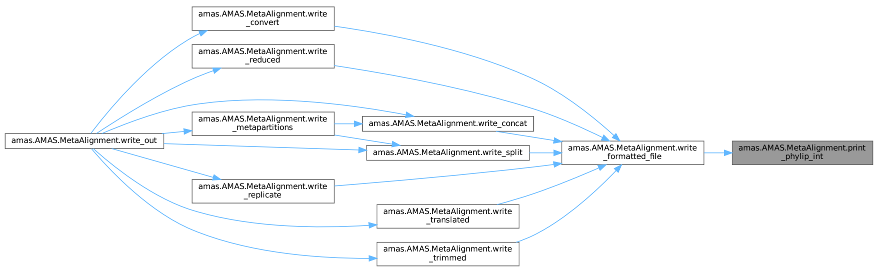
```
amas.AMAS.MetaAlignment.print_phylip_int (
                self,
                source_dict )
```

Definition at line 1869 of file AMAS.py.

```
01869     def print_phylip_int(self, source_dict):
01870         # print phylip interleaved-formatted string from a dictionary
01871         taxa_list = list(source_dict.keys())
01872         no_taxa = len(taxa_list)
01873         pad_longest_name = len(max(taxa_list, key=len)) + 3
01874         seq_length = len(next(iter(source_dict.values())))
01875         header = str(len(source_dict)) + " " + str(seq_length)
01876         phylip_int_string = header + "\n\n"
01877         # this will be a list of tuples to hold taxa names and sequences
01878         seq_matrix = []
01879 
01880         # each sequence line will have 500 characters
01881         n = 500
01882 
01883         # recreate sequence matrix
01884         add_to_matrix = seq_matrix.append
01885         for taxon, seq in sorted(source_dict.items()):
01886             add_to_matrix((taxon, [seq[i:i+n] for i in range(0, len(seq), n)]))
01887 
01888         first_seq = seq_matrix[0][1]
01889         for index, item in enumerate(first_seq):
01890             for taxon, sequence in seq_matrix:
01891                 if index == 0:
01892                     phylip_int_string += taxon.ljust(pad_longest_name, ' ') + sequence[index] + "\n"
01893                 else:
01894                     phylip_int_string += sequence[index] + "\n"
01895             phylip_int_string += "\n"
01896 
01897         return phylip_int_string
01898 
```

Referenced by amas.AMAS.MetaAlignment.write_formatted_file().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_phylip_int

7.6.3.25 print_raxml_partitions()

```
amas.AMAS.MetaAlignment.print_raxml_partitions (
                self,
                data_type,
                codons )
```

Definition at line 2062 of file AMAS.py.

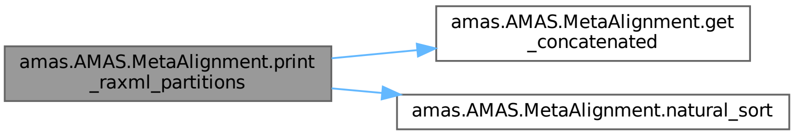
```
02062     def print_raxml_partitions(self, data_type, codons):
02063         # print partitions for concatenated alignment
02064         part_string = ""
02065         part_dict = self.get_concatenated(self.parsed_alignments)[1]
02066         part_list = self.natural_sort(part_dict.keys())
```

```

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += "DNA, " + key + " = " + str(part_dict[key]) + "\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "DNA, " + key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
                    part_string += "DNA, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end +
"\\2" + "\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "DNA, " + key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
                    part_string += "DNA, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end +
"\\3" + "\n"
                    part_string += "DNA, " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end +
"\\3" + "\n"

        elif data_type == "aa":
            for key in part_list:
                part_string += "WAG, " + key + " = " + str(part_dict[key]) + "\n"

            #  aa-partition files with strides are probably not useful? (original below)
#            elif codons == "12":
#                for key in part_list:
#                    start, end = str(part_dict[key]).split("-")
#                    part_string += "WAG, " + key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
#                    part_string += "WAG, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end
+ "\\2" + "\n"
#            elif codons == "123":
#                for key in part_list:
#                    start, end = str(part_dict[key]).split("-")
#                    part_string += "WAG, " + key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
#                    part_string += "WAG, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end
+ "\\3" + "\n"
#                    part_string += "WAG, " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end
+ "\\3" + "\n"
        return part_string

```

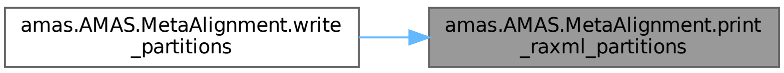
References amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.natural_sort(), amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.split.

Referenced by amas.AMAS.MetaAlignment.write_partitions().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.print_raxml_partitions
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.natural_sort

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.print_raxml_partitions

7.6.3.26 print_unspecified_partitions()

```
amas.AMAS.MetaAlignment.print_unspecified_partitions (
                self,
                data_type,
                codons )
```

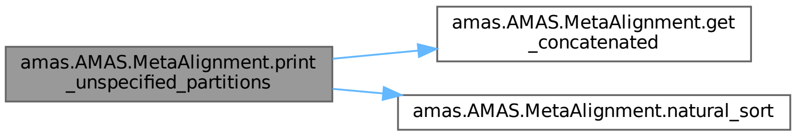
Definition at line 1968 of file AMAS.py.

```
    def print_unspecified_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += key + " = " + str(part_dict[key]) + "\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
                    part_string += key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\2" +
"\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
                    part_string += key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" +
"\n"
                    part_string += key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" +
"\n"

        elif data_type == "aa":
            for key in part_list:
                part_string += key + " = " + str(part_dict[key]) + "\n"

        return part_string

```

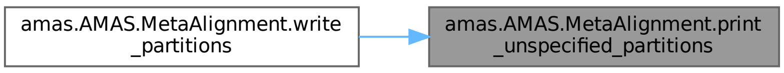
References amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.natural_sort(), amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.split.

Referenced by amas.AMAS.MetaAlignment.write_partitions().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.print_unspecified_partitions
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.natural_sort

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.print_unspecified_partitions

7.6.3.27 remove_empty_sequences()

```
amas.AMAS.MetaAlignment.remove_empty_sequences (
                self,
                split_alignment )
```

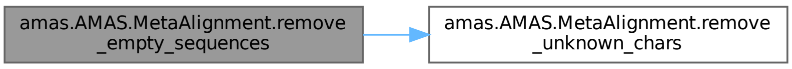
Definition at line 1510 of file AMAS.py.

```
01510     def remove_empty_sequences(self, split_alignment):
01511         # remove taxa from alignment if they are composed of only empty sequences
01512         new_alignment = {taxon : seq for taxon, seq in split_alignment.items() if
      self.remove_unknown_chars(seq)}
01513
01514         return new_alignment
01515
```

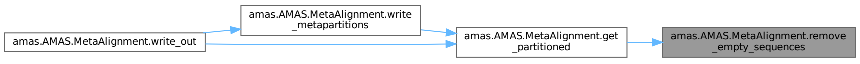
References amas.AMAS.MetaAlignment.remove_unknown_chars().

Referenced by amas.AMAS.MetaAlignment.get_partitioned().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.remove
_empty_sequences
amas.AMAS.MetaAlignment.remove
_unknown_chars

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write
_metapartitions
amas.AMAS.MetaAlignment.get
_partitioned
amas.AMAS.MetaAlignment.remove
_empty_sequences

7.6.3.28 remove_from_alignment()

```
amas.AMAS.MetaAlignment.remove_from_alignment (
                self,
                alignment,
                species_to_remove_set,
                index )
```

Definition at line 1809 of file AMAS.py.

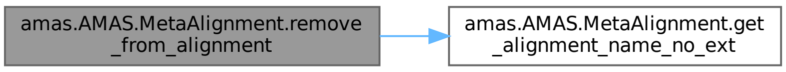
```
01809     def remove_from_alignment(self, alignment, species_to_remove_set, index):
01810         # remove taxa from alignment
01811         aln_name = self.get_alignment_name_no_ext(index)
01812         for taxon in species_to_remove_set:
01813             if taxon not in alignment.keys():
01814                 print(
01815                     "WARNING: Taxon '" + taxon + "' not found in '" + aln_name + "'.\nIf you expected
      it to be there, "
01816                     "make sure to replace all taxon name spaces with underscores and that you are not
      using quotes."
01817                 )
01818         # originally within for-loop scope (redundancy)
01819         new_alignment = {species: seq for species, seq in alignment.items() if species not in
      species_to_remove_set}
01820
```

```
        return aln_name, new_alignment

```

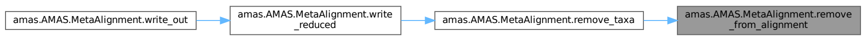
References amas.AMAS.MetaAlignment.get_alignment_name_no_ext().

Referenced by amas.AMAS.MetaAlignment.remove_taxa().

Here is the call graph for this function:



Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write
_reduced
amas.AMAS.MetaAlignment.remove_taxa
amas.AMAS.MetaAlignment.remove
_from_alignment

7.6.3.29 remove_taxa()

```
amas.AMAS.MetaAlignment.remove_taxa (
                self,
                species_to_remove_set )
```

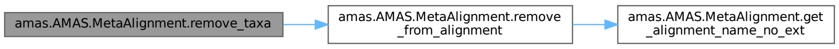
Definition at line 1823 of file AMAS.py.

```
    def remove_taxa(self, species_to_remove_set):
        new_alns = {}
        for index, alignment in enumerate(self.parsed_alignments):
            aln_name, aln_dict = self.remove_from_alignment(alignment, species_to_remove_set, index)
            # check if alignment is not empty:
            if aln_dict:
                new_alns[aln_name] = aln_dict
            else:
                print("ERROR: You asked to remove all taxa from the alignment " + aln_name + ". No
      output file will be written.")

        return new_alns

```

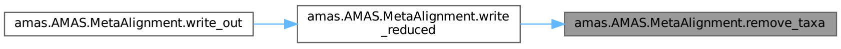
References amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.remove_from_alignment().

Referenced by amas.AMAS.MetaAlignment.write_reduced().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.remove_taxa
amas.AMAS.MetaAlignment.remove
_from_alignment
amas.AMAS.MetaAlignment.get
_alignment_name_no_ext

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write
_reduced
amas.AMAS.MetaAlignment.remove_taxa

7.6.3.30 remove_unknown_chars()

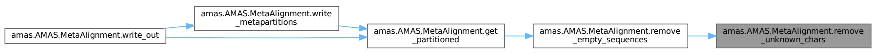
```
amas.AMAS.MetaAlignment.remove_unknown_chars (
                self,
                seq )
```

Definition at line 1504 of file AMAS.py.

```
def remove_unknown_chars(self, seq):
    # remove unknown characters from sequence
    new_seq = seq.replace("?", "").replace("-", "")

    return new_seq

```

Referenced by amas.AMAS.MetaAlignment.remove_empty_sequences().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write _metapartitions
amas.AMAS.MetaAlignment.get _partitioned
amas.AMAS.MetaAlignment.remove _empty_sequences
amas.AMAS.MetaAlignment.remove _unknown_chars

7.6.3.31 replace_string_in_file()

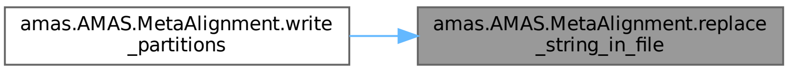
```
amas.AMAS.MetaAlignment.replace_string_in_file (
                self,
                file_name,
                old_string,
                new_string )
```

Definition at line 2102 of file AMAS.py.

```
def replace_string_in_file(self, file_name, old_string, new_string):
    # global string replacement in file
    with open(file_name, "r", encoding="utf-8") as file:
        file_content = file.read()
    # write globally replaced content back to file
    glb_replaced_content = file_content.replace(old_string, new_string)
    with open(file_name, "w", encoding="utf-8") as file:
        file.write(glb_replaced_content)

```

Referenced by amas.AMAS.MetaAlignment.write_partitions().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write _partitions
amas.AMAS.MetaAlignment.replace _string_in_file

7.6.3.32 summarize_alignments()

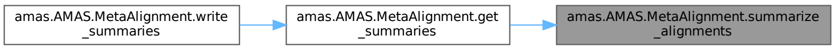
```
amas.AMAS.MetaAlignment.summarize_alignments (
              self,
              alignment )
```

Definition at line 1648 of file AMAS.py.

```
    def summarize_alignments(self, alignment):
        # helper function to summarize alignments
        summary = alignment.get_summary()
        return summary

```

Referenced by amas.AMAS.MetaAlignment.get_summaries().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_summaries
amas.AMAS.MetaAlignment.get_summaries
amas.AMAS.MetaAlignment.summarize_alignments

7.6.3.33 summarize_alignments_taxa()

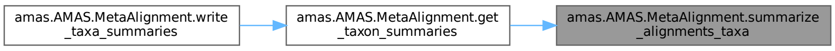
```
amas.AMAS.MetaAlignment.summarize_alignments_taxa (
              self,
              alignment )
```

Definition at line 1693 of file AMAS.py.

```
    def summarize_alignments_taxa(self, alignment):
        # helper function to summarize alignments by taxon
        summary = alignment.get_taxa_summary()
        return summary

```

Referenced by amas.AMAS.MetaAlignment.get_taxon_summaries().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_taxa_summaries
amas.AMAS.MetaAlignment.get_taxon_summaries
amas.AMAS.MetaAlignment.summarize_alignments_taxa

7.6.3.34 translate_dict()

```
amas.AMAS.MetaAlignment.translate_dict (
              self,
              source_dict )
```

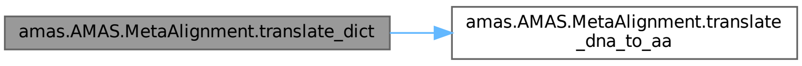
Definition at line 1467 of file AMAS.py.

```
    def translate_dict(self, source_dict):
        translation_table = self.codes.get(self.genetic_code)
        translated_dict = {}
        for taxon, seq in sorted(source_dict.items()):
            translated_seq = self.translate_dna_to_aa(seq, translation_table, self.reading_frame)
            if "*" in translated_seq:
                print("WARNING: stop codon(s), indicated as *, found in {} sequence".format(taxon))
            translated_dict[taxon] = translated_seq

        return translated_dict

```

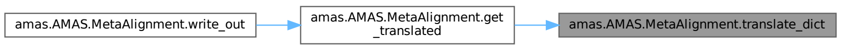
References amas.AMAS.MetaAlignment.codes, amas.AMAS.MetaAlignment.genetic_code, amas.AMAS.MetaAlignment.reading_frame, and amas.AMAS.MetaAlignment.translate_dna_to_aa().

Referenced by amas.AMAS.MetaAlignment.get_translated().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.translate_dict
amas.AMAS.MetaAlignment.translate _dna_to_aa

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get _translated
amas.AMAS.MetaAlignment.translate_dict

7.6.3.35 translate_dna_to_aa()

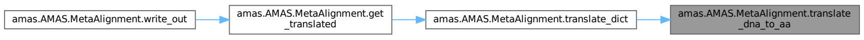
```
amas.AMAS.MetaAlignment.translate_dna_to_aa (
              self,
              seq,
              translation_table,
              frame )
```

Definition at line 1446 of file AMAS.py.

```
    def translate_dna_to_aa(self, seq, translation_table, frame):
        # translate DNA string into amino acids
        # where the last codon starts
        last_codon_start = len(seq) - 2
        # where the first codon starts
        if frame == 1:
            first = 0
        elif frame == 2:
            first = 1
        elif frame == 3:
            first = 2
        # create protein sequence by growing list
        protein = []
        add_to_protein = protein.append
        for start in range(first, last_codon_start, 3):
            codon = seq[start : start + 3]
            aa = translation_table.get(codon.upper(), 'X')
            add_to_protein(aa)

        return "".join(protein)

```

Referenced by amas.AMAS.MetaAlignment.translate_dict().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_translated
amas.AMAS.MetaAlignment.translate_dict
amas.AMAS.MetaAlignment.translate_dna_to_aa

7.6.3.36 trim_dict()

```
amas.AMAS.MetaAlignment.trim_dict (
                self,
                alignment )
```

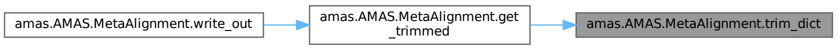
Definition at line 1487 of file AMAS.py.

```
    def trim_dict(self, alignment):
        trim_vector = alignment.get_trim_selection(self.trim_fraction, self.parsimony_check)
        aln_dict = alignment.parsed_aln
        for key in aln_dict:
            aln_dict[key] = ".join(list(compress(aln_dict[key], trim_vector)))

        return aln_dict

```

References amas.AMAS.MetaAlignment.parsimony_check, and amas.AMAS.MetaAlignment.trim_fraction.

Referenced by amas.AMAS.MetaAlignment.get_trimmed().

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_trimmed
amas.AMAS.MetaAlignment.trim_dict

7.6.3.37 write_concat()

```
amas.AMAS.MetaAlignment.write_concat (
                self,
                file_format )
```

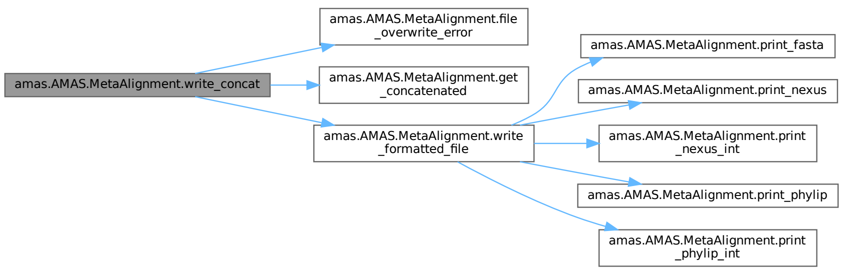
Definition at line 2190 of file AMAS.py.

```
    def write_concat(self, file_format):
        # write concatenated alignment into a file
        concatenated_alignment = self.get_concatenated(self.parsed_alignments)[0]
        file_name = self.concat_out
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, concatenated_alignment)

        print("Wrote concatenated sequences to " + file_format + " file '" + file_name + "'")

```

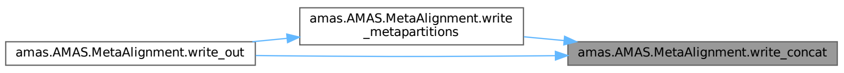
References amas.AMAS.MetaAlignment.concat_out, amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.parsed_alignments, and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_concat

7.6.3.38 write_convert()

```
amas.AMAS.MetaAlignment.write_convert (
                self,
                index,
                alignment,
                file_format,
                extension )
```

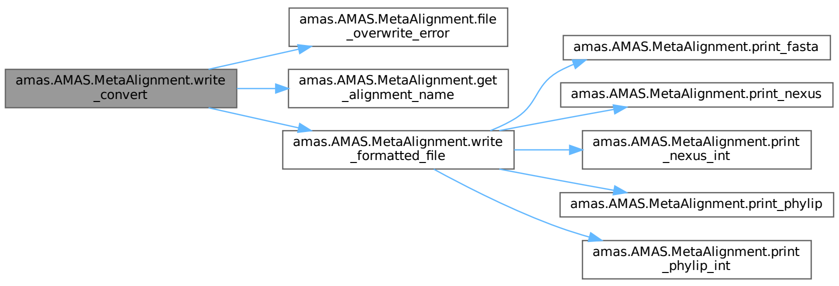
Definition at line 2199 of file AMAS.py.

```
    def write_convert(self, index, alignment, file_format, extension):
        # write converted alignment into a file
        file_name = self.get_alignment_name(index, extension)
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, alignment)

```

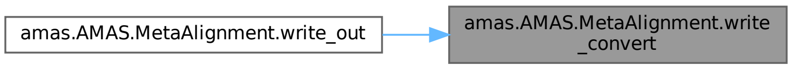
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.get_alignment_name(), and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_alignment_name
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_convert

7.6.3.39 write_formatted_file()

```
amas.AMAS.MetaAlignment.write_formatted_file (
            self,
            file_format,
            file_name,
            alignment )
```

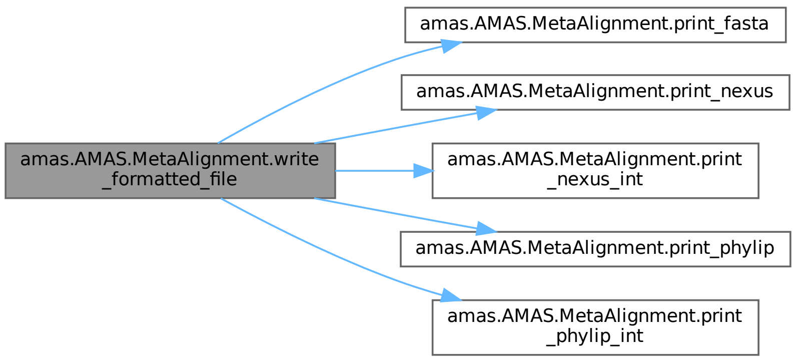
Definition at line 2164 of file AMAS.py.

```
    def write_formatted_file(self, file_format, file_name, alignment):
        # write the correct format string into a file
        with open(file_name, "w", encoding="utf-8") as out_file:
            if file_format == "phylip":
                out_file.write(self.print_phylip(alignment))
            elif file_format == "fasta":
                out_file.write(self.print_fasta(alignment))
            elif file_format == "phylip-int":
                out_file.write(self.print_phylip_int(alignment))
            elif file_format == "nexus":
                out_file.write(self.print_nexus(alignment))
            elif file_format == "nexus-int":
                out_file.write(self.print_nexus_int(alignment))

```

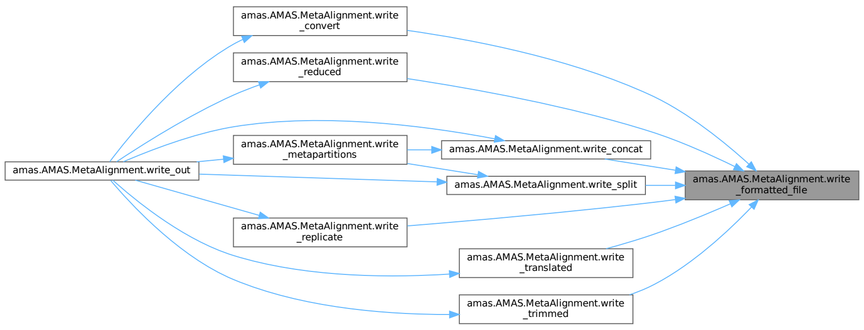
References amas.AMAS.MetaAlignment.print_fasta(), amas.AMAS.MetaAlignment.print_nexus(), amas.AMAS.MetaAlignment.print_nexus_int(), amas.AMAS.MetaAlignment.print_phylip(), and amas.AMAS.MetaAlignment.print_phylip_int().

Referenced by amas.AMAS.MetaAlignment.write_concat(), amas.AMAS.MetaAlignment.write_convert(), amas.AMAS.MetaAlignment.write_reduced(), amas.AMAS.MetaAlignment.write_replicate(), amas.AMAS.MetaAlignment.write_split(), amas.AMAS.MetaAlignment.write_translated(), and amas.AMAS.MetaAlignment.write_trimmed().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write
_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print
_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print
_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write
_convert
amas.AMAS.MetaAlignment.write
_reduced
amas.AMAS.MetaAlignment.write
_metapartitions
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write
_replicate
amas.AMAS.MetaAlignment.write
_translated
amas.AMAS.MetaAlignment.write
_trimmed
amas.AMAS.MetaAlignment.write
_formatted_file

7.6.3.40 write_metapartitions()

```
amas.AMAS.MetaAlignment.write_metapartitions (
                self,
                file_format )
```

Definition at line 2265 of file AMAS.py.

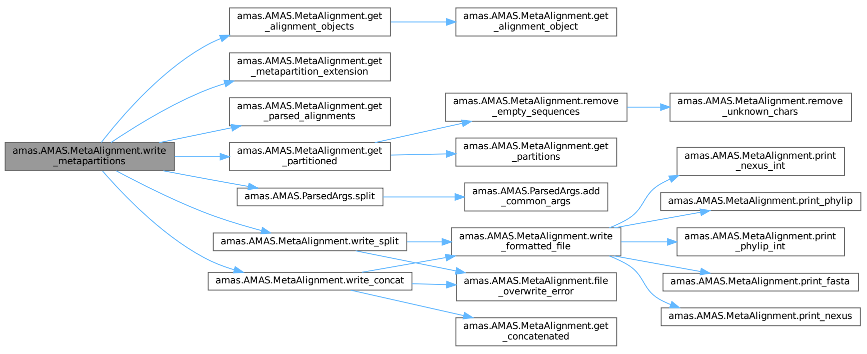
```
02265     def write_metapartitions(self, file_format):
02266         # write metapartitions - combines split and concat
02267         print("write_out elif action == metapartitions")
02268         metapartition_extension = self.get_metapartition_extension(file_format)
02269         list_of_alignments = self.get_partitioned(self.split)
02270         written_split_files = []
02271         err_indx = 0
02272 
02273         for item in list_of_alignments:
02274             try:
02275                 for split_file in self.write_split(item, file_format, metapartition_extension):
02276                     written_split_files.append(split_file)
02277             except ValueError as e:
02278                     print("WARNING: ", e)
02279                     err_indx += 1
02280         if len(written_split_files) > 0:
02281             print("Wrote %d %s metapartition files from partitions provided" %
      (len(written_split_files), file_format))
```

```
        if err_indx > 0:
            print("WARNING: %d file(s) raised an error while writing (see above)." % err_indx)

        # now set inputs to be the collated metapartition alignment files
        self.in_files = written_split_files
        self.alignment_objects = self.get_alignment_objects()
        self.parsed_alignments = self.get_parsed_alignments()

        # concat metapartition alignment files
        self.write_concat(file_format)

```

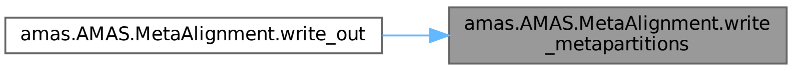
References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.MetaAlignment.get_alignment_objects(), amas.AMAS.MetaAlignment.get_metapartition_extension(), amas.AMAS.MetaAlignment.get_parsed_alignments(), amas.AMAS.MetaAlignment.get_partitioned(), amas.AMAS.MetaAlignment.in_files, amas.AMAS.MetaAlignment.parsed_alignments, amas.AMAS.ParsedArgs.split(), amas.AMAS.MetaAlignment.split, amas.AMAS.MetaAlignment.write_concat(), and amas.AMAS.MetaAlignment.write_split().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_alignment_objects
amas.AMAS.MetaAlignment.get_alignment_object
amas.AMAS.MetaAlignment.get_metapartition_extension
amas.AMAS.MetaAlignment.get_parsed_alignments
amas.AMAS.MetaAlignment.remove_empty_sequences
amas.AMAS.MetaAlignment.remove_unknown_chars
amas.AMAS.MetaAlignment.get_partitioned
amas.AMAS.MetaAlignment.get_partitions
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.ParsedArgs.split
amas.AMAS.ParsedArgs.add_common_args
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_phylip_int
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.get_concatenated

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions

7.6.3.41 write_out()

```
amas.AMAS.MetaAlignment.write_out (
                self,
                action,
                file_format )
```

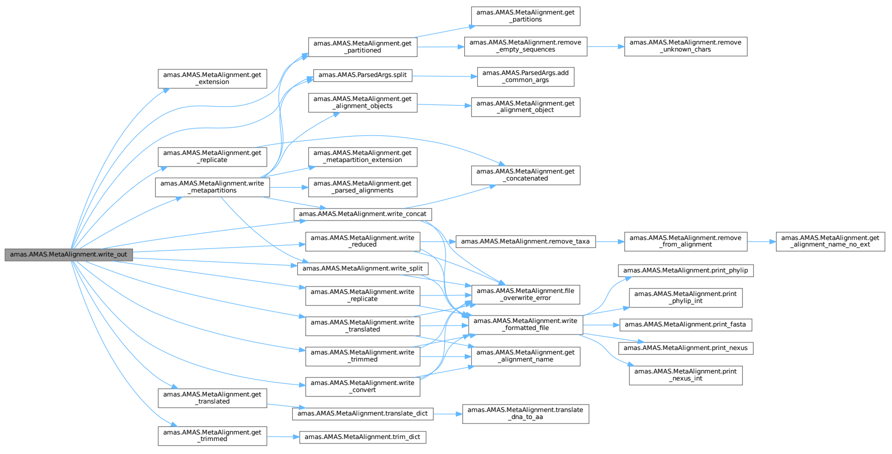
Definition at line 2293 of file AMAS.py.

```
02293     def write_out(self, action, file_format):
02294         # write other output files depending on command (action)
02295         extension = self.get_extension(file_format)
02296
```

```
        if action == "concat":
            self.write_concat(file_format)

        elif action == "convert":
            length = len(self.alignment_objects)
            [
                self.write_convert(i, alignment, file_format, extension)
                for i, alignment in enumerate(self.parsed_alignments)
            ]
            print("Converted " + str(length) + " files from " + self.in_format + " to " + file_format)

        elif action == "replicate":
            [
                self.write_replicate(i, alignment, file_format, extension)
                for i, alignment in enumerate(self.get_replicate(self.no_replicates, self.no_loci))
            ]

            print("Constructed " + str(self.no_replicates) + " replicate data sets, each from " +
str(self.no_loci) + " alignments")

        elif action == "split":
            list_of_alignments = self.get_partitioned(self.split)
            written_split_files = []
            err_indx = 0

            for item in list_of_alignments:
                try:
                    for split_file in self.write_split(item, file_format, extension):
                        written_split_files.append(split_file)
                except ValueError as e:
                        print("WARNING: ", e)
                        err_indx += 1
            if len(written_split_files) > 0:
                print("Wrote %d %s files from partitions provided" % (len(written_split_files),
file_format))
            if err_indx > 0:
                print("WARNING: %d file(s) raised an error while writing (see above)." % err_indx)

        elif action == "metapartitions":
            self.write_metapartitions(file_format)

        elif action == "remove":
            aln_no = self.write_reduced(file_format, extension)
            if aln_no:
                print("Wrote " + str(aln_no) + " " + str(file_format) + " files with reduced taxon
set")

        elif action == "translate":
            if self.data_type == "aa":
                print("ERROR: cannot translate; you said your alignment already contains amino acids")
                sys.exit()
            translated_alignment_dicts = self.get_translated(self.genetic_code, self.reading_frame)
            length = len(self.alignment_objects)
            [
                self.write_translated(i, alignment, file_format, extension)
                for i, alignment in enumerate(translated_alignment_dicts)
            ]
            print("Translated " + str(length) + " files to amino acid sequences")

        elif action == "trim": # self.trim_fraction, self.parsimony_check
            trimmed_alignment_dicts = self.get_trimmed(self.trim_fraction, self.parsimony_check)
            length = len(self.alignment_objects)
            [
                self.write_trimmed(i, alignment, file_format, extension)
                for i, alignment in enumerate(trimmed_alignment_dicts)
            ]
            print("Trimmed", str(length), "file(s) to have", self.trim_fraction, "minimum occupancy
per alignment column")


```

References amas.AMAS.MetaAlignment.alignment_objects, amas.AMAS.Alignment.data_type, amas.AMAS.MetaAlignment.data_type, amas.AMAS.MetaAlignment.genetic_code, amas.AMAS.MetaAlignment.get_extension(), amas.AMAS.MetaAlignment.get_partitioned(), amas.AMAS.MetaAlignment.get_replicate(), amas.AMAS.MetaAlignment.get_translated(), amas.AMAS.MetaAlignment.get_trimmed(), amas.AMAS.Alignment.in_format, amas.AMAS.MetaAlignment.in_format, amas.AMAS.MetaAlignment.no_loci, amas.AMAS.MetaAlignment.no_replicates, amas.AMAS.MetaAlignment.parsed_alignments, amas.AMAS.MetaAlignment.parsimony_check, amas.AMAS.MetaAlignment.reading_frame, amas.AMAS.ParsedArgs.split(), amas.AMAS.MetaAlignment.split, amas.AMAS.MetaAlignment.trim_fraction, amas.AMAS.MetaAlignment.write_concat(), amas.AMAS.MetaAlignment.write_convert(), amas.AMAS.MetaAlignment.write_metapartitions(), amas.AMAS.MetaAlignment.write_reduced(), amas.AMAS.MetaAlignment.write_replicate(), amas.AMAS.MetaAlignment.write_split(), amas.AMAS.MetaAlignment.write_translated(), and amas.AMAS.MetaAlignment.write_trimmed().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.get_extension
amas.AMAS.MetaAlignment.get_replicate
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.get_translated
amas.AMAS.MetaAlignment.get_trimmed
amas.AMAS.MetaAlignment.get_partitioned
amas.AMAS.ParsedArgs.split
amas.AMAS.MetaAlignment.get_alignment_objects
amas.AMAS.MetaAlignment.get_metapartition_extension
amas.AMAS.MetaAlignment.get_parsed_alignments
amas.AMAS.MetaAlignment.write_concat
amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.write_convert
amas.AMAS.MetaAlignment.translate_dict
amas.AMAS.MetaAlignment.trim_dict
amas.AMAS.MetaAlignment.get_partitions
amas.AMAS.MetaAlignment.remove_empty_sequences
amas.AMAS.MetaAlignment.remove_unknown_chars
amas.AMAS.ParsedArgs.add_common_args
amas.AMAS.MetaAlignment.get_alignment_object
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.remove_taxa
amas.AMAS.MetaAlignment.remove_from_alignment
amas.AMAS.MetaAlignment.get_alignment_name_no_ext
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.print_phylip_int
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.get_alignment_name
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.translate_dna_to_aa

7.6.3.42 write_partitions()

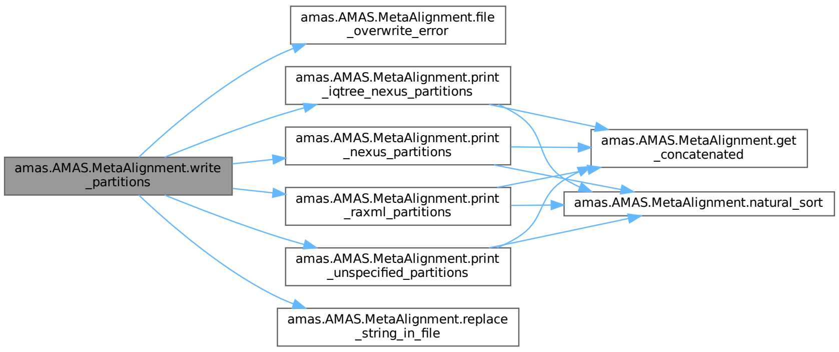
```
amas.AMAS.MetaAlignment.write_partitions (
            self,
            file_name,
            part_format,
            data_type,
            codons )
```

Definition at line 2111 of file AMAS.py.

```
    def write_partitions(self, file_name, part_format, data_type, codons):
        # write partitions file for concatenated alignment
        self.file_overwrite_error(file_name)
        with open(file_name, "w", encoding="utf-8") as part_file:
            if part_format == "nexus":
                part_file.write(self.print_nexus_partitions(data_type, codons))
            if part_format == "iqtree-nexus":
                part_file.write(self.print_iqtree_nexus_partitions(data_type, codons))
            if part_format == "raxml":
                part_file.write(self.print_raxml_partitions(data_type, codons))
            if part_format == "unspecified":
                part_file.write(self.print_unspecified_partitions(data_type, codons))

            if self.using_metapartitions:
                self.replace_string_in_file(file_name, '-meta =', ' =')

        print("Wrote partitions for the concatenated file to '" + file_name + "'")

```

References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions(), amas.AMAS.MetaAlignment.print_nexus_partitions(), amas.AMAS.MetaAlignment.print_raxml_partitions(), amas.AMAS.MetaAlignment.print_unspecified_partitions(), amas.AMAS.MetaAlignment.replace_string_in_file(), and amas.AMAS.MetaAlignment.using_metapartitions.

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_partitions
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions
amas.AMAS.MetaAlignment.print_nexus_partitions
amas.AMAS.MetaAlignment.print_raxml_partitions
amas.AMAS.MetaAlignment.print_unspecified_partitions
amas.AMAS.MetaAlignment.replace_string_in_file
amas.AMAS.MetaAlignment.get_concatenated
amas.AMAS.MetaAlignment.natural_sort

7.6.3.43 write_reduced()

```
amas.AMAS.MetaAlignment.write_reduced (
                self,
                file_format,
                extension )
```

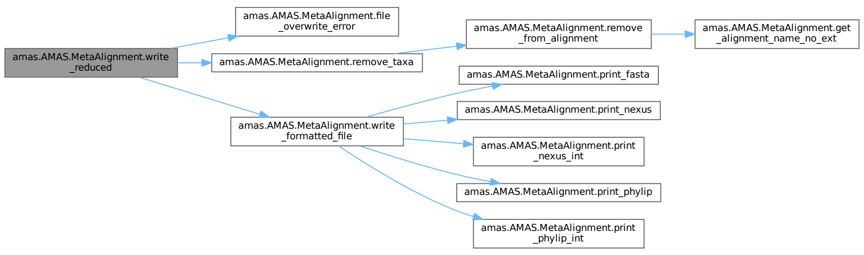
Definition at line 2236 of file AMAS.py.

```
02236     def write_reduced(self, file_format, extension):
02237         # write alignment with taxa removed into a file
02238         prefix = self.reduced_file_prefix
02239         alns = self.remove_taxa(self.species_to_remove)
02240         for file_name, aln_dict in alns.items():
02241             out_file_name = prefix + file_name + extension
02242             self.file_overwrite_error(out_file_name)
02243             self.write_formatted_file(file_format, out_file_name, aln_dict)
02244         return len(alns)
02245
```

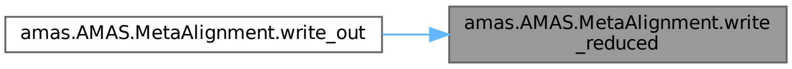
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.reduced_file_prefix, amas.AMAS.MetaAlignment.remove_taxa(), amas.AMAS.MetaAlignment.species_to_remove, and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_reduced
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.remove_taxa
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.remove_from_alignment
amas.AMAS.MetaAlignment.get_alignment_name_no_ext
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_reduced

7.6.3.44 write_replicate()

```
amas.AMAS.MetaAlignment.write_replicate (
                self,
                index,
                alignment,
                file_format,
                extension )
```

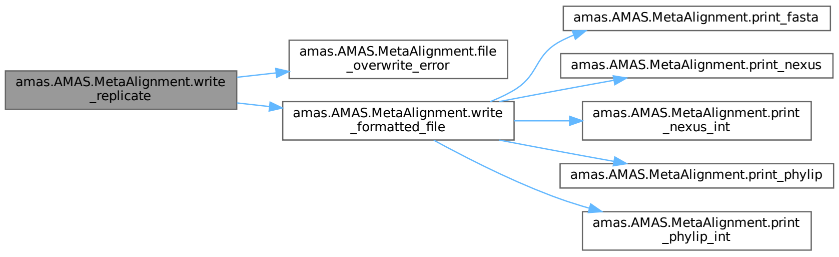
Definition at line 2205 of file AMAS.py.

```
    def write_replicate(self, index, alignment, file_format, extension):
        # write replicate alignment into a file
        file_name = "replicate" + str(index + 1) + "_" + str(self.no_loci) + "-loci" + extension
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, alignment)
```

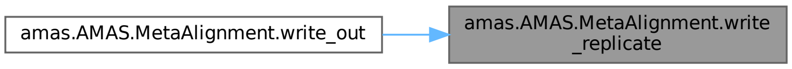
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.no_loci, and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_replicate
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_replicate

7.6.3.45 write_split()

```
amas.AMAS.MetaAlignment.write_split (
                self,
                item,
                file_format,
                extension )
```

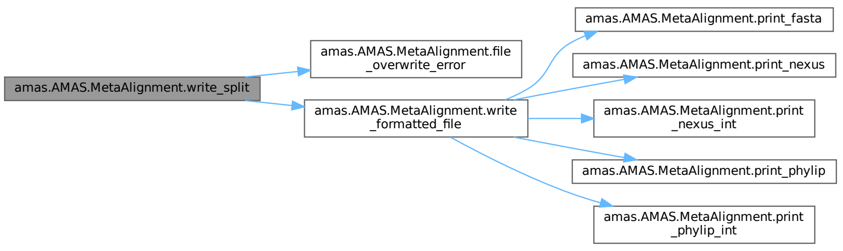
Definition at line 2211 of file AMAS.py.

```
    def write_split(self, item, file_format, extension):
        # write split alignments from partitions file
        # bad practice with the dicts; figure out better solution
        partition_name = list(item.keys())[0]
        alignment = item[partition_name]

        if not alignment:
            # If the alignment dict is empty, i.e. no alignment associated with partition name, raise
      error
            raise ValueError("Partition '%s' is empty. No sequences to write." % partition_name)

        # implementation of option --no-san (don't prepend input superalignment filename to the
      `split` outputs)
        if self.no_sup_aln_name:
            file_name = partition_name + extension
        else:
            file_name = str(self.in_files[0].split('.')[0]) + "_" + partition_name + extension

        try:
            self.file_overwrite_error(file_name)
            self.write_formatted_file(file_format, file_name, alignment)
            yield file_name
        except ValueError as e:
            print("There was an issue writing file '%s': %s" % (file_name, str(e)))
            remove(file_name)
            raise

```

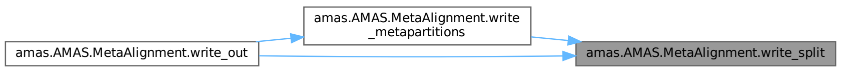
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.in_files, amas.AMAS.MetaAlignment.no_sup_aln_name, amas.AMAS.MetaAlignment.split, and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_split
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_metapartitions
amas.AMAS.MetaAlignment.write_split

7.6.3.46 write_summaries()

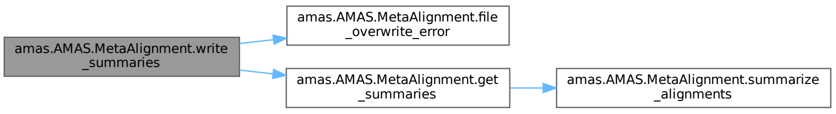
```
amas.AMAS.MetaAlignment.write_summaries (
                self,
                file_name )
```

Definition at line 1698 of file AMAS.py.

```
    def write_summaries(self, file_name):
        # write summaries to file

        self.file_overwrite_error(file_name)

        with open(file_name, "w", encoding="utf-8") as summary_file:
            summary_out = self.get_summaries()
            header = '\t'.join(summary_out[0])
            new_summ = ['\t'.join(summary) for summary in summary_out[1]]
            summary_file.write(header + '\n')
            summary_file.write('\n'.join(new_summ))
            summary_file.write('\n')
            print("Wrote summaries to file '" + file_name + "'")

```

References amas.AMAS.MetaAlignment.file_overwrite_error(), and amas.AMAS.MetaAlignment.get_summaries().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_summaries
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_summaries
amas.AMAS.MetaAlignment.summarize_alignments

7.6.3.47 write_taxa_summaries()

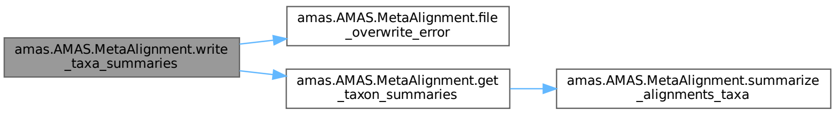
```
amas.AMAS.MetaAlignment.write_taxa_summaries (
                self )
```

Definition at line 1712 of file AMAS.py.

```
    def write_taxa_summaries(self):
        # write by-taxon summaries to file
        for index, in_file_name in enumerate(self.in_files):
            out_file_name = in_file_name + "-seq-summary.txt"
            self.file_overwrite_error(out_file_name)
            with open(out_file_name, "w", encoding="utf-8") as summary_file:
                summary_out = self.get_taxon_summaries()
                header = '\t'.join(summary_out[0])
                summ = [[str(col) for col in element] for element in summary_out[1][index]]
                new_summ = ['\t'.join(row) for row in summ]
                summary_file.write(header + '\n')
                summary_file.write('\n'.join(new_summ))
                summary_file.write('\n')

```

References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.get_taxon_summaries(), and amas.AMAS.MetaAlignment.in_files.

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_taxa_summaries
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_taxon_summaries
amas.AMAS.MetaAlignment.summarize_alignments_taxa

7.6.3.48 write_translated()

```
amas.AMAS.MetaAlignment.write_translated (
              self,
              index,
              alignment,
              file_format,
              extension )
```

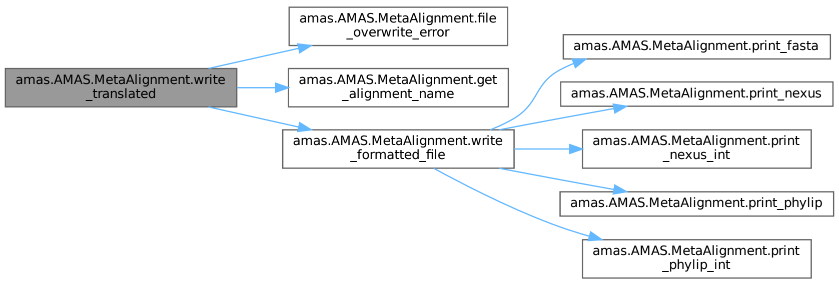
Definition at line 2246 of file AMAS.py.

```
    def write_translated(self, index, alignment, file_format, extension):
        # write alignments translated into amino acids
        prefix = "translated_"
        file_name = self.get_alignment_name(index, extension)
        out_file_name = prefix + file_name + extension
        self.file_overwrite_error(out_file_name)
        self.write_formatted_file(file_format, out_file_name, alignment)

```

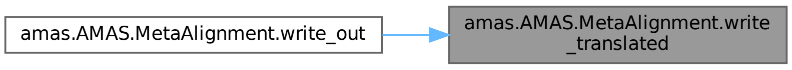
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.get_alignment_name(), and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_translated
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_alignment_name
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_translated

7.6.3.49 write_trimmed()

```
amas.AMAS.MetaAlignment.write_trimmed (
              self,
              index,
              alignment,
```

file_format,
extension)

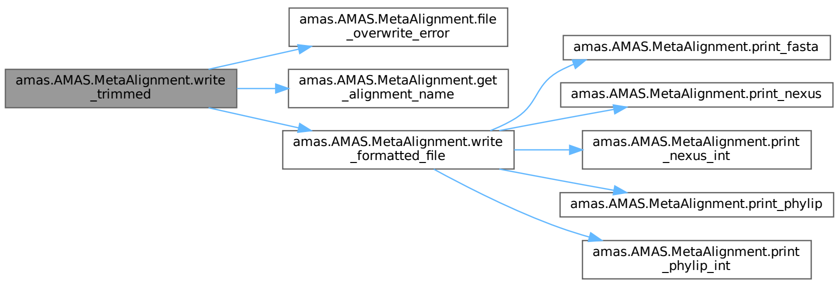
Definition at line 2254 of file AMAS.py.

```
    def write_trimmed(self, index, alignment, file_format, extension):
        # write trimmed alignments
        if self.trim_out:
            out_file_name = self.trim_out
        else:
            prefix = "trimmed_"
            file_name = self.get_alignment_name(index, extension)
            out_file_name = prefix + file_name
        self.file_overwrite_error(out_file_name)
        self.write_formatted_file(file_format, out_file_name, alignment)

```

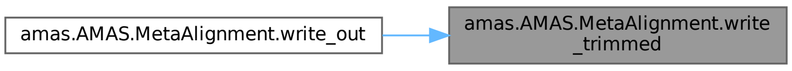
References amas.AMAS.MetaAlignment.file_overwrite_error(), amas.AMAS.MetaAlignment.get_alignment_name(), amas.AMAS.MetaAlignment.trim_out, and amas.AMAS.MetaAlignment.write_formatted_file().

Referenced by amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:


amas.AMAS.MetaAlignment.write_trimmed
amas.AMAS.MetaAlignment.file_overwrite_error
amas.AMAS.MetaAlignment.get_alignment_name
amas.AMAS.MetaAlignment.write_formatted_file
amas.AMAS.MetaAlignment.print_fasta
amas.AMAS.MetaAlignment.print_nexus
amas.AMAS.MetaAlignment.print_nexus_int
amas.AMAS.MetaAlignment.print_phylip
amas.AMAS.MetaAlignment.print_phylip_int

Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write_out
amas.AMAS.MetaAlignment.write_trimmed

7.6.4 Member Data Documentation

7.6.4.1 alignment_objects

`amas.AMAS.MetaAlignment.alignment_objects`

Definition at line 1224 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_name(), amas.AMAS.MetaAlignment.get_alignment_name_no_ext(), amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.get_parsed_alignments(), amas.AMAS.MetaAlignment.get_summaries(), amas.AMAS.MetaAlignment.get_taxon_summaries(), amas.AMAS.MetaAlignment.get_trimmed(), amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.2 by_taxon_summary

```
amas.AMAS.MetaAlignment.by_taxon_summary
```

Definition at line 1178 of file AMAS.py.

7.6.4.3 check_align

```
amas.AMAS.MetaAlignment.check_align
```

Definition at line 1176 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_parsed_alignments().

7.6.4.4 check_taxa

```
amas.AMAS.MetaAlignment.check_taxa
```

Definition at line 1213 of file AMAS.py.

7.6.4.5 codes

```
amas.AMAS.MetaAlignment.codes
```

Definition at line 1424 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.translate_dict().

7.6.4.6 codes_list

```
amas.AMAS.MetaAlignment.codes_list
```

Definition at line 1228 of file AMAS.py.

7.6.4.7 codons

```
amas.AMAS.MetaAlignment.codons
```

Definition at line 1183 of file AMAS.py.

7.6.4.8 command

```
amas.AMAS.MetaAlignment.command
```

Definition at line 1173 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.print_nexus().

7.6.4.9 concat_out

```
amas.AMAS.MetaAlignment.concat_out
```

Definition at line 1174 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_concat().

7.6.4.10 cores

```
amas.AMAS.MetaAlignment.cores
```

Definition at line 1177 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_objects(), amas.AMAS.MetaAlignment.get_summaries(), amas.AMAS.MetaAlignment.get_taxon_summaries(), amas.AMAS.MetaAlignment.get_translated(), and amas.AMAS.MetaAlignment.get_trimmed().

7.6.4.11 data_type

```
amas.AMAS.MetaAlignment.data_type
```

Definition at line 1172 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_object(), amas.AMAS.MetaAlignment.get_summaries(), amas.AMAS.MetaAlignment.get_taxon_summaries(), amas.AMAS.MetaAlignment.print_nexus(), amas.AMAS.MetaAlignment.print_nexus_int(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.12 gencode_NCBI_1

```
amas.AMAS.MetaAlignment.gencode_NCBI_1
```

Definition at line 1251 of file AMAS.py.

7.6.4.13 gencode_NCBI_10

```
amas.AMAS.MetaAlignment.gencode_NCBI_10
```

Definition at line 1364 of file AMAS.py.

7.6.4.14 gencode_NCBI_11

```
amas.AMAS.MetaAlignment.gencode_NCBI_11
```

Definition at line 1368 of file AMAS.py.

7.6.4.15 gencode_NCBI_12

`amas.AMAS.MetaAlignment.gencode_NCBI_12`

Definition at line 1371 of file AMAS.py.

7.6.4.16 gencode_NCBI_13

`amas.AMAS.MetaAlignment.gencode_NCBI_13`

Definition at line 1375 of file AMAS.py.

7.6.4.17 gencode_NCBI_14

`amas.AMAS.MetaAlignment.gencode_NCBI_14`

Definition at line 1382 of file AMAS.py.

7.6.4.18 gencode_NCBI_16

`amas.AMAS.MetaAlignment.gencode_NCBI_16`

Definition at line 1390 of file AMAS.py.

7.6.4.19 gencode_NCBI_2

`amas.AMAS.MetaAlignment.gencode_NCBI_2`

Definition at line 1322 of file AMAS.py.

7.6.4.20 gencode_NCBI_21

`amas.AMAS.MetaAlignment.gencode_NCBI_21`

Definition at line 1394 of file AMAS.py.

7.6.4.21 gencode_NCBI_22

`amas.AMAS.MetaAlignment.gencode_NCBI_22`

Definition at line 1402 of file AMAS.py.

7.6.4.22 gencode_NCBI_23

`amas.AMAS.MetaAlignment.gencode_NCBI_23`

Definition at line 1407 of file AMAS.py.

7.6.4.23 gencode_NCBI_24

`amas.AMAS.MetaAlignment.gencode_NCBI_24`

Definition at line 1411 of file AMAS.py.

7.6.4.24 gencode_NCBI_25

`amas.AMAS.MetaAlignment.gencode_NCBI_25`

Definition at line 1417 of file AMAS.py.

7.6.4.25 gencode_NCBI_26

`amas.AMAS.MetaAlignment.gencode_NCBI_26`

Definition at line 1421 of file AMAS.py.

7.6.4.26 gencode_NCBI_3

`amas.AMAS.MetaAlignment.gencode_NCBI_3`

Definition at line 1329 of file AMAS.py.

7.6.4.27 gencode_NCBI_4

`amas.AMAS.MetaAlignment.gencode_NCBI_4`

Definition at line 1341 of file AMAS.py.

7.6.4.28 gencode_NCBI_5

`amas.AMAS.MetaAlignment.gencode_NCBI_5`

Definition at line 1345 of file AMAS.py.

7.6.4.29 gencode_NCBI_6

`amas.AMAS.MetaAlignment.gencode_NCBI_6`

Definition at line 1352 of file AMAS.py.

7.6.4.30 gencode_NCBI_9

`amas.AMAS.MetaAlignment.gencode_NCBI_9`

Definition at line 1357 of file AMAS.py.

7.6.4.31 genetic_code

```
amas.AMAS.MetaAlignment.genetic_code
```

Definition at line 1217 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.translate_dict(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.32 in_files

```
amas.AMAS.MetaAlignment.in_files
```

Definition at line 1170 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_objects(), amas.AMAS.MetaAlignment.write_metapartitions(), amas.AMAS.MetaAlignment.write_split(), and amas.AMAS.MetaAlignment.write_taxa_summaries().

7.6.4.33 in_format

```
amas.AMAS.MetaAlignment.in_format
```

Definition at line 1171 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_alignment_object(), amas.AMAS.Alignment.get_parsed_aln(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.34 no_loci

```
amas.AMAS.MetaAlignment.no_loci
```

Definition at line 1190 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_out(), and amas.AMAS.MetaAlignment.write_replicate().

7.6.4.35 no_mpan

```
amas.AMAS.MetaAlignment.no_mpan
```

Definition at line 1180 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_concatenated().

7.6.4.36 no_replicates

```
amas.AMAS.MetaAlignment.no_replicates
```

Definition at line 1189 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_out().

7.6.4.37 no_sup_aln_name

```
amas.AMAS.MetaAlignment.no_sup_aln_name
```

Definition at line 1179 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_split().

7.6.4.38 parsed_alignments

```
amas.AMAS.MetaAlignment.parsed_alignments
```

Definition at line 1225 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_partitioned(), amas.AMAS.MetaAlignment.get_replicate(), amas.AMAS.MetaAlignment.get_summaries(), amas.AMAS.MetaAlignment.get_taxon_summaries(), amas.AMAS.MetaAlignment.get_translated(), amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions(), amas.AMAS.MetaAlignment.print_nexus_partitions(), amas.AMAS.MetaAlignment.print_raxml_partitions(), amas.AMAS.MetaAlignment.print_unspecified_partitions(), amas.AMAS.MetaAlignment.remove_taxa(), amas.AMAS.MetaAlignment.write_concat(), amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.39 parsimony_check

```
amas.AMAS.MetaAlignment.parsimony_check
```

Definition at line 1222 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.trim_dict(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.40 prepend_label

```
amas.AMAS.MetaAlignment.prepend_label
```

Definition at line 1203 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_concatenated().

7.6.4.41 reading_frame

```
amas.AMAS.MetaAlignment.reading_frame
```

Definition at line 1216 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.translate_dict(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.42 reduced_file_prefix

```
amas.AMAS.MetaAlignment.reduced_file_prefix
```

Definition at line 1212 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_reduced().

7.6.4.43 remove_empty

```
amas.AMAS.MetaAlignment.remove_empty
```

Definition at line 1194 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_partitioned().

7.6.4.44 species_to_remove

```
amas.AMAS.MetaAlignment.species_to_remove
```

Definition at line 1210 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_reduced().

7.6.4.45 species_to_remove_set

```
amas.AMAS.MetaAlignment.species_to_remove_set
```

Definition at line 1211 of file AMAS.py.

7.6.4.46 split

```
amas.AMAS.MetaAlignment.split
```

Definition at line 1193 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_concatenated(), amas.AMAS.MetaAlignment.print_iqtree_nexus_partitions(), amas.AMAS.MetaAlignment.print_nexus_partitions(), amas.AMAS.MetaAlignment.print_raxml_partitions(), amas.AMAS.MetaAlignment.print_unspecified_partitions(), amas.AMAS.MetaAlignment.write_metapartitions(), amas.AMAS.MetaAlignment.write_out(), and amas.AMAS.MetaAlignment.write_split().

7.6.4.47 trim_fraction

```
amas.AMAS.MetaAlignment.trim_fraction
```

Definition at line 1220 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.trim_dict(), and amas.AMAS.MetaAlignment.write_out().

7.6.4.48 trim_out

```
amas.AMAS.MetaAlignment.trim_out
```

Definition at line 1221 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.write_trimmed().

7.6.4.49 using_metapartitions

```
amas.AMAS.MetaAlignment.using_metapartitions
```

Definition at line 1175 of file AMAS.py.

Referenced by amas.AMAS.MetaAlignment.get_concatenated(), and amas.AMAS.MetaAlignment.write_partitions().

The documentation for this class was generated from the following file:

- amas/AMAS.py

7.7 amas.AMAS.ParsedArgs Class Reference

Public Member Functions

- __init__ (self)
- add_common_args (self, parser)
- trim (self)
- summary (self)
- concat (self)
- convert (self)
- replicate (self)
- split (self)
- metapartitions (self)
- translate (self)
- remove (self)
- get_args_dict (self)

Public Attributes

- args

7.7.1 Detailed Description

Definition at line 50 of file AMAS.py.

7.7.2 Constructor & Destructor Documentation

7.7.2.1 __init__()

```
amas.AMAS.ParsedArgs.__init__ (
                self )
```

Definition at line 52 of file AMAS.py.

```
    def __init__(self):
        parser = argparse.ArgumentParser(
            usage="'AMAS <command> [<args>]

The AMAS commands are:
  concat            Concatenate input alignments.
  convert           Convert to other file format.
  replicate         Create replicate data sets for phylogenetic jackknife.
  split             Split alignment according to a partitions file.
  metapartitions    Runs `split` and concatenates the output.
  summary           Write alignment summary.
  remove            Remove taxa from alignment.
  translate         Translate DNA alignment into protein alignment.
  trim              Remove columns from alignment.


Use AMAS <command> -h for help with arguments of the command of interest
"'
        )

        parser.add_argument(
            "command",
            help="Subcommand to run"
        )

        # parse_args defaults to [1:] for args, but you need to
        # exclude the rest of the args too, or validation will fail
        self.args = parser.parse_args(sys.argv[1:2])
        if not hasattr(self, self.args.command):
            print('Unrecognized command')
            parser.print_help()
            exit(1)
        # use dispatch pattern to invoke method with same name
        getattr(self, self.args.command)()

```

7.7.3 Member Function Documentation

7.7.3.1 add_common_args()

```
amas.AMAS.ParsedArgs.add_common_args (
                self,
                parser )
```

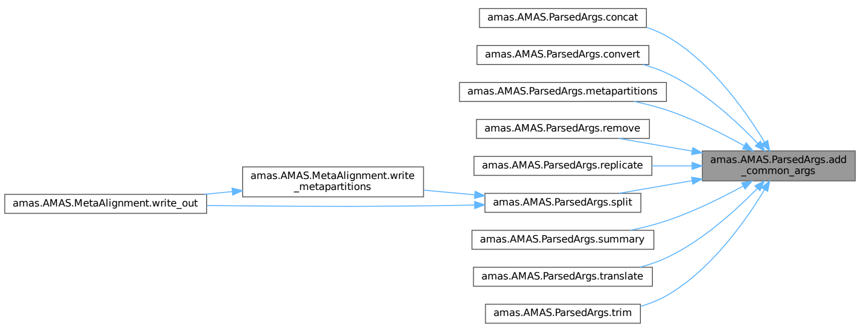
Definition at line 87 of file AMAS.py.

```
    def add_common_args(self, parser):
        # define required arguments for every command
        requiredNamed = parser.add_argument_group('required arguments')
        parser.add_argument(
            "-e",
            "--check-align",
            dest = "check_align",
            action = "store_true",
            default = False,
            help = "Check if input sequences are aligned. Default: no check"
        )
        parser.add_argument(
            # parallelization is used for file parsing and calculating summary stats
            "-c",
            "--cores",
            dest = "cores",
            default = 1,
            help = "Number of cores used. Default: 1"
        )

```

```
00107         requiredNamed.add_argument(
00108             "-i",
00109             "--in-files",
00110             nargs = "+",
00111             type = str,
00112             dest = "in_files",
00113             required = True,
00114             help = """Alignment files to be taken as input.
00115             You can specify multiple files using wildcards (e.g. --in-files *fasta)"""
00116         )
00117         requiredNamed.add_argument(
00118             "-f",
00119             "--in-format",
00120             dest = "in_format",
00121             required = True,
00122             choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
00123             help = "The format of input alignment"
00124         )
00125         requiredNamed.add_argument(
00126             "-d",
00127             "--data-type",
00128             dest = "data_type",
00129             required = True,
00130             choices = ["aa", "dna"],
00131             help = "Type of data"
00132         )
00133 
```

Referenced by amas.AMAS.ParsedArgs.concat(), amas.AMAS.ParsedArgs.convert(), amas.AMAS.ParsedArgs.metapartitions(), amas.AMAS.ParsedArgs.remove(), amas.AMAS.ParsedArgs.replicate(), amas.AMAS.ParsedArgs.split(), amas.AMAS.ParsedArgs.summary(), amas.AMAS.ParsedArgs.translate(), and amas.AMAS.ParsedArgs.trim().

Here is the caller graph for this function:


amas.AMAS.ParsedArgs.concat
amas.AMAS.ParsedArgs.convert
amas.AMAS.ParsedArgs.metapartitions
amas.AMAS.ParsedArgs.remove
amas.AMAS.ParsedArgs.replicate
amas.AMAS.ParsedArgs.add
_common_args
amas.AMAS.MetaAlignment.write
_metapartitions
amas.AMAS.MetaAlignment.write_out
amas.AMAS.ParsedArgs.split
amas.AMAS.ParsedArgs.summary
amas.AMAS.ParsedArgs.translate
amas.AMAS.ParsedArgs.trim

7.7.3.2 concat()

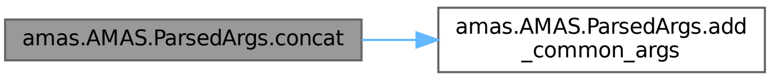
```
amas.AMAS.ParsedArgs.concat (
                self )
```

Definition at line 201 of file AMAS.py.

```
00201     def concat(self):
00202         # concat command
00203         parser = argparse.ArgumentParser(
00204             description="Concatenate input alignments"
00205         )
00206         parser.add_argument(
00207             "-p",
00208             "--concat-part",
00209             dest = "concat_part",
00210             default = "partitions.txt",
00211             help = "File name for the concatenated alignment partitions. Default: 'partitions.txt'"
00212         )
00213         parser.add_argument(
00214             "-t",
            "--concat-out",
            dest = "concat_out",
            default = "concatenated.out",
            help = "File name for the concatenated alignment. Default: 'concatenated.out'"
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-y",
            "--part-format",
            dest = "part_format",
            choices = ["nexus", "iqtree-nexus", "raxml", "unspecified"],
            default = "unspecified",
            help = "Format of the partitions file. Default: 'unspecified'"
        )
        parser.add_argument(
            "-n",
            "--codons",
            dest = "codons",
            choices = ["none", "12", "123"],
            default = "none",
            help = "Use codon partitioning for 1st and 2nd or all three positions. Default: Don't use"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:



7.7.3.3 convert()

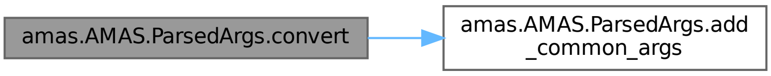
```
amas.AMAS.ParsedArgs.convert (
                self )
```

Definition at line 249 of file AMAS.py.

```
    def convert(self):
        # convert command
        parser = argparse.ArgumentParser(
            description="Convert to other file format",
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:


amas.AMAS.ParsedArgs.convert
amas.AMAS.ParsedArgs.add_common_args

7.7.3.4 get_args_dict()

```
amas.AMAS.ParsedArgs.get_args_dict (
                self )
```

Definition at line 508 of file AMAS.py.

```
    def get_args_dict(self):
        # store arguments in a dictionary
        command = self.args.__dict__
        arguments = getattr(self, self.args.command)().__dict__
        argument_dictionary = command.copy()
        argument_dictionary.update(arguments)

        return argument_dictionary


```

References amas.AMAS.ParsedArgs.args.

7.7.3.5 metapartitions()

```
amas.AMAS.ParsedArgs.metapartitions (
                self )
```

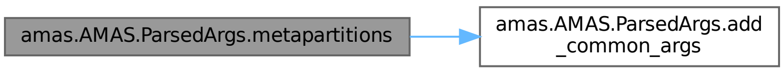
Definition at line 334 of file AMAS.py.

```
    def metapartitions(self):
        # metapartitions command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawTextHelpFormatter,
            description="'Split alignment according to a partition file, then concatenate the
      output."'
            "'\n\nuse case:\n"'
            "'    Some utilities cannot parse partition definitions containing strides (\\) and/or
      discontinuous ranges.\n"'
            "'    In such case, running `split` + `concat` in separate passes can convert a
      corresponding (super)alignment it into an\n"'
            "'    equivalent compatible form with contiguous (meta)partitions; this may also require
      renaming metapartiton alignments\n"'
            "'    and partition file entries in order to remove tags applied by each respective
      operation.\n\n"'
            "'    `metapartitions` combines these steps into one command, with the options `--prepend`
      and `--no-mpan`\n"'
            "'    providing additional control over the collated (meta)partition names (see their
      respective help entries).\n\n"'
            "'    Note: in this mode, the format of the input (super)alignment file determines that of
      all outputs (-u|--out-format is disabled)!\n\n"'
        )
        parser.add_argument(
            "-p",
            "--concat-part",
            dest = "concat_part",
            default = "metapartitions.txt",
            help = "Partition file(name) for the final concatenated alignment of metapartitions.
      Default: 'metapartitions.txt'"
```

```
        )
        parser.add_argument(
            "-t",
            "--concat-out",
            dest = "concat_out",
            default = "concatenated-meta.out",
            help = "File name for the concatenated alignment of metapartitions. Default: 'concatenated-meta.out'"
        )
        parser.add_argument(
            "-y",
            "--part-format",
            dest = "part_format",
            choices = ["nexus", "iqtree-nexus", "raxml", "unspecified"],
            default = "unspecified",
            help = "Partitions file format for the final concatenated alignment of metapartitions. Default: 'unspecified'"
        )
        parser.add_argument(
            "-l",
            "--split-by",
            dest = "split_by",
            help = "Partition file(name) to be used for splitting the initial concatenated alignment.",
            required = True
        )
        parser.add_argument(
            "-j",
            "--remove-empty",
            dest = "remove_empty",
            action = "store_true",
            default = False,
            help = "Remove taxa with sequences composed of only undetermined characters? Default: Don't remove"
        )
        parser.add_argument(
            "--no-san",
            dest = "no_sup_aln_name",
            action = "store_true",
            default = False,
            help = "'Don't prepend the input (super)alignment filename to the (meta)partition-alignment filenames output by `split`"'
        )
        parser.add_argument(
            "--prepend",
            dest = "prepend_label",
            default = None,
            help = "'Prepend <string> to the partition counter in partition file, e.g."'
            "'\n            --prepend <string>:  <string>_p001_metapartition_alignment_name = 1-1200 ..."'
            "'\n                 Default (None):           p001_metapartition_alignment_name = 1-1200 ..."'
            "'\n--no-mpan + --prepend <string>:  <string>_p001 = 1-1200 ..."'
        )
        parser.add_argument(
            "--no-mpan",
            dest = "no_mpan",
            action = "store_true",
            default = False,
            help = "'Omits (meta)partition alignment names when printing partition file, e.g."'
            "'\n                      --no-mpan:          p001 = 1-1200 ..."'
            "'\n                Default (False):          p001_metapartition_alignment_name = 1-1200 ..."'
            "'\n--prepend <string> + --no-mpan: <string>_p001 = 1-1200 ..."'
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:


amas.AMAS.ParsedArgs.metapartitions
amas.AMAS.ParsedArgs.add_common_args

7.7.3.6 remove()

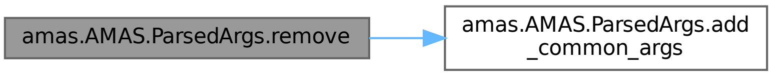
```
amas.AMAS.ParsedArgs.remove (
              self )
```

Definition at line 474 of file AMAS.py.

```
    def remove(self):
        # remove taxa command
        parser = argparse.ArgumentParser(
            description="Remove taxa from alignment",
        )
        parser.add_argument(
            "-x",
            "--taxa-to-remove",
            nargs = "+",
            type = str,
            dest = "taxa_to_remove",
            help = "Taxon/sequence names to be removed.",
            required = True
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-g",
            "--out-prefix",
            dest = "out_prefix",
            default = "reduced_",
            help = "File name prefix for the concatenated alignment. Default: 'reduced_'"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args
```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:


amas.AMAS.ParsedArgs.remove
amas.AMAS.ParsedArgs.add_common_args

7.7.3.7 replicate()

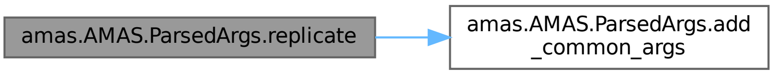
```
amas.AMAS.ParsedArgs.replicate (
              self )
```

Definition at line 267 of file AMAS.py.

```
    def replicate(self):
        # replicate command
        parser = argparse.ArgumentParser(
            description="Create replicate datasets for phylogenetic jackknife",
        )
        parser.add_argument(
            "-r",
            "--rep-aln",
            nargs = 2,
            type = int,
            dest = "replicate_args",
            help = "Create replicate data sets for phylogenetic jackknife [replicates, no alignments
      for each replicate]",
            required = True
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:


amas.AMAS.ParsedArgs.replicate
amas.AMAS.ParsedArgs.add_common_args

7.7.3.8 split()

```
amas.AMAS.ParsedArgs.split (
              self )
```

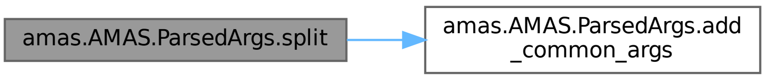
Definition at line 294 of file AMAS.py.

```
    def split(self):
        # split command
        parser = argparse.ArgumentParser(
            description="Split alignment according to a partitions file",
        )
        parser.add_argument(
            "-l",
            "--split-by",
            dest = "split_by",
            help = "File name for partitions to be used for alignment splitting.",
            required = True
        )
        parser.add_argument(
            "-j",
            "--remove-empty",
            dest = "remove_empty",
            action = "store_true",
            default = False,
            help = "Remove taxa with sequences composed of only undetermined characters? Default:
      Don't remove"
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "--no-san",
            dest = "no_sup_aln_name",
            action = "store_true",
            default = False,
            help = "'Don't prepend the input (super)alignment filename to the partition-alignment
filenames output by `split`"'
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

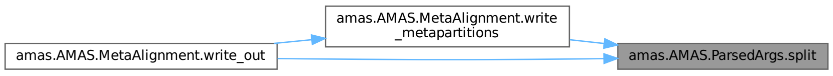
References amas.AMAS.ParsedArgs.add_common_args().

Referenced by amas.AMAS.MetaAlignment.write_metapartitions(), and amas.AMAS.MetaAlignment.write_out().

Here is the call graph for this function:



Here is the caller graph for this function:


amas.AMAS.MetaAlignment.write
_metapartitions
amas.AMAS.MetaAlignment.write_out
amas.AMAS.ParsedArgs.split

7.7.3.9 summary()

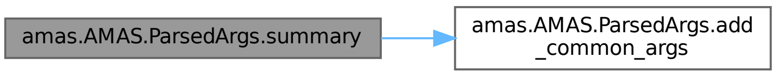
```
amas.AMAS.ParsedArgs.summary (
                self )
```

Definition at line 176 of file AMAS.py.

```
    def summary(self):
        # summary command
        parser = argparse.ArgumentParser(
            description="Write alignment summary",
        )
        parser.add_argument(
            "-o",
            "--summary-out",
            dest = "summary_out",
            default = "summary.txt",
            help = "File name for the alignment summary. Default: 'summary.txt'"
        )
        parser.add_argument(
            "-s",
            "--by-taxon",
            dest = "by_taxon_summary",
            action = "store_true",
            default = False,
            help = "In addition to alignment summary, write by sequence/taxon summaries. Default:
Don't write"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:



7.7.3.10 translate()

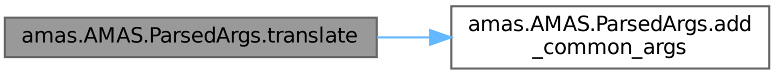
```
amas.AMAS.ParsedArgs.translate (
                self )
```

Definition at line 416 of file AMAS.py.

```
    def translate(self):
        # translate command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawTextHelpFormatter,
            description="Translate a protein-coding DNA alignment into amino acids"
        )
        parser.add_argument(
            "-b",
            "--code",
            type = int,
            dest = "genetic_code",
            choices = [1, 2, 3, 4, 5, 6, 9, 10, 11, 12, 13, 14, 16, 21, 22, 23, 24, 25, 26],
            default = 1,
            help = "'\nNCBI genetic code to use (Default: 1):"'
"'
   1. The Standard Code
   2. The Vertebrate Mitochondrial Code
   3. The Yeast Mitochondrial Code
   4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code
   5. The Invertebrate Mitochondrial Code
   6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
   9. The Echinoderm and Flatworm Mitochondrial Code
  10. The Euplotid Nuclear Code
  11. The Bacterial, Archaeal and Plant Plastid Code
  12. The Alternative Yeast Nuclear Code
  13. The Ascidian Mitochondrial Code
  14. The Alternative Flatworm Mitochondrial Code
  16. Chlorophycean Mitochondrial Code
  21. Trematode Mitochondrial Code
  22. Scenedesmus obliquus Mitochondrial Code
  23. Thraustochytrium Mitochondrial Code
  24. Pterobranchia Mitochondrial Code
  25. Candidate Division SR1 and Gracilibacteria Code
  26. Pachysolen tannophilus Nuclear Code\n
"'
        )
        parser.add_argument(
            "-k",
            "--reading-frame",
            type = int,
            dest = "reading_frame",
            choices = [1, 2, 3],
            default = 1,
            help = "Number specifying reading frame; i.e. '2' means codons start at the second
character of the alignment. Default: 1",
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:



7.7.3.11 trim()

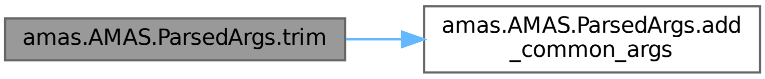
```
amas.AMAS.ParsedArgs.trim (
               self )
```

Definition at line 134 of file AMAS.py.

```
    def trim(self):
        # trim command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawDescriptionHelpFormatter,
            description="'Trim alignment by occupancy. Optionally removes sites that are not parsimony
informative."'
            "'\nCAUTION: when running on amino acids stop codons marked with * will be treated as
missing data!"'
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-o",
            "--trim-out",
            dest = "trim_out",
            help = "File name for the trimmed alignment when providing a single file as input."
        )
        parser.add_argument(
            "-t",
            "--trim-fraction",
            type = proportion,
            dest = "trim_fraction",
            default = 0.6,
            help = "Columns in the alignments with occupancy lower than this value will be removed.
Default: 0.6"
        )
        parser.add_argument(
            "-p",
            "--retain-only-parsimony-sites",
            dest = "parsimony_check",
            action = "store_true",
            default = False,
            help = "Only write parsimony informative columns in trimmed alignment Default: write all
columns"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

```

References amas.AMAS.ParsedArgs.add_common_args().

Here is the call graph for this function:



7.7.4 Member Data Documentation

7.7.4.1 args

```
amas.AMAS.ParsedArgs.args
```

Definition at line 79 of file AMAS.py.

Referenced by amas.AMAS.ParsedArgs.get_args_dict().

The documentation for this class was generated from the following file:

- amas/AMAS.py

Chapter 8

File Documentation

8.1 amas/__init__.py File Reference

Namespaces

- namespace amas

Variables

- str amas.__author__ = 'Marek Borowiec'
- str amas.__email__ = 'petiolus@gmail.com'
- str amas.__version__ = '1.02'
- amas.__all__ = dir()

8.2 __init__.py

Go to the documentation of this file.

```
# -*- coding: utf-8 -*-

__author__ = 'Marek Borowiec'
__email__ = 'petiolus@gmail.com'
__version__ = '1.02'
__all__ = dir()
```

8.3 amas/AMAS.py File Reference

Classes

- class amas.AMAS.ParsedArgs
- class amas.AMAS.FileHandler
- class amas.AMAS.FileParser
- class amas.AMAS.Alignment
- class amas.AMAS.AminoAcidAlignment
- class amas.AMAS.DNAAlignment
- class amas.AMAS.MetaAlignment

Namespaces

- namespace amas
- namespace amas.AMAS

Functions

- amas.AMAS.proportion (x)
- amas.AMAS.main ()
- amas.AMAS.run ()

8.4 AMAS.py

Go to the documentation of this file.

```
#! /usr/bin/env python3
# -*- coding: utf-8 -*-
# vim:fileencoding=utf-8

#   Program to calculate various statistics on a multiple sequence alignment
#   and allow efficient manipulation of phylogenomic data sets

#   Copyright (C) 2015 Marek Borowiec

#   This program is free software: you can redistribute it and/or modify
#   it under the terms of the GNU General Public License as published by
#   the Free Software Foundation, either version 3 of the License, or
#   (at your option) any later version.

#   This program is distributed in the hope that it will be useful,
#   but WITHOUT ANY WARRANTY; without even the implied warranty of
#   MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.  See the
#   GNU General Public License for more details.

#   You should have received a copy of the GNU General Public License
#   along with this program.  If not, see <http://www.gnu.org/licenses/>.

"""
This stand-alone program allows manipulations of multiple sequence
alignments. It supports sequential FASTA, PHYLIP, NEXUS, and interleaved PHYLIP
and NEXUS formats for DNA and aino acid sequences. It can print summary statistics,
convert among formats, and concatenate alignments.

Current statistics include the number of taxa, alignment length, total number
of matrix cells, overall number of undetermined characters, percent of missing
data, AT and GC contents (for DNA alignments), number and proportion of
variable sites, number and proportion of parsimony informative sites,
and counts of all characters present in the relevant (nucleotide or amino acid) alphabet.
"""


import argparse, multiprocessing as mp, re, sys
from random import sample
from os import path, remove
from collections import defaultdict, Counter
from itertools import compress

def proportion(x):
    # needed to prevent input of invalid floats in trim mode
    x = float(x)
    if x < 0.0 or x > 1.0:
        raise argparse.ArgumentTypeError("%r not in range [0.0, 1.0]" % (x,))
    return x

class ParsedArgs:

    def __init__(self):
        parser = argparse.ArgumentParser(
            usage="'AMAS <command> [<args>]

The AMAS commands are:
  concat            Concatenate input alignments.
  convert           Convert to other file format.
  replicate         Create replicate data sets for phylogenetic jackknife.
  split             Split alignment according to a partitions file.
  metapartitions    Runs `split` and concatenates the output.
  summary           Write alignment summary.
  remove            Remove taxa from alignment.
  translate         Translate DNA alignment into protein alignment.
  trim              Remove columns from alignment.


Use AMAS <command> -h for help with arguments of the command of interest
"'
        )

        parser.add_argument(
            "command",
            help="Subcommand to run"
        )

        # parse_args defaults to [1:] for args, but you need to
        # exclude the rest of the args too, or validation will fail
        self.args = parser.parse_args(sys.argv[1:2])
        if not hasattr(self, self.args.command):
            print('Unrecognized command')
            parser.print_help()
            exit(1)
        # use dispatch pattern to invoke method with same name
        getattr(self, self.args.command)()

    def add_common_args(self, parser):
        # define required arguments for every command
        requiredNamed = parser.add_argument_group('required arguments')
        parser.add_argument(
            "-e",
            "--check-align",
            dest = "check_align",
            action = "store_true",
            default = False,
            help = "Check if input sequences are aligned. Default: no check"
        )
        parser.add_argument(
            # parallelization is used for file parsing and calculating summary stats
            "-c",
            "--cores",
            dest = "cores",
            default = 1,
            help = "Number of cores used. Default: 1"
        )

        requiredNamed.add_argument(
            "-i",
            "--in-files",
            nargs = "+",
            type = str,
            dest = "in_files",
            required = True,
            help = """Alignment files to be taken as input.
            You can specify multiple files using wildcards (e.g. --in-files *fasta)"""
        )
        requiredNamed.add_argument(
            "-f",
            "--in-format",
            dest = "in_format",
            required = True,
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            help = "The format of input alignment"
        )
        requiredNamed.add_argument(
            "-d",
            "--data-type",
            dest = "data_type",
            required = True,
            choices = ["aa", "dna"],
            help = "Type of data"
        )

    def trim(self):
        # trim command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawDescriptionHelpFormatter,
            description="'Trim alignment by occupancy. Optionally removes sites that are not parsimony
informative."'
            "'\nCAUTION: when running on amino acids stop codons marked with * will be treated as
missing data!"'
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-o",
            "--trim-out",
            dest = "trim_out",
            help = "File name for the trimmed alignment when providing a single file as input."
        )
        parser.add_argument(
            "-t",
            "--trim-fraction",
            type = proportion,
            dest = "trim_fraction",
            default = 0.6,
            help = "Columns in the alignments with occupancy lower than this value will be removed.
Default: 0.6"
        )
        parser.add_argument(
            "-p",
            "--retain-only-parsimony-sites",
            dest = "parsimony_check",
            action = "store_true",
            default = False,
            help = "Only write parsimony informative columns in trimmed alignment Default: write all
columns"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def summary(self):
       # summary command
        parser = argparse.ArgumentParser(
            description="Write alignment summary",
        )
        parser.add_argument(
            "-o",
            "--summary-out",
            dest = "summary_out",
            default = "summary.txt",
            help = "File name for the alignment summary. Default: 'summary.txt'"
        )
        parser.add_argument(
            "-s",
            "--by-taxon",
            dest = "by_taxon_summary",
            action = "store_true",
            default = False,
            help = "In addition to alignment summary, write by sequence/taxon summaries. Default:
Don't write"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def concat(self):
        # concat command
        parser = argparse.ArgumentParser(
            description="Concatenate input alignments"
        )
        parser.add_argument(
            "-p",
            "--concat-part",
            dest = "concat_part",
            default = "partitions.txt",
            help = "File name for the concatenated alignment partitions. Default: 'partitions.txt'"
        )
        parser.add_argument(
            "-t",
            "--concat-out",
            dest = "concat_out",
            default = "concatenated.out",
            help = "File name for the concatenated alignment. Default: 'concatenated.out'"
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-y",
            "--part-format",
            dest = "part_format",
            choices = ["nexus", "iqtree-nexus", "raxml", "unspecified"],
            default = "unspecified",
            help = "Format of the partitions file. Default: 'unspecified'"
        )
        parser.add_argument(
            "-n",
            "--codons",
            dest = "codons",
            choices = ["none", "12", "123"],
            default = "none",
            help = "Use codon partitioning for 1st and 2nd or all three positions. Default: Don't use"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def convert(self):
        # convert command
        parser = argparse.ArgumentParser(
            description="Convert to other file format",
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def replicate(self):
        # replicate command
        parser = argparse.ArgumentParser(
            description="Create replicate datasets for phylogenetic jackknife",
        )
        parser.add_argument(
            "-r",
            "--rep-aln",
            nargs = 2,
            type = int,
            dest = "replicate_args",
            help = "Create replicate data sets for phylogenetic jackknife [replicates, no alignments
     for each replicate]",
            required = True
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def split(self):
        # split command
        parser = argparse.ArgumentParser(
            description="Split alignment according to a partitions file",
        )
        parser.add_argument(
            "-l",
            "--split-by",
            dest = "split_by",
            help = "File name for partitions to be used for alignment splitting.",
            required = True
        )
        parser.add_argument(
            "-j",
            "--remove-empty",
            dest = "remove_empty",
            action = "store_true",
            default = False,
            help = "Remove taxa with sequences composed of only undetermined characters? Default:
     Don't remove"
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "--no-san",
            dest = "no_sup_aln_name",
            action = "store_true",
            default = False,
            help = "'Don't prepend the input (super)alignment filename to the partition-alignment filenames output by `split`"'
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def metapartitions(self):
        # metapartitions command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawTextHelpFormatter,
            description="'Split alignment according to a partition file, then concatenate the output."'
            "'\n\nuse case:\n"'
            "'    Some utilities cannot parse partition definitions containing strides (\\) and/or discontinuous ranges.\n"'
            "'    In such case, running `split` + `concat` in separate passes can convert a corresponding (super)alignment it into an\n"'
            "'    equivalent compatible form with contiguous (meta)partitions; this may also require renaming metapartiton alignments\n"'
            "'    and partition file entries in order to remove tags applied by each respective operation.\n\n"'
            "'    `metapartitions` combines these steps into one command, with the options `--prepend` and `--no-mpan`\n"'
            "'    providing additional control over the collated (meta)partition names (see their respective help entries).\n\n"'
            "'    Note: in this mode, the format of the input (super)alignment file determines that of all outputs (-u|--out-format is disabled)!\n\n"'
        )
        parser.add_argument(
            "-p",
            "--concat-part",
            dest = "concat_part",
            default = "metapartitions.txt",
            help = "Partition file(name) for the final concatenated alignment of metapartitions. Default: 'metapartitions.txt'"
        )
        parser.add_argument(
            "-t",
            "--concat-out",
            dest = "concat_out",
            default = "concatenated-meta.out",
            help = "File name for the concatenated alignment of metapartitions. Default: 'concatenated-meta.out'"
        )
        parser.add_argument(
            "-y",
            "--part-format",
            dest = "part_format",
            choices = ["nexus", "iqtree-nexus", "raxml", "unspecified"],
            default = "unspecified",
            help = "Partitions file format for the final concatenated alignment of metapartitions. Default: 'unspecified'"
        )
        parser.add_argument(
            "-l",
            "--split-by",
            dest = "split_by",
            help = "Partition file(name) to be used for splitting the initial concatenated alignment.",
            required = True
        )
        parser.add_argument(
            "-j",
            "--remove-empty",
            dest = "remove_empty",
            action = "store_true",
            default = False,
            help = "Remove taxa with sequences composed of only undetermined characters? Default: Don't remove"
        )
        parser.add_argument(
            "--no-san",
            dest = "no_sup_aln_name",
            action = "store_true",
            default = False,
            help = ”’Don’t prepend the input (super)alignment filename to the (meta)partition-alignment filenames output by `split`”’
        )
        parser.add_argument(
            "--prepend",
            dest = "prepend_label",
            default = None,
            help = ”’Prepend <string> to the partition counter in partition file, e.g.”’
            ”’\n            --prepend <string>:  <string>_p001_metapartition_alignment_name = 1-1200 ...”’
            ”’\n                Default (None):           p001_metapartition_alignment_name = 1-1200 ...”’
            ”’\n--no-mpan + --prepend <string>:  <string>_p001 = 1-1200 ...”’
        )
        parser.add_argument(
            "--no-mpan",
            dest = "no_mpan",
            action = "store_true",
            default = False,
            help = ”’Omits (meta)partition alignment names when printing partition file, e.g.”’
            ”’\n                     --no-mpan:          p001 = 1-1200 ...”’
            ”’\n               Default (False):          p001_metapartition_alignment_name = 1-1200 ...”’
            ”’\n--prepend <string> + --no-mpan: <string>_p001 = 1-1200 ...”’
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def translate(self):
        # translate command
        parser = argparse.ArgumentParser(
            formatter_class=argparse.RawTextHelpFormatter,
            description="Translate a protein-coding DNA alignment into amino acids"
        )
        parser.add_argument(
            "-b",
            "--code",
            type = int,
            dest = "genetic_code",
            choices = [1, 2, 3, 4, 5, 6, 9, 10, 11, 12, 13, 14, 16, 21, 22, 23, 24, 25, 26],
            default = 1,
            help = ”’\nNCBI genetic code to use (Default: 1):”’
”’
   1. The Standard Code
   2. The Vertebrate Mitochondrial Code
   3. The Yeast Mitochondrial Code
   4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code
   5. The Invertebrate Mitochondrial Code
   6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
   9. The Echinoderm and Flatworm Mitochondrial Code
  10. The Euplotid Nuclear Code
  11. The Bacterial, Archaeal and Plant Plastid Code
  12. The Alternative Yeast Nuclear Code
  13. The Ascidian Mitochondrial Code
  14. The Alternative Flatworm Mitochondrial Code
  16. Chlorophycean Mitochondrial Code
  21. Trematode Mitochondrial Code
  22. Scenedesmus obliquus Mitochondrial Code
  23. Thraustochytrium Mitochondrial Code
  24. Pterobranchia Mitochondrial Code
  25. Candidate Division SR1 and Gracilibacteria Code
  26. Pachysolen tannophilus Nuclear Code\n
”’
        )
        parser.add_argument(
            "-k",
            "--reading-frame",
            type = int,
            dest = "reading_frame",
            choices = [1, 2, 3],
            default = 1,
            help = "Number specifying reading frame; i.e. ’2’ means codons start at the second character of the alignment. Default: 1",
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def remove(self):
        # remove taxa command
        parser = argparse.ArgumentParser(
            description="Remove taxa from alignment",
        )
        parser.add_argument(
            "-x",
            "--taxa-to-remove",
            nargs = "+",
            type = str,
            dest = "taxa_to_remove",
            help = "Taxon/sequence names to be removed.",
            required = True
        )
        parser.add_argument(
            "-u",
            "--out-format",
            dest = "out_format",
            choices = ["fasta", "phylip", "nexus", "phylip-int", "nexus-int"],
            default = "fasta",
            help = "File format for the output alignment. Default: fasta"
        )
        parser.add_argument(
            "-g",
            "--out-prefix",
            dest = "out_prefix",
            default = "reduced_",
            help = "File name prefix for the concatenated alignment. Default: 'reduced_'"
        )
        # add shared arguments
        self.add_common_args(parser)
        args = parser.parse_args(sys.argv[2:])
        return args

    def get_args_dict(self):
        # store arguments in a dictionary
        command = self.args.__dict__
        arguments = getattr(self, self.args.command)().__dict__
        argument_dictionary = command.copy()
        argument_dictionary.update(arguments)

        return argument_dictionary


class FileHandler:
    """Define file handle that closes when out of scope"""

    def __init__(self, file_name):
        self.file_name = file_name

    def __enter__(self):
        try:
            self.in_file = open(self.file_name, "r", encoding="utf-8")
        except FileNotFoundError:
            print("ERROR: File '" + self.file_name + "' not found.")
            sys.exit()
        return self.in_file

    def __exit__(self, *args):
        self.in_file.close()

    def get_file_name(self):
        return self.file_name

class FileParser:
    """Parse file contents and return sequences and sequence names"""

    def __init__(self, in_file):
        self.in_file = in_file
        with FileHandler(in_file) as handle:
            self.in_file_lines = handle.read().rstrip("\r\n")

    def fasta_parse(self):
        # use regex to parse names and sequences in sequential fasta files
        matches = re.finditer(
            r"^>(.*[^$])([^>]*)",
            self.in_file_lines, re.MULTILINE
        )
        records = {}

        for match in matches:
            name_match = match.group(1).replace("\n", "")
            seq_match = match.group(2).replace("\n", "").upper()
            seq_match = self.translate_ambiguous(seq_match)
            records[name_match] = seq_match

        return records

    def phylip_parse(self):
        # use regex to parse names and sequences in sequential phylip files
        matches = re.finditer(
            r"^(\s+)?(\S+)\s+([A-Za-z*?.{}-]+)",
            self.in_file_lines, re.MULTILINE
        )

        records = {}

        for match in matches:
            name_match = match.group(2).replace("\n", "")
            seq_match = match.group(3).replace("\n", "").upper()
            seq_match = self.translate_ambiguous(seq_match)
            records[name_match] = seq_match

        return records

    def phylip_interleaved_parse(self):
    # use regex to parse names and sequences in interleaved phylip files
        tax_chars_matches = re.finditer(
            r"^(\s+)?([0-9]+)[ \t]+([0-9]+)",
            self.in_file_lines, re.MULTILINE
        )
        name_matches = re.finditer(
            r"^(\s+)?(\S+)[ \t]+[A-Za-z*?.{}-]+",
            self.in_file_lines, re.MULTILINE
        )
        seq_matches = re.finditer(
            r"(^(\s+)?\S+[ \t]+|^)([A-Za-z*?.{}-]+)$",
            self.in_file_lines, re.MULTILINE
        )
        # get number of taxa and chars
        for match in tax_chars_matches:
            tax_match = match.group(2)
            chars_match = match.group(3)

        # initiate lists for taxa names and sequence strings on separate lines
        taxa = []
        sequences = []
        # initiate a dictionary for the name:sequence records
        records = {}
        # initiate a counter to keep track of sequences strung together
        # from separate lines
        counter = 0

        for match in name_matches:
            name_match = match.group(2).replace("\n", "")
            taxa.append(name_match)

        for match in seq_matches:
            seq_match = match.group(3).replace("\n", "").upper()
            seq_match = self.translate_ambiguous(seq_match)
            sequences.append(seq_match)
        # try parsing PHYLUCE-style interleaved phylip
        if len(taxa) != int(tax_match):
            taxa = []
            sequences = []
            matches = re.finditer(
                r"(^(\s+)?(\S+)( ){2,}|^\s+)([ A-Za-z*?.{}-]+)",
                self.in_file_lines, re.MULTILINE
            )

            for match in matches:
                try:
                    name_match = match.group(3).replace("\n", "")
                    taxa.append(name_match)
                except AttributeError:
                    pass
                seq_match = match.group(5).replace("\n", "").upper()
                seq_match = "".join(seq_match.split())
                seq_match = self.translate_ambiguous(seq_match)
                sequences.append(seq_match)

        for taxon_no in range(len(taxa)):
            sequence = ""
            for index in range(counter,len(sequences),len(taxa)):
                sequence += sequences[index]

            records[taxa[taxon_no]] = sequence
            counter += 1

        return records

    def nexus_parse(self):
        # use regex to parse names and sequences in sequential nexus files
        # find the matrix block
        matches = re.finditer(
            r"(\s+)?(MATRIX\n|matrix\n|MATRIX\r\n|matrix\r\n)(.*?;)",
            self.in_file_lines, re.DOTALL
        )

        records = {}
        # get names and sequences from the matrix block

        for match in matches:
            matrix_match = match.group(3)
            seq_matches = re.finditer(
                r"^(\s+)?[’]?(\S+\s\S+|\S+)[’]?\s+([A-Za-z*?.{}-]+)($|\s+\[[0-9]+\]$)",
                matrix_match, re.MULTILINE
            )

            for match in seq_matches:
                name_match = match.group(2).replace("\n", "")
                seq_match = match.group(3).replace("\n", "").upper()
                seq_match = self.translate_ambiguous(seq_match)
                records[name_match] = seq_match

        return records

    def nexus_interleaved_parse(self):
        # use regex to parse names and sequences in sequential nexus files
        # find the matrix block
        matches = re.finditer(
            r"(\s+)?(MATRIX\n|matrix\n|MATRIX\r\n|matrix\r\n)(.*?;)",
            self.in_file_lines, re.DOTALL
        )
        # initiate lists for taxa names and sequence strings on separate lines
        taxa = []
        sequences = []
        # initiate a dictionary for the name:sequence records
        records = {}

        for match in matches:
            matrix_match = match.group(3)
            # get names and sequences from the matrix block
            seq_matches = re.finditer(
                r"^(\s+)?[’]?(\S+\s\S+|\S+)[’]?\s+([A-Za-z*?.{}-]+)($|\s+\[[0-9]+\]$)",
                matrix_match, re.MULTILINE
            )

            for match in seq_matches:
                name_match = match.group(2)
                if name_match not in taxa:
                    taxa.append(name_match)
                seq_match = match.group(3)

                sequences.append(seq_match)

        # initiate a counter to keep track of sequences strung together
        # from separate lines
        counter = 0

        for taxon_no in range(len(taxa)):

            full_length_sequence = "".join([sequences[index] for index in range(counter,len(sequences),len(taxa))])
            records[taxa[taxon_no]] = self.translate_ambiguous(full_length_sequence).replace("\n", "").upper()
            counter += 1

        return records

    def translate_ambiguous(self, seq):
        # translate ambiguous characters from curly bracket format
        # to single letter format
        # also remove spaces from sequences
        seq = seq.replace("{GT}", "K")
        seq = seq.replace("{AC}", "M")
        seq = seq.replace("{AG}", "R")
        seq = seq.replace("{CT}", "Y")
        seq = seq.replace("{CG}", "S")
        seq = seq.replace("{AT}", "W")
        seq = seq.replace("{CGT}", "B")
        seq = seq.replace("{ACG}", "V")
        seq = seq.replace("{ACT}", "H")
        seq = seq.replace("{AGT}", "D")
        seq = seq.replace("{GATC}", "N")
        seq = seq.replace(" ", "")

        return seq

    def partitions_parse(self):
        # parse partitions file using regex
        # original: `matches = re.finditer(r"^(\s+)?([^ =]+)[ =]+([\\0-9, -]+)", self.in_file_lines, re.MULTILINE)`
        # new version: more permissive -> handles PartionFinder/RAxML/(IQ-TREE 2)best_scheme.nex format partition files
        matches = re.finditer(
            r"""^[ \t]*                                         # start line w/ 0+ whitespaces/tabs
                (
                 (?P<nexus>charset[ ]+)                         # <1>: best_scheme.nex partition directive
                 |
                 (?P<raxml>[A-Za-z0-9_+.\{\}\/-]+,[ \t]+)       # <2>: RAxML(-NG) model(+pars)
                )?
                (?P<partition_name>[A-Za-z0-9_&.-]+)            # partition name
                [ ]*=[ ]*                                       # whitespace-(un)padded '='
                (?P<numbers>[\\0-9, -]+)                        # position ranges w/stride (multiple intervals)
                (?P<nexus_term>[ ]*[;])?                        # whitespace-(un)prepended ';' (nexus terminator)
            """,
            self.in_file_lines,
            re.MULTILINE | re.VERBOSE
        )

        # initiate list to store dictionaries with lists
        # of slice positions as values
        partitions = []
        add_to_partitions = partitions.append

        for match in matches:
            # initiate dictionary of partition name as key
            dict_of_dicts = {}
            # and list of dictionaries with slice positions
            list_of_dicts = []
            add_to_list_of_dicts = list_of_dicts.append
            # get parition name and numbers from parsed partition strings
            partition_name = match.group('partition_name')
            numbers = match.group('numbers')
            # remove any whitespace padding '-' (to be consistent with partition-writing format)
            numbers = re.sub(r"[ ]*-[ ]*", "-", numbers)
            # find all numbers that will be used to parse positions
            positions = re.findall(r"([^ ,]+)", numbers)

            for position in positions:
                # create dictionary for slicing input sequence
                # conditioning on whether positions are represented
                # by range, range with stride, or single number
                pos_dict = {}

                if "-" in position:
                    m = re.search(r"([0-9]+)-([0-9]+)", position)
                    pos_dict["start"] = int(m.group(1)) - 1
                    pos_dict["stop"] = int(m.group(2))
                else:
                    pos_dict["start"] = int(position) - 1
                    pos_dict["stop"] = int(position)

                if "\\" in position:
                    # Note: the value of `N` in `...\N` isn't read: the script simply assumes `N` is consistent with the number of
                    # increments per interval when the alignment is parsed with a stride of 3 (designating each cpos).
                    # E.g. For the partition file:
                    #       ...`1-N\2`
                    #       ...`2-N\2`
                    #       ...`(N+1)-M\2`
                    #       ...`(N+2)-M\2`
                    # 3'cpos are ignored due to the absence of intervals `3-N...`, `(N+3)-M...`, not because the associated stride values are`\2`
                    pos_dict["stride"] = 3
                elif "\\" not in position:
                    pos_dict["stride"] = 1

                add_to_list_of_dicts(pos_dict)

            dict_of_dicts[partition_name] = list_of_dicts
            add_to_partitions(dict_of_dicts)

        return partitions


class Alignment:
    """Base class: Gets in parsed sequences as input and summarizes their stats.
    Based on the data type, the subclasses AminoAcidAlignment & DNAAlignment define the attributes:
    `alphabet`, `missing_ambiguous_chars`, `missing_chars`, `non_alphabet`
    """

    def __init__(self, in_file, in_format, data_type):
        # initialize alignment class with parsed records and alignment name as arguments,
        # create empty lists for list of sequences, sites without
        # ambiguous or missing characters, and initialize variable for the number
        # of parsimony informative sites
        self.in_file = in_file
        self.in_format = in_format
        self.data_type = data_type

        self.parsed_aln = self.get_parsed_aln()

    def __str__(self):
        #  purpose of override? (originally returned method object)
        return self.get_name()

    def get_aln_input(self):
        # open and parse input file
        aln_input = FileParser(self.in_file)
        return aln_input

    def get_parsed_aln(self):
        # parse according to the given format
        aln_input = self.get_aln_input()
        if self.in_format == "fasta":
            parsed_aln = aln_input.fasta_parse()
        elif self.in_format == "phylip":
            parsed_aln = aln_input.phylip_parse()
        elif self.in_format == "phylip-int":
            parsed_aln = aln_input.phylip_interleaved_parse()
        elif self.in_format == "nexus":
            parsed_aln = aln_input.nexus_parse()
        elif self.in_format == "nexus-int":
            parsed_aln = aln_input.nexus_interleaved_parse()

        return parsed_aln

    def summarize_alignment(self):
        # call methods to create sequences list, matrix, sites without ambiguous or
        # missing characters; get and summarize alignment statistics
        summary = []
        self.length = str(self.get_alignment_length())
        self.matrix = self.matrix_creator()
        self.no_missing_ambiguous = self.get_sites_no_missing_ambiguous()
        self.variable_sites = self.get_variable()
        self.prop_variable = self.get_prop_variable()
        self.parsimony_informative = self.get_parsimony_informative()
        self.prop_parsimony = self.get_prop_parsimony()
        self.missing_records = self.get_missing_from_parsed()
        name = str(self.get_name())
        taxa_no = str(self.get_taxa_no())
        cells = str(self.get_matrix_cells())
        missing = str(self.get_missing())
        missing_percent = str(self.get_missing_percent())
        self.check_data_type()
        summary = [
            name,
            taxa_no,
            self.length,
            cells,
            missing,
            missing_percent,
            str(self.variable_sites),
            str(self.prop_variable),
            str(self.parsimony_informative),
            str(self.prop_parsimony)
        ]
        return summary

    def summarize_alignment_by_taxa(self):
        # get summary for all taxa/sequences in alignment
        per_taxon_summary = []
        taxa_no = self.get_taxa_no()
        self.missing_records = self.get_missing_from_parsed()
        self.length = self.get_alignment_length()
        lengths = (self.length for i in range(taxa_no))
        name = self.get_name()
        names = (name for i in range(taxa_no))
        taxa_names = (
            taxon.replace(" ", "_").replace(".", "_").replace("'", "")
            for taxon, missing_count, missing_percent in self.missing_records
        )
        missing = (missing_count for taxon, missing_count, missing_percent in self.missing_records)
        missing_percent = (missing_percent for taxon, missing_count, missing_percent in
self.missing_records)
        self.check_data_type()
        per_taxon_summary = (names, taxa_names, lengths, missing, missing_percent)
        zipped = list(zip(*per_taxon_summary))
        return zipped

    def get_char_summary(self):
        # get summary of frequencies for all characters
        characters = []
        counts = []
        add_to_chars = characters.append
        add_to_counts = counts.append
        char_count_dicts = self.get_counts()
        for char in self.alphabet:
            add_to_chars(char)
            if char in char_count_dicts.keys():
                add_to_counts(str(char_count_dicts[char]))
            else:
                add_to_counts("0")
        return characters, counts

    def get_taxon_char_summary(self):
        # get summary of frequencies for all characters
        records = (self.append_count(char_dict) for taxon, char_dict in self.get_counts_from_parsed())
        return records

    def append_count(self, char_dict):
        count_list = []
        for char in self.alphabet:
            if char in char_dict.keys():
                count_list.append(char_dict[char])
            else:
                count_list.append(0)
        return count_list

    def matrix_creator(self):
        # decompose character matrix into a two-dimensional list
        matrix = [list(sequence) for sequence in self.parsed_aln.values()]
        return matrix

    def get_column(self, i):
        # get site from the character matrix
        return [row[i] for row in self.matrix]

    def all_same(self, site):
        # check if all elements of a site are the same
        return not site or site.count(site[0]) == len(site)

    def get_sites_no_missing_ambiguous(self):
        # get each site without missing or ambiguous characters
        no_missing_ambiguous_sites = [self.get_site_no_missing_ambiguous(column) for column in range(self.get_alignment_length())]
        return no_missing_ambiguous_sites

    def get_site_no_missing_ambiguous(self, column):
        site = self.get_column(column)
        return [char for char in site if char not in self.missing_ambiguous_chars]

    def replace_missing(self, column):
        return ["-" if x in self.missing_chars else x for x in self.get_column(column)]

    def get_trim_selection(self, trim_fraction, parsimony_check):
        # this checks each column of alignment for minimum occupancy
        self.matrix = self.matrix_creator()
        trim_vector = []
        for column in range(self.get_alignment_length()):
            site = self.replace_missing(column)
            occ = (len(site) - site.count("-")) / len(site)
            if parsimony_check:
                unique_chars = set(site)
                try:
                    unique_chars.remove("-")
                except KeyError:
                    pass # this occurs if we have no missing data
                pattern = [base for base in unique_chars if site.count(base) >= 2]
                trim_vector.append(len(pattern) >= 2 and occ >= trim_fraction)
            else:
                trim_vector.append(occ >= trim_fraction)
        return trim_vector

    def get_variable(self):
        # if all elements of a site without missing or ambiguous characters
        # are not the same, consider it variable
        variable = len([site for site in self.no_missing_ambiguous if not self.all_same(site)])
        return variable

    def get_parsimony_informative(self):
        # if the count for a unique character in a site is at least two,
        # and there are at least two such characters in a site without missing
        # or ambiguous characters, consider it parsimony informative
        parsimony_informative = 0
        for site in self.no_missing_ambiguous:
            unique_chars = set(site)
            pattern = [base for base in unique_chars if site.count(base) >= 2]
            no_patterns = len(pattern)

            if no_patterns >= 2:
                parsimony_informative += 1
        return parsimony_informative

    def get_prop_variable(self):
        # get proportion of variable sites to all sites
        prop_variable = self.variable_sites / int(self.length)
        return round(prop_variable, 3)

    def get_prop_parsimony(self):
        # get proportion of parsimony informative sites to all sites
        prop_parsimony = self.parsimony_informative / int(self.length)
        return round(prop_parsimony, 3)

    def get_name(self):
        # get input file name
        in_filename = path.basename(self.in_file)
        return in_filename

    def get_taxa_no(self):
        # get number of taxa
        return len(self.parsed_aln.values())

    def get_alignment_length(self):
        # get alignment length by just checking the first seq length
        # this assumes that all sequences are of equal length
        return len(next(iter(self.parsed_aln.values())))

    def get_matrix_cells(self):
    # count all matrix cells
        self.all_matrix_cells = len(self.parsed_aln.values()) * int(self.length)
        return self.all_matrix_cells

    def get_missing(self):
        # count missing characters from the list of missing for all sequences
        self.missing = sum(count for taxon, count, percent in self.missing_records)
        return self.missing

    def get_missing_percent(self):
        # get missing percent
        missing_percent = round((self.missing / self.all_matrix_cells * 100), 3)
        return missing_percent

    def get_missing_from_parsed(self):
        # get missing count and percent from parsed alignment
        # return a list of tuples with taxon name, count, and percent missing
        self.missing_records = sorted(
            [
                (taxon, self.get_missing_from_seq(seq), self.get_missing_percent_from_seq(seq))
                for taxon, seq in self.parsed_aln.items()
            ]
        )
        return self.missing_records

    def get_missing_from_seq(self, seq):
        # count missing characters for individual sequence
        missing_count = sum(seq.count(char) for char in self.missing_chars)
        return missing_count

    def get_missing_percent_from_seq(self, seq):
        # get missing percent from individual sequence
        missing_seq_percent = round((self.get_missing_from_seq(seq) / self.get_alignment_length() * 100), 3)
        return missing_seq_percent

    def get_counts(self):
        # get counts of each character in the used alphabet for all sequences
        counters = [Counter(chars) for taxon, chars in self.get_counts_from_parsed()]
        all_counts = sum(counters, Counter())
        counts_dict = dict(all_counts)
        return counts_dict

    def get_counts_from_parsed(self):
        # get counts of all characters from parsed alignment
        # return a list of tuples with taxon name and counts
        return sorted(
            [
                (taxon, self.get_counts_from_seq(seq))
                for taxon, seq in self.parsed_aln.items()
            ]
        )

    def get_counts_from_seq(self, seq):
        # get all alphabet chars count for individual sequence
        char_counts = {char : seq.count(char) for char in self.alphabet}
        return char_counts

    def check_data_type(self):
        # check if the data type is correct; only one seq to save on computation
        seq = next(iter(self.parsed_aln.values()))
        self.check = any(char in self.non_alphabet for char in seq)
        if self.check is True:
            print(
                "WARNING: found non-" + self.data_type + " characters. "
                "Are you sure you specified the right data type?"
            )


class AminoAcidAlignment(Alignment):
    """Alphabets specific to amino acid alignments"""

    alphabet = ["A", "C", "D", "E", "F", "G", "H", "I", "K", "L", "M", "N", "P", "Q", "R", "S", "T",
"V", "W", "Y", "B", "J", "Z", "X", ".", "*", "-", "?"]
    missing_ambiguous_chars = ["B", "J", "Z", "X", ".", "*", "-", "?"]
    missing_chars = ["X", ".", "*", "-", "?"]
    non_alphabet = ["O"]

    def get_summary(self):
        # get alignment summary specific to amino acids
        data = self.summarize_alignment()
        new_data = data + list(self.get_char_summary()[1])
        return new_data

    def get_taxa_summary(self):
        # get per-taxon/sequence alignment summary specific to amino acids
        data = self.summarize_alignment_by_taxa()
        aa_summary = (data, self.get_taxon_char_summary())
        zipped_list = list(zip(*aa_summary))
        new_data = [list(data_tupl) + chars for data_tupl, chars in zipped_list]
        return new_data

class DNAAlignment(Alignment):
    """Alphabets specific to DNA alignments"""

    alphabet = ["A", "C", "G", "T", "K", "M", "R", "Y", "S", "W", "B", "V", "H", "D", "X", "N", "O",
"-", "?"]
    missing_ambiguous_chars = ["K", "M", "R", "Y", "S", "W", "B", "V", "H", "D", "X", "N", "O", "-",
"?"]
    missing_chars = ["X", "N", "O", "-", "?"]
    non_alphabet = ["E", "F", "I", "L", "P", "Q", "J", "Z", ".", "*"]

    def get_summary(self):
        # get alignment summarry specific to nucleotide
        data = self.summarize_alignment()
        new_data = data + self.get_atgc_content() + list(self.get_char_summary()[1])
        return new_data

    def get_taxa_summary(self):
        # get per-taxon/sequence alignment summary specific to nucleotides
        data = self.summarize_alignment_by_taxa()
        dna_summary = (data, self.get_list_from_atgc(), self.get_taxon_char_summary())
        zipped_list = list(zip(*dna_summary))
        new_data = [list(data_tupl) + list(atgc) + chars for data_tupl, atgc, chars in zipped_list]
        return new_data

    def get_atgc_content(self):
        # get AC and GC contents for all sequences
        # AT content is the first element of AT, GC content tuple
        # returned by get_atgc_from_seq()
        atgc_records = self.get_atgc_from_parsed()
        at_content = round(sum(atgc[0] for taxon, atgc in atgc_records) / self.get_taxa_no(), 3)
        gc_content = round(1 - float(at_content), 3)

        atgc_content = [str(at_content), str(gc_content)]
        return atgc_content

    def get_list_from_atgc(self):
        records = (atgc for taxon, atgc in self.get_atgc_from_parsed())
        return records

    def get_atgc_from_parsed(self):
        # get AT and GC contents from parsed alignment dictionary
        # return a list of tuples with taxon name, AT content, and GC content
        return sorted([(taxon, self.get_atgc_from_seq(seq)) for taxon, seq in
self.parsed_aln.items()])

    def get_atgc_from_seq(self, seq):
        # get AT and GC contents from individual sequences

        at_count = seq.count("A") + seq.count("T") + seq.count("W")
        gc_count = seq.count("G") + seq.count("C") + seq.count("S")

        try:
            at_content = round(at_count / (at_count + gc_count), 3)
            gc_content = round(1 - float(at_content), 3)

        except ZeroDivisionError:
            at_content = 0
            gc_content = 0

        return at_content, gc_content

class MetaAlignment:
    """Class of multiple sequence alignments"""

    def __init__(self, **kwargs):
        # set defaults and get values from kwargs
        self.in_files = kwargs.get("in_files")
        self.in_format = kwargs.get("in_format")
        self.data_type = kwargs.get("data_type")
        self.command = kwargs.get("command")
        self.concat_out = kwargs.get("concat_out", "concatenated.out")
        self.using_metapartitions = False
        self.check_align = kwargs.get("check_align", False)
        self.cores = kwargs.get("cores")
        self.by_taxon_summary = kwargs.get("by_taxon_summary")
        self.no_sup_aln_name = False
        self.no_mpan = False

        if self.command == "concat":
            self.codons = kwargs.get("codons", "none")
            if self.data_type == "aa" and self.codons != "none":
                print("ERROR: when option -d|--data-type is set to 'aa', option -n|--codons must be
set to 'none'.")
                sys.exit(1)

        if self.command == "replicate":
            self.no_replicates = kwargs.get("replicate_args")[0]
            self.no_loci = kwargs.get("replicate_args")[1]

        if self.command == "split":
            self.split = kwargs.get("split_by")
            self.remove_empty = kwargs.get("remove_empty", False)
            self.no_sup_aln_name = kwargs.get("no_sup_aln_name", False)

        if self.command == "metapartitions":
            self.using_metapartitions = True
            self.split = kwargs.get("split_by")
            self.remove_empty = kwargs.get("remove_empty", False)
            self.no_sup_aln_name = kwargs.get("no_sup_aln_name", False)
            self.no_mpan = kwargs.get("no_mpan", False)
            self.prepend_label = kwargs.get("prepend_label")
            if self.prepend_label is not None and isinstance(self.prepend_label, str):
                self.prepend_label = self.prepend_label + "_"
            else:
                self.prepend_label = ""

        if self.command == "remove":
            self.species_to_remove = kwargs.get("taxa_to_remove")
            self.species_to_remove_set = set(self.species_to_remove)
            self.reduced_file_prefix = kwargs.get("out_prefix")
            self.check_taxa = kwargs.get("check_taxa", False)

        if self.command == "translate":
            self.reading_frame = kwargs.get("reading_frame")
            self.genetic_code = kwargs.get("genetic_code")

        if self.command == "trim":
            self.trim_fraction = kwargs.get("trim_fraction")
            self.trim_out = kwargs.get("trim_out")
            self.parsimony_check = kwargs.get("parsimony_check", False)

        self.alignment_objects = self.get_alignment_objects()
        self.parsed_alignments = self.get_parsed_alignments()

        # The code list:
        self.codes_list = """
         1. The Standard Code
         2. The Vertebrate Mitochondrial Code
         3. The Yeast Mitochondrial Code
         4. The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma
Code
         5. The Invertebrate Mitochondrial Code
         6. The Ciliate, Dasycladacean and Hexamita Nuclear Code
         9. The Echinoderm and Flatworm Mitochondrial Code
        10. The Euplotid Nuclear Code
        11. The Bacterial, Archaeal and Plant Plastid Code
        12. The Alternative Yeast Nuclear Code
        13. The Ascidian Mitochondrial Code
        14. The Alternative Flatworm Mitochondrial Code
        16. Chlorophycean Mitochondrial Code
        21. Trematode Mitochondrial Code
        22. Scenedesmus obliquus Mitochondrial Code
        23. Thraustochytrium Mitochondrial Code
        24. Pterobranchia Mitochondrial Code
        25. Candidate Division SR1 and Gracilibacteria Code
        26. Pachysolen tannophilus Nuclear Code
        """

        # 1: The Standard Code
        self.gencode_NCBI_1 = {
        "TTT" : "F", # Phe
        "TCT" : "S", # Ser
        "TAT" : "Y", # Tyr
        "TGT" : "C", # Cys
        "TTC" : "F", # Phe
        "TCC" : "S", # Ser
        "TAC" : "Y", # Tyr
        "TGC" : "C", # Cys
        "TTA" : "L", # Leu
        "TCA" : "S", # Ser
        "TAA" : "*", # Ter
        "TGA" : "*", # Ter
        "TTG" : "L", # Leu i
        "TCG" : "S", # Ser
        "TAG" : "*", # Ter
        "TGG" : "W", # Trp
        "CTT" : "L", # Leu
        "CCT" : "P", # Pro
        "CAT" : "H", # His
        "CGT" : "R", # Arg
        "CTC" : "L", # Leu
        "CCC" : "P", # Pro
        "CAC" : "H", # His
        "CGC" : "R", # Arg
        "CTA" : "L", # Leu
        "CCA" : "P", # Pro
        "CAA" : "Q", # Gln
        "CGA" : "R", # Arg
        "CTG" : "L", # Leu i
        "CCG" : "P", # Pro
        "CAG" : "Q", # Gln
        "CGG" : "R", # Arg
        "ATT" : "I", # Ile
        "ACT" : "T", # Thr
        "AAT" : "N", # Asn
        "AGT" : "S", # Ser
        "ATC" : "I", # Ile
        "ACC" : "T", # Thr
        "AAC" : "N", # Asn
        "AGC" : "S", # Ser
        "ATA" : "I", # Ile
        "ACA" : "T", # Thr
        "AAA" : "K", # Lys
        "AGA" : "R", # Arg
        "ATG" : "M", # Met i
        "ACG" : "T", # Thr
        "AAG" : "K", # Lys
        "AGG" : "R", # Arg
        "GTT" : "V", # Val
        "GCT" : "A", # Ala
        "GAT" : "D", # Asp
        "GGT" : "G", # Gly
        "GTC" : "V", # Val
        "GCC" : "A", # Ala
        "GAC" : "D", # Asp
        "GGC" : "G", # Gly
        "GTA" : "V", # Val
        "GCA" : "A", # Ala
        "GAA" : "E", # Glu
        "GGA" : "G", # Gly
        "GTG" : "V", # Val
        "GCG" : "A", # Ala
        "GAG" : "E", # Glu
        "GGG" : "G", # Gly
        "---" : "-", # Gap
        "???" : "?", # Unk
        "NNN" : "X", # Unk
        }

        # 2: The Vertebrate Mitochondrial Code
        self.gencode_NCBI_2 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_2["AGA"] = "*" # Ter
        self.gencode_NCBI_2["AGG"] = "*" # Ter
        self.gencode_NCBI_2["ATA"] = "M" # Met
        self.gencode_NCBI_2["TGA"] = "W" # Trp

        # 3: The Yeast Mitochondrial Code
        self.gencode_NCBI_3 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_3["ATA"] = "M" # Met
        self.gencode_NCBI_3["CTT"] = "T" # Thr
        self.gencode_NCBI_3["CTC"] = "T" # Thr
        self.gencode_NCBI_3["CTA"] = "T" # Thr
        self.gencode_NCBI_3["CTG"] = "T" # Thr
        self.gencode_NCBI_3["TGA"] = "W" # Trp

        del self.gencode_NCBI_3["CGA"]
        del self.gencode_NCBI_3["CGC"]

        # 4: The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma
      Code
        self.gencode_NCBI_4 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_4["TGA"] = "W" # Trp

        # 5: The Invertebrate Mitochondrial Code
        self.gencode_NCBI_5 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_5["AGA"] = "S" # Ser
        self.gencode_NCBI_5["AGG"] = "S" # Ser
        self.gencode_NCBI_5["ATA"] = "M" # Met
        self.gencode_NCBI_5["TGA"] = "W" # Trp

        # 6: The Ciliate, Dasycladacean and Hexamita Nuclear Code
        self.gencode_NCBI_6 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_6["TAA"] = "Q" # Gln
        self.gencode_NCBI_6["TAG"] = "Q" # Gln

        # 9: The Echinoderm and Flatworm Mitochondrial Code
        self.gencode_NCBI_9 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_9["AAA"] = "N" # Asn
        self.gencode_NCBI_9["AGA"] = "S" # Ser
        self.gencode_NCBI_9["AGG"] = "S" # Ser
        self.gencode_NCBI_9["TGA"] = "W" # Trp

        # 10: The Euplotid Nuclear Code
        self.gencode_NCBI_10 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_10["TGA"] = "C" # Cys

        # 11: The Bacterial, Archaeal and Plant Plastid Code
        self.gencode_NCBI_11 = self.gencode_NCBI_1.copy()

        # 12: The Alternative Yeast Nuclear Code
        self.gencode_NCBI_12 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_12["CTG"] = "S" # Ser

        # 13: The Ascidian Mitochondrial Code
        self.gencode_NCBI_13 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_13["AGA"] = "G" # Gly
        self.gencode_NCBI_13["AGG"] = "G" # Gly
        self.gencode_NCBI_13["ATA"] = "M" # Met
        self.gencode_NCBI_13["TGA"] = "W" # Trp

        # 14: The Alternative Flatworm Mitochondrial Code
        self.gencode_NCBI_14 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_14["AAA"] = "N" # Asn
        self.gencode_NCBI_14["AGA"] = "S" # Ser
        self.gencode_NCBI_14["AGG"] = "S" # Ser
        self.gencode_NCBI_14["TAA"] = "Y" # Tyr
        self.gencode_NCBI_14["TGA"] = "W" # Trp

        # 16: Chlorophycean Mitochondrial Code
        self.gencode_NCBI_16 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_16["TAG"] = "L" # Leu

        # 21: Trematode Mitochondrial Code
        self.gencode_NCBI_21 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_21["TGA"] = "W" # Trp
        self.gencode_NCBI_21["ATA"] = "M" # Met
        self.gencode_NCBI_21["AGA"] = "S" # Ser
        self.gencode_NCBI_21["AGG"] = "S" # Ser
        self.gencode_NCBI_21["AAA"] = "N" # Asn

        # 22: Scenedesmus obliquus Mitochondrial Code
        self.gencode_NCBI_22 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_22["TCA"] = "*" # Ter
        self.gencode_NCBI_22["TAG"] = "L" # Leu

        # 23: Thraustochytrium Mitochondrial Code
        self.gencode_NCBI_23 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_23["TTA"] = "*" # Ter

        # 24: Pterobranchia Mitochondrial Code
        self.gencode_NCBI_24 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_24["AGA"] = "S" # Ser
        self.gencode_NCBI_24["AGG"] = "K" # Lys
        self.gencode_NCBI_24["TGA"] = "W" # Trp

        # 25: Candidate Division SR1 and Gracilibacteria Code
        self.gencode_NCBI_25 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_25["TGA"] = "G" # Gly

        # 26: Pachysolen tannophilus Nuclear Code
        self.gencode_NCBI_26 = self.gencode_NCBI_1.copy()
        self.gencode_NCBI_26["CTG"] = "A" # Ala

        self.codes = {
        1 : self.gencode_NCBI_1,
        2 : self.gencode_NCBI_2,
        3 : self.gencode_NCBI_3,
        4 : self.gencode_NCBI_4,
        5 : self.gencode_NCBI_5,
        6 : self.gencode_NCBI_6,
        9 : self.gencode_NCBI_9,
        10 : self.gencode_NCBI_10,
        11 : self.gencode_NCBI_11,
        12 : self.gencode_NCBI_12,
        13 : self.gencode_NCBI_13,
        14 : self.gencode_NCBI_14,
        16 : self.gencode_NCBI_16,
        21 : self.gencode_NCBI_21,
        22 : self.gencode_NCBI_22,
        23 : self.gencode_NCBI_23,
        24 : self.gencode_NCBI_24,
        25 : self.gencode_NCBI_25,
        26 : self.gencode_NCBI_26
        }

    def translate_dna_to_aa(self, seq, translation_table, frame):
        # translate DNA string into amino acids
        # where the last codon starts
        last_codon_start = len(seq) - 2
        # where the first codon starts
        if frame == 1:
            first = 0
        elif frame == 2:
            first = 1
        elif frame == 3:
            first = 2
        # create protein sequence by growing list
        protein = []
        add_to_protein = protein.append
        for start in range(first, last_codon_start, 3):
            codon = seq[start : start + 3]
            aa = translation_table.get(codon.upper(), ’X’)
            add_to_protein(aa)

        return "".join(protein)

    def translate_dict(self, source_dict):
        translation_table = self.codes.get(self.genetic_code)
        translated_dict = {}
        for taxon, seq in sorted(source_dict.items()):
            translated_seq = self.translate_dna_to_aa(seq, translation_table, self.reading_frame)
            if "*" in translated_seq:
                print("WARNING: stop codon(s), indicated as *, found in {} sequence".format(taxon))
            translated_dict[taxon] = translated_seq

        return translated_dict

    def get_translated(self, translation_table, reading_frame):
        if int(self.cores) == 1:
            translated_alignments = [self.translate_dict(alignment) for alignment in self.parsed_alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            translated_alignments = pool.map(self.translate_dict, self.parsed_alignments)

        return translated_alignments

    def trim_dict(self, alignment):
        trim_vector = alignment.get_trim_selection(self.trim_fraction, self.parsimony_check)
        aln_dict = alignment.parsed_aln
        for key in aln_dict:
            aln_dict[key] = ”.join(list(compress(aln_dict[key], trim_vector)))

        return aln_dict

    def get_trimmed(self, trim_fraction, parsimony_check):
        if int(self.cores) == 1:
            trimmed_alignments = [self.trim_dict(alignment) for alignment in self.alignment_objects]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            trimmed_alignments = pool.map(self.trim_dict, self.alignment_objects)

        return trimmed_alignments

    def remove_unknown_chars(self, seq):
        # remove unknown characters from sequence
        new_seq = seq.replace("?", "").replace("-", "")

        return new_seq

    def remove_empty_sequences(self, split_alignment):
        # remove taxa from alignment if they are composed of only empty sequences
        new_alignment = {taxon : seq for taxon, seq in split_alignment.items() if self.remove_unknown_chars(seq)}

        return new_alignment

    def get_partitions(self, partitions_file):
        # parse and get partitions from partitions file
        partitions = FileParser(partitions_file)
        parsed_partitions = partitions.partitions_parse()

        return parsed_partitions

    def get_alignment_object(self, alignment):
        # parse according to the given alphabet;
        # Note:('alignment') <=> `in_file` outside MetaAlignment, e.g.
        # AminoAcidAlignment(Alignment<-.get_parsed_aln<-.get_aln_input)<-FileParser.__init__(in_file)<-FileHandler(...open(self.
        if self.data_type == "aa":
            aln = AminoAcidAlignment(alignment, self.in_format, self.data_type)
        elif self.data_type == "dna":
            aln = DNAAlignment(alignment, self.in_format, self.data_type)
        return aln

    def get_alignment_objects(self):
        # get alignment objects on which statistics can be computed
        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            alignments = [self.get_alignment_object(alignment) for alignment in self.in_files]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            alignments = pool.map(self.get_alignment_object, self.in_files)
        return alignments

    def get_parsed_alignments(self):
        # get parsed dictionaries with taxa and sequences
        parsed_alignments = []
        add_to_parsed_alignments = parsed_alignments.append
        for alignment in self.alignment_objects:
            parsed = alignment.parsed_aln
            add_to_parsed_alignments(parsed)
            # checking if every seq has the same length or if parsed is not empty; exit if false
            if self.check_align:
                equal = all(
                    x == [len(list(parsed.values())[i]) for i in range(0,len(list(parsed.values())))][0]
                    for x in [len(list(parsed.values())[i]) for i in range(0,len(list(parsed.values())))]
                )
                if equal is False:
                    print("ERROR: Sequences in input are of varying lengths. Be sure to align them first.")
                    sys.exit()

            if not parsed.keys() or not any(parsed.values()):
                print(
                    "ERROR: Parsed sequences of " + alignment.in_file + " are empty. "
                    "Are you sure you specified the right input format and/or that input is a valid alignment?"
                )
                sys.exit()

        return parsed_alignments

    def get_partitioned(self, partitions_file):
        # partition alignment according to a partitions file
        partitions = self.get_partitions(partitions_file)
        alignment = self.parsed_alignments[0]

        # initiate list of newly partitioned alignments
        list_of_parts = []
        add_to_list_of_parts = list_of_parts.append
        for partition in partitions:
            # loop over all parsed partitions, adding taxa and sliced sequences
            for name, elements in partition.items():
                new_dict = {}

                for taxon, seq in alignment.items():
                    new_seq = ""

                    for dictionary in elements:
                        new_seq = new_seq +
seq[dictionary["start"]:dictionary["stop"]:dictionary["stride"]]
                        new_dict[taxon] = new_seq

                if self.remove_empty:
                    # check if remove empty sequences
                    no_empty_dict = self.remove_empty_sequences(new_dict)
                    add_to_list_of_parts({name : no_empty_dict})
                else:
                    # add partition name : dict of taxa and sequences to the list
                    add_to_list_of_parts({name : new_dict})

        return list_of_parts

    def get_summaries(self):
        # get summaries for all alignment objects

        # define different headers for aa and dna alignments
        aa_header = [
            "Alignment_name",
            "No_of_taxa",
            "Alignment_length",
            "Total_matrix_cells",
            "Undetermined_characters",
            "Missing_percent",
            "No_variable_sites",
            "Proportion_variable_sites",
            "Parsimony_informative_sites",
            "Proportion_parsimony_informative"
        ]

        dna_header = [
            "Alignment_name",
            "No_of_taxa",
            "Alignment_length",
            "Total_matrix_cells",
            "Undetermined_characters",
            "Missing_percent",
            "No_variable_sites",
            "Proportion_variable_sites",
            "Parsimony_informative_sites",
            "Proportion_parsimony_informative",
            "AT_content",
            "GC_content"
        ]

        alignments = self.alignment_objects
        parsed_alignments = self.parsed_alignments
        freq_header = [char for char in alignments[0].alphabet]

        if self.data_type == "aa":
            header = aa_header + freq_header
        elif self.data_type == "dna":
            header = dna_header + freq_header

        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            summaries = [alignment.get_summary() for alignment in alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            summaries = pool.map(self.summarize_alignments, alignments)
        return header, summaries

    def summarize_alignments(self, alignment):
        # helper function to summarize alignments
        summary = alignment.get_summary()
        return summary

    def get_taxon_summaries(self):
        # get per-sequence summaries for all alignment objects

        # define different headers for aa and dna alignments
        aa_header = [
            "Alignment_name",
            "Taxon_name",
            "Sequence_length",
            "Undetermined_characters",
            "Missing_percent"
        ]

        dna_header = [
            "Alignment_name",
            "Taxon_name",
            "Sequence_length",
            "Undetermined_characters",
            "Missing_percent",
            "AT_content",
            "GC_content"
        ]

        alignments = self.alignment_objects
        parsed_alignments = self.parsed_alignments
        freq_header = alignments[0].alphabet

        if self.data_type == "aa":
            header = aa_header + freq_header
        elif self.data_type == "dna":
            header = dna_header + freq_header

        # use multiprocessing if more than one core specified
        if int(self.cores) == 1:
            summaries = [alignment.get_taxa_summary() for alignment in alignments]
        elif int(self.cores) > 1:
            pool = mp.Pool(int(self.cores))
            summaries = pool.map(self.summarize_alignments_taxa, alignments)

        return header, summaries

    def summarize_alignments_taxa(self, alignment):
        # helper function to summarize alignments by taxon
        summary = alignment.get_taxa_summary()
        return summary

    def write_summaries(self, file_name):
        # write summaries to file

        self.file_overwrite_error(file_name)

        with open(file_name, "w", encoding="utf-8") as summary_file:
            summary_out = self.get_summaries()
            header = '\t'.join(summary_out[0])
            new_summ = ['\t'.join(summary) for summary in summary_out[1]]
            summary_file.write(header + '\n')
            summary_file.write('\n'.join(new_summ))
            summary_file.write('\n')
            print("Wrote summaries to file '" + file_name + "'")

    def write_taxa_summaries(self):
        # write by-taxon summaries to file
        for index, in_file_name in enumerate(self.in_files):
            out_file_name = in_file_name + "-seq-summary.txt"
            self.file_overwrite_error(out_file_name)
            with open(out_file_name, "w", encoding="utf-8") as summary_file:
                summary_out = self.get_taxon_summaries()
                header = '\t'.join(summary_out[0])
                summ = [[str(col) for col in element] for element in summary_out[1][index]]
                new_summ = ['\t'.join(row) for row in summ]
                summary_file.write(header + '\n')
                summary_file.write('\n'.join(new_summ))
                summary_file.write('\n')

    def get_replicate(self, no_replicates, no_loci):
        # construct replicate data sets for phylogenetic jackknife
        replicates = []
        add_to_replicates = replicates.append
        counter = 1
        for replicate in range(no_replicates):

            try:
                random_alignments = sample(self.parsed_alignments, no_loci)
            except ValueError:
                print("ERROR: You specified more loci per replicate than there are in your input.")
                sys.exit()

            random_alignments = sample(self.parsed_alignments, no_loci)
            concat_replicate = self.get_concatenated(random_alignments)[0]
            add_to_replicates(concat_replicate)
            counter += 1

        return replicates

    def get_concatenated(self, alignments):
        # concatenate muntiple input alignments
        # create empty dictionary of lists
        concatenated = defaultdict(list)

        # first create list of taxa in all alignments
        # you need this to insert empty seqs in
        # the concatenated alignment
        all_taxa = []
        for alignment in alignments:
            for taxon in alignment.keys():
                if taxon not in all_taxa:
                    all_taxa.append(taxon)

        # start counters to keep track of partitions
        partition_counter = 1
        position_counter = 1
        # get dict for alignment name and partition
        partitions = {}
        digits_to_pad = len(str(len(alignments)))

        for alignment in alignments:
            # get alignment length from a random taxon
            partition_length = len(alignment[list(alignment.keys())[0]])
            # get base name of each alignment for use when writing partitions file
            # NOTE: the base name here is whatever comes before fist period in the file name
            alignment_name = self.alignment_objects[partition_counter - 1].get_name().split(’.’)[0]

            if self.using_metapartitions:
                #  Implementation of `--no-mpan‘, i.e. ’no metapartition alignment name’.
                #  `prepend_label‘ either assigned to `<str>_‘ via option `--prepend <str>‘
                #  or empty ("") -> see def MetaAlignment.__init__()
                if self.no_mpan:
                    # omit original alignment names from the printed partition file
                    partition_name = self.prepend_label + "p" + str(partition_counter).zfill(digits_to_pad)
                else:
                    # keep original alignment names in the printed partition file
                    partition_name = self.prepend_label + "p" + str(partition_counter).zfill(digits_to_pad) + "_" + alignment_name
            else:
                partition_name = "p" + str(partition_counter) + "_" + alignment_name

            start = position_counter
            position_counter += partition_length
            end = position_counter - 1
            partitions[partition_name] = str(start) + "-" + str(end)
            partition_counter += 1

            # get empty sequence if there is missing taxon
            # getting length from first element of list of keys
            # created from the original dict for this alignment
            empty_seq = ’?’ * partition_length

            for taxon in all_taxa:

                if taxon not in alignment.keys():
                    concatenated[taxon].append(empty_seq)
                else:
                    concatenated[taxon].append(alignment[taxon])

        concatenated = {taxon:”.join(seqs) for taxon, seqs in concatenated.items()}

        return concatenated, partitions

    def remove_from_alignment(self, alignment, species_to_remove_set, index):
        # remove taxa from alignment
        aln_name = self.get_alignment_name_no_ext(index)
        for taxon in species_to_remove_set:
            if taxon not in alignment.keys():
                print(
                    "WARNING: Taxon ’" + taxon + "’ not found in ’" + aln_name + "’.\nIf you expected it to be there, "
                    "make sure to replace all taxon name spaces with underscores and that you are not using quotes."
                )
        # originally within for-loop scope (redundancy)
        new_alignment = {species: seq for species, seq in alignment.items() if species not in species_to_remove_set}

        return aln_name, new_alignment

    def remove_taxa(self, species_to_remove_set):
        new_alns = {}
        for index, alignment in enumerate(self.parsed_alignments):
            aln_name, aln_dict = self.remove_from_alignment(alignment, species_to_remove_set, index)
            # check if alignment is not empty:
            if aln_dict:
                new_alns[aln_name] = aln_dict
            else:
                print("ERROR: You asked to remove all taxa from the alignment " + aln_name + ". No
output file will be written.")

        return new_alns

    def print_fasta(self, source_dict):
        # print fasta-formatted string from a dictionary
        fasta_string = ""
        # each sequence line will have 80 characters
        n = 80

        for taxon, seq in sorted(source_dict.items()):
            # split dictionary values to a list of string, each n chars long
            seq = [seq[i:i+n] for i in range(0, len(seq), n)]
            # in case there are unwanted spaces in taxon names
            taxon = taxon.replace(" ", "_").strip("'")
            fasta_string += ">" + taxon + "\n"
            for element in seq:
                fasta_string += element + "\n"

        return fasta_string

    def print_phylip(self, source_dict):
        # print phylip-formatted string from a dictionary
        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        # figure out the max length of a taxon for nice padding of sequences
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        # get sequence length from a random value
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        phylip_string = header + "\n"
        for taxon, seq in sorted(source_dict.items()):
            taxon = taxon.replace(" ", "_").strip("'")
            # left-justify taxon names relative to sequences
            phylip_string += taxon.ljust(pad_longest_name, ' ') + seq + "\n"

        return phylip_string

    def print_phylip_int(self, source_dict):
        # print phylip interleaved-formatted string from a dictionary
        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        phylip_int_string = header + "\n\n"
        # this will be a list of tuples to hold taxa names and sequences
        seq_matrix = []

        # each sequence line will have 500 characters
        n = 500

        # recreate sequence matrix
        add_to_matrix = seq_matrix.append
        for taxon, seq in sorted(source_dict.items()):
            add_to_matrix((taxon, [seq[i:i+n] for i in range(0, len(seq), n)]))

        first_seq = seq_matrix[0][1]
        for index, item in enumerate(first_seq):
            for taxon, sequence in seq_matrix:
                if index == 0:
                    phylip_int_string += taxon.ljust(pad_longest_name, ' ') + sequence[index] + "\n"
                else:
                    phylip_int_string += sequence[index] + "\n"
            phylip_int_string += "\n"

        return phylip_int_string

    def print_nexus(self, source_dict):
        # print nexus-formatted string from a dictionary
        if self.data_type == "aa" or self.command == "translate":
            data_type = "PROTEIN"
        elif self.data_type == "dna":
            data_type = "DNA"

        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        nexus_string = (
            "#NEXUS\n\nBEGIN DATA;\n\tDIMENSIONS  NTAX=" + str(no_taxa) + " NCHAR=" + str(seq_length)
            + ";\n\tFORMAT DATATYPE=" + data_type + "  GAP = - MISSING = ?;\n\tMATRIX\n"
        )

        for taxon, seq in sorted(source_dict.items()):
            taxon = taxon.replace(" ", "_").strip("'")
            nexus_string += "\t" + taxon.ljust(pad_longest_name, ' ') + seq + "\n"
        nexus_string += "\n;\n\nEND;"

        return nexus_string

    def print_nexus_int(self, source_dict):
        # print nexus interleaved-formatted string from a dictionary
        if self.data_type == "aa":
            data_type = "PROTEIN"
        elif self.data_type == "dna":
            data_type = "DNA"

        taxa_list = list(source_dict.keys())
        no_taxa = len(taxa_list)
        pad_longest_name = len(max(taxa_list, key=len)) + 3
        seq_length = len(next(iter(source_dict.values())))
        header = str(len(source_dict)) + " " + str(seq_length)
        # this will be a list of tuples to hold taxa names and sequences
        seq_matrix = []
        nexus_int_string = (
            "#NEXUS\n\nBEGIN DATA;\n\tDIMENSIONS  NTAX=" + str(no_taxa) + " NCHAR=" + str(seq_length)
            + ";\n\tFORMAT   INTERLEAVE" + "   DATATYPE=" + data_type + "  GAP = - MISSING =
?;\n\tMATRIX\n"
        )
        # each sequence line will have 500 characters
        n = 500

        # recreate sequence matrix
        add_to_matrix = seq_matrix.append
        for taxon, seq in sorted(source_dict.items()):
            add_to_matrix((taxon, [seq[i:i+n] for i in range(0, len(seq), n)]))

        first_seq = seq_matrix[0][1]
        for index, item in enumerate(first_seq):
            for taxon, sequence in seq_matrix:
                if index == 0:
                    nexus_int_string += taxon.ljust(pad_longest_name, ' ') + sequence[index] + "\n"
                else:
                    nexus_int_string += sequence[index] + "\n"
            nexus_int_string += "\n"

        nexus_int_string += "\n;\n\nEND;"

        return nexus_int_string

    def natural_sort(self, a_list):
        # create a function that does 'human sort' on a list
        convert = lambda text: int(text) if text.isdigit() else text.lower()
        alphanum_key = lambda key: [convert(c) for c in re.split('([0-9]+)', key)]
        return sorted(a_list, key = alphanum_key)

    def print_unspecified_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += key + " = " + str(part_dict[key]) + "\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
                    part_string += key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\2" +
"\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
                    part_string += key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" +
"\n"
                    part_string += key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" +
"\n"

        elif data_type == "aa":
            for key in part_list:
                part_string += key + " = " + str(part_dict[key]) + "\n"

        return part_string

    def print_nexus_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())
        # write beginning of nexus sets
        part_string += "#NEXUS\n\n"
        part_string += "BEGIN SETS;\n"

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += "\tcharset " + key + " = " + str(part_dict[key]) + ";\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "\tcharset " + key + "_pos1" + " = " + start + "-" + end + "\\2" + ";\n"
                    part_string += "\tcharset " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\2" + ";\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "\tcharset " + key + "_pos1" + " = " + start + "-" + end + "\\3" + ";\n"
                    part_string += "\tcharset " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" + ";\n"
                    part_string += "\tcharset " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" + ";\n"
            part_string += "END;"

        elif data_type == "aa":
            for key in part_list:
                part_string += "\tcharset " + key + " = " + str(part_dict[key]) + ";\n"
            part_string += "END;"

        return part_string

    def print_iqtree_nexus_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())
        # write beginning of nexus sets
        part_string += "#nexus\n"
        part_string += "begin sets;\n"

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += "  charset " + key + " = " + str(part_dict[key]) + ";\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "  charset " + key + "_pos1" + " = " + start + " - " + end + "\\2" + ";\n"
                    part_string += "  charset " + key + "_pos2" + " = " + str(int(start) + 1) + " - " + end + "\\2" + ";\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "  charset " + key + "_pos1" + " = " + start + " - " + end + "\\3" + ";\n"
                    part_string += "  charset " + key + "_pos2" + " = " + str(int(start) + 1) + " - " + end + "\\3" + ";\n"
                    part_string += "  charset " + key + "_pos3" + " = " + str(int(start) + 2) + " - " + end + "\\3" + ";\n"
            part_string += "end;\n"

        elif data_type == "aa":
            for key in part_list:
                part_string += "  charset " + key + " = " + str(part_dict[key]) + ";\n"
            part_string += "end;\n"

        return part_string

    def print_raxml_partitions(self, data_type, codons):
        # print partitions for concatenated alignment
        part_string = ""
        part_dict = self.get_concatenated(self.parsed_alignments)[1]
        part_list = self.natural_sort(part_dict.keys())

        if data_type == "dna":
            if codons == "none":
                for key in part_list:
                    part_string += "DNA, " + key + " = " + str(part_dict[key]) + "\n"
            elif codons == "12":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "DNA, " + key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
                    part_string += "DNA, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end +
"\\2" + "\n"
            elif codons == "123":
                for key in part_list:
                    start, end = str(part_dict[key]).split("-")
                    part_string += "DNA, " + key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
                    part_string += "DNA, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" + "\n"
                    part_string += "DNA, " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" + "\n"

        elif data_type == "aa":
            for key in part_list:
                part_string += "WAG, " + key + " = " + str(part_dict[key]) + "\n"

            #  aa-partition files with strides are probably not useful? (original below)
#            elif codons == "12":
#                for key in part_list:
#                    start, end = str(part_dict[key]).split("-")
#                    part_string += "WAG, " + key + "_pos1" + " = " + start + "-" + end + "\\2" + "\n"
#                    part_string += "WAG, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\2" + "\n"
#            elif codons == "123":
#                for key in part_list:
#                    start, end = str(part_dict[key]).split("-")
#                    part_string += "WAG, " + key + "_pos1" + " = " + start + "-" + end + "\\3" + "\n"
#                    part_string += "WAG, " + key + "_pos2" + " = " + str(int(start) + 1) + "-" + end + "\\3" + "\n"
#                    part_string += "WAG, " + key + "_pos3" + " = " + str(int(start) + 2) + "-" + end + "\\3" + "\n"
        return part_string

    def replace_string_in_file(self, file_name, old_string, new_string):
        # global string replacement in file
        with open(file_name, "r", encoding="utf-8") as file:
            file_content = file.read()
        # write globally replaced content back to file
        glb_replaced_content = file_content.replace(old_string, new_string)
        with open(file_name, "w", encoding="utf-8") as file:
            file.write(glb_replaced_content)

    def write_partitions(self, file_name, part_format, data_type, codons):
        # write partitions file for concatenated alignment
        self.file_overwrite_error(file_name)
        with open(file_name, "w", encoding="utf-8") as part_file:
            if part_format == "nexus":
                part_file.write(self.print_nexus_partitions(data_type, codons))
            if part_format == "iqtree-nexus":
                part_file.write(self.print_iqtree_nexus_partitions(data_type, codons))
            if part_format == "raxml":
                part_file.write(self.print_raxml_partitions(data_type, codons))
            if part_format == "unspecified":
                part_file.write(self.print_unspecified_partitions(data_type, codons))

            if self.using_metapartitions:
                self.replace_string_in_file(file_name, '-meta =', ' =')

        print("Wrote partitions for the concatenated file to '" + file_name + "'")

    def get_extension(self, file_format):
        # get proper extension string
        if file_format == "phylip":
            extension = "-out.phy"
        elif file_format == "phylip-int":
            extension = "-out.int-phy"
        elif file_format == "fasta":
            extension = "-out.fas"
        elif file_format == "nexus":
            extension = "-out.nex"
        elif file_format == "nexus-int":
            extension = "-out.int-nex"

        return extension

    def get_metapartition_extension(self, file_format):
        # get proper metapartition_extension string
        if file_format == "phylip":
            metapartition_extension = "-meta.phy"
        elif file_format == "phylip-int":
            metapartition_extension = "-meta.int-phy"
        elif file_format == "fasta":
            metapartition_extension = "-meta.fas"
        elif file_format == "nexus":
            metapartition_extension = "-meta.nex"
        elif file_format == "nexus-int":
            metapartition_extension = "-meta.int-nex"

        return metapartition_extension

    def file_overwrite_error(self, file_name):
        # print warning when overwriting a file
        if path.exists(file_name):
            print("WARNING: You are overwriting '" + file_name + "'")

    def write_formatted_file(self, file_format, file_name, alignment):
        # write the correct format string into a file
        with open(file_name, "w", encoding="utf-8") as out_file:
            if file_format == "phylip":
                out_file.write(self.print_phylip(alignment))
            elif file_format == "fasta":
                out_file.write(self.print_fasta(alignment))
            elif file_format == "phylip-int":
                out_file.write(self.print_phylip_int(alignment))
            elif file_format == "nexus":
                out_file.write(self.print_nexus(alignment))
            elif file_format == "nexus-int":
                out_file.write(self.print_nexus_int(alignment))

    def get_alignment_name(self, i, extension):
        # get file name
        file_name = self.alignment_objects[i].get_name() + extension

        return file_name

    def get_alignment_name_no_ext(self, i):
        # get file name without extension
        file_name = self.alignment_objects[i].get_name()

        return file_name

    def write_concat(self, file_format):
        # write concatenated alignment into a file
        concatenated_alignment = self.get_concatenated(self.parsed_alignments)[0]
        file_name = self.concat_out
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, concatenated_alignment)

        print("Wrote concatenated sequences to " + file_format + " file '" + file_name + "'")

    def write_convert(self, index, alignment, file_format, extension):
        # write converted alignment into a file
        file_name = self.get_alignment_name(index, extension)
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, alignment)

    def write_replicate(self, index, alignment, file_format, extension):
        # write replicate alignment into a file
        file_name = "replicate" + str(index + 1) + "_" + str(self.no_loci) + "-loci" + extension
        self.file_overwrite_error(file_name)
        self.write_formatted_file(file_format, file_name, alignment)

    def write_split(self, item, file_format, extension):
        # write split alignments from partitions file
        # bad practice with the dicts; figure out better solution
        partition_name = list(item.keys())[0]
        alignment = item[partition_name]

        if not alignment:
            # If the alignment dict is empty, i.e. no alignment associated with partition name, raise
    error
            raise ValueError("Partition '%s' is empty. No sequences to write." % partition_name)

        # implementation of option --no-san (don't prepend input superalignment filename to the
    `split` outputs)
        if self.no_sup_aln_name:
            file_name = partition_name + extension
        else:
            file_name = str(self.in_files[0].split('.')[0]) + "_" + partition_name + extension

        try:
            self.file_overwrite_error(file_name)
            self.write_formatted_file(file_format, file_name, alignment)
            yield file_name
        except ValueError as e:
            print("There was an issue writing file '%s': %s" % (file_name, str(e)))
            remove(file_name)
            raise

    def write_reduced(self, file_format, extension):
        # write alignment with taxa removed into a file
        prefix = self.reduced_file_prefix
        alns = self.remove_taxa(self.species_to_remove)
        for file_name, aln_dict in alns.items():
            out_file_name = prefix + file_name + extension
            self.file_overwrite_error(out_file_name)
            self.write_formatted_file(file_format, out_file_name, aln_dict)
        return len(alns)

    def write_translated(self, index, alignment, file_format, extension):
        # write alignments translated into amino acids
        prefix = "translated_"
        file_name = self.get_alignment_name(index, extension)
        out_file_name = prefix + file_name + extension
        self.file_overwrite_error(out_file_name)
        self.write_formatted_file(file_format, out_file_name, alignment)

    def write_trimmed(self, index, alignment, file_format, extension):
        # write trimmed alignments
        if self.trim_out:
            out_file_name = self.trim_out
        else:
            prefix = "trimmed_"
            file_name = self.get_alignment_name(index, extension)
            out_file_name = prefix + file_name
        self.file_overwrite_error(out_file_name)
        self.write_formatted_file(file_format, out_file_name, alignment)

    def write_metapartitions(self, file_format):
        # write metapartitions - combines split and concat
        print("write_out elif action == metapartitions")
        metapartition_extension = self.get_metapartition_extension(file_format)
        list_of_alignments = self.get_partitioned(self.split)
        written_split_files = []
        err_indx = 0

        for item in list_of_alignments:
            try:
                for split_file in self.write_split(item, file_format, metapartition_extension):
                    written_split_files.append(split_file)
            except ValueError as e:
                    print("WARNING: ", e)
                    err_indx += 1
        if len(written_split_files) > 0:
            print("Wrote %d %s metapartition files from partitions provided" %
(len(written_split_files), file_format))
        if err_indx > 0:
            print("WARNING: %d file(s) raised an error while writing (see above)." % err_indx)

        # now set inputs to be the collated metapartition alignment files
        self.in_files = written_split_files
        self.alignment_objects = self.get_alignment_objects()
        self.parsed_alignments = self.get_parsed_alignments()

        # concat metapartition alignment files
        self.write_concat(file_format)

    def write_out(self, action, file_format):
        # write other output files depending on command (action)
        extension = self.get_extension(file_format)

        if action == "concat":
            self.write_concat(file_format)

        elif action == "convert":
            length = len(self.alignment_objects)
            [
                self.write_convert(i, alignment, file_format, extension)
                for i, alignment in enumerate(self.parsed_alignments)
            ]
            print("Converted " + str(length) + " files from " + self.in_format + " to " + file_format)

        elif action == "replicate":
            [
                self.write_replicate(i, alignment, file_format, extension)
                for i, alignment in enumerate(self.get_replicate(self.no_replicates, self.no_loci))
            ]

            print("Constructed " + str(self.no_replicates) + " replicate data sets, each from " +
str(self.no_loci) + " alignments")

        elif action == "split":
            list_of_alignments = self.get_partitioned(self.split)
            written_split_files = []
            err_indx = 0

            for item in list_of_alignments:
                try:
                    for split_file in self.write_split(item, file_format, extension):
                        written_split_files.append(split_file)
                except ValueError as e:
                        print("WARNING: ", e)
                        err_indx += 1
            if len(written_split_files) > 0:
                print("Wrote %d %s files from partitions provided" % (len(written_split_files),
file_format))
            if err_indx > 0:
                print("WARNING: %d file(s) raised an error while writing (see above)." % err_indx)

        elif action == "metapartitions":
            self.write_metapartitions(file_format)

        elif action == "remove":
            aln_no = self.write_reduced(file_format, extension)
            if aln_no:
                print("Wrote " + str(aln_no) + " " + str(file_format) + " files with reduced taxon
set")

        elif action == "translate":
            if self.data_type == "aa":
                print("ERROR: cannot translate; you said your alignment already contains amino acids")
                sys.exit()
            translated_alignment_dicts = self.get_translated(self.genetic_code, self.reading_frame)
            length = len(self.alignment_objects)
            [
                self.write_translated(i, alignment, file_format, extension)
                for i, alignment in enumerate(translated_alignment_dicts)
            ]
            print("Translated " + str(length) + " files to amino acid sequences")

        elif action == "trim": # self.trim_fraction, self.parsimony_check
            trimmed_alignment_dicts = self.get_trimmed(self.trim_fraction, self.parsimony_check)
            length = len(self.alignment_objects)
            [
                self.write_trimmed(i, alignment, file_format, extension)
                for i, alignment in enumerate(trimmed_alignment_dicts)
            ]
            print("Trimmed", str(length), "file(s) to have", self.trim_fraction, "minimum occupancy
per alignment column")


def main():

    # initialize parsed arguments and meta alignment objects
    kwargs = run()
    meta_aln = MetaAlignment(**kwargs)

    if meta_aln.command == "summary":
        meta_aln.write_summaries(kwargs["summary_out"])

    if meta_aln.by_taxon_summary:
        print("Printing taxon summaries")
        meta_aln.write_taxa_summaries()

    if meta_aln.command == "convert":
        meta_aln.write_out("convert", kwargs["out_format"])

    if meta_aln.command == "concat":
        meta_aln.write_out("concat", kwargs["out_format"])
        meta_aln.write_partitions(kwargs["concat_part"], kwargs["part_format"], kwargs["data_type"],
kwargs["codons"])

    if meta_aln.command == "replicate":
        meta_aln.write_out("replicate", kwargs["out_format"])

    if meta_aln.command == "split":
        meta_aln.write_out("split", kwargs["out_format"])

    if meta_aln.command == "metapartitions":
        # `metapartitions` is essentially `split` + `concat`. Currently you can't set an out_format:
        # it's automatically set to match the in_format because the intermediate `split` outputs
become
        # the 'new' in_files for the `concat` operation, and then calling either:
        #  -> AminoAcidAlignment(Alignment.__init__(self, in_file, in_format, data_type))
        #  -> DNAAlignment(Alignment.__init__(self, in_file, in_format, data_type))
        # through MetaAlignment.get_alignment_object(alignment, self.in_format, self.data_type)
        meta_aln.write_out("metapartitions", kwargs["in_format"])
        meta_aln.write_partitions(kwargs["concat_part"], kwargs["part_format"], kwargs["data_type"],
"none")

    if meta_aln.command == "remove":
        meta_aln.write_out("remove", kwargs["out_format"])

    if meta_aln.command == "translate":
        meta_aln.write_out("translate", kwargs["out_format"])

    if meta_aln.command == "trim":
        meta_aln.write_out("trim", kwargs["out_format"])

        # meta_aln.write_out("translate", kwargs["out_format"])
```

```

def run():

    # initialize parsed arguments
    config = ParsedArgs()
    # get arguments
    config_dict = config.get_args_dict()
    return config_dict

if __name__ == '__main__':
    main()
```

8.5 README.md File Reference

Index