taxon_pair + taxon + protein_start + protein end - listParseData - listStructData - listTaxa + getVariables() + print() + has_data() + taxon_pair() + taxon pair() + initList() + free_taxonPairList() + init_taxon_pair() + assert_class() **listPair** pipe_struct - MODE_PAIRWISE_OUTPUT_ABC - MODE_PAIRWISE_OUTPUT_MCL - PRINT_IN_ABC_FORMAT - PRINT_IN_MCL_FORMAT - SORT_ABC_DATA - PRINT_NORMALIXATION_BASIS - DEBUG_NORM - MODE_PAIRWISE_OUTPUT - MODE INTEGER OUTPUT - DIVIDE_BY_NORMALIZATION_VALUE_FOR_ABC_FORMAT - DIVIDE_BY_NORMALIZATION_VALUE_FOR_MCL_FORMAT - listStructData - listParseData - max input value - g_protein_length - g_taxon_length SIZE_BUFFER - USE EVERYREL AS ARRNORM BASIS LENGTH KEY NAMES WIDTH_DISTANCE - lock_set_ps_id - OPT_GET_FILE_LOCALLY + getFromBufferToStruct() + finalize_memory() - init_arrNorm() produce_row() - build_normArr() insert_into_stack_rel() - insertOrthologs() - insertInpaInpaRelations()

- taxon_length

- listOrtho - listTaxa - stackRel

- log - n_threads - in_use

- list_pair_pos - PIPE_TYPE

- arrAvgNorm

- listPair

- I arrNorm - mcIData

+ operator()() + free_mem() + pipe_struct()