
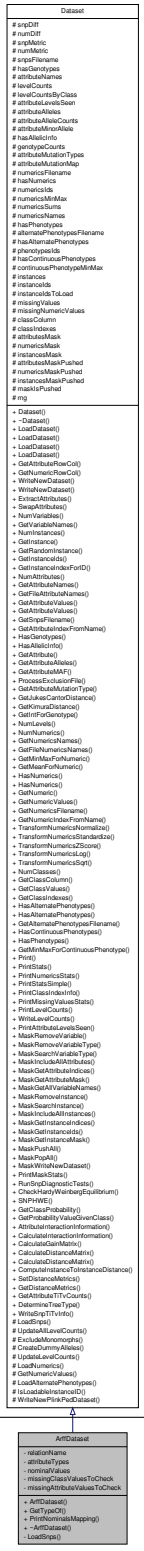
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attributeMutationTypes
attributeMutationMap
numericsFilename
hasNumerics
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hasPhenotypes
alternatePhenotypesFilename
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hasContinuousPhenotypes
continuousPhenotypeMinMax
instances
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instanceIdsToLoad
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+ GetJukesCantorDistance()
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+ PrintMaskStats()
+ RunSnpDiagnosticTests()
+ CheckHardyWeinbergEquilibrium()
+ SNPHWE()
+ GetClassProbability()
+ GetProbabilityValueGivenClass()
+ AttributeInteractionInformation()
+ CalculateInteractionInformation()
+ CalculateGainMatrix()
+ CalculateDistanceMatrix()
+ CalculateDistanceMatrix()
+ ComputeInstanceToInstanceDistance()
+ SetDistanceMetrics()
+ GetDistanceMetrics()
+ GetAttributeTiTv Counts()
+ DetermineTreeType()
+ WriteSnpTiTvInfo()
LoadSnps()
UpdateAllLevelCounts()
ExcludeMonomorphic()
CreateDummyAlleles()
UpdateLevelCounts()
LoadNumerics()
GetNumericValues()
LoadAlternatePhenotypes()
IsLoadableInstanceID()
WriteNewPlinkPedDataset()
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- attributeTypes
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+ GetTypeOf()
+ PrintNominalsMapping()
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- LoadSnps()


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genotypeCounts
attributeMutationTypes
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numericsFilename
hasNumerics
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hasPhenotypes
alternatePhenotypesFilename
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hasContinuousPhenotypes
continuousPhenotypesMinMax
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+ CheckHardyWeinbergEquilibrium()
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UpdateAllLevelCounts()
ExcludeMonomorphs()
CreateDummyAlleles()
UpdateLevelCounts()
LoadNumerics()
GetNumericValues()
LoadAlternatePhenotypes()
IsLoadableInstanceID()
WriteInstancesFromPlinkDataset()
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levelCounts
levelCountsByClass
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attributeMinorAllele
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genotypeCounts
attributeMutationTypes
attributeMutationMap
numericsFilename
hasNumerics
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hasPhenotypes
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+ CheckHardyWeinbergEquilibrium()
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+ GetClassProbability()
+ GetProbabilityValueGivenClass()
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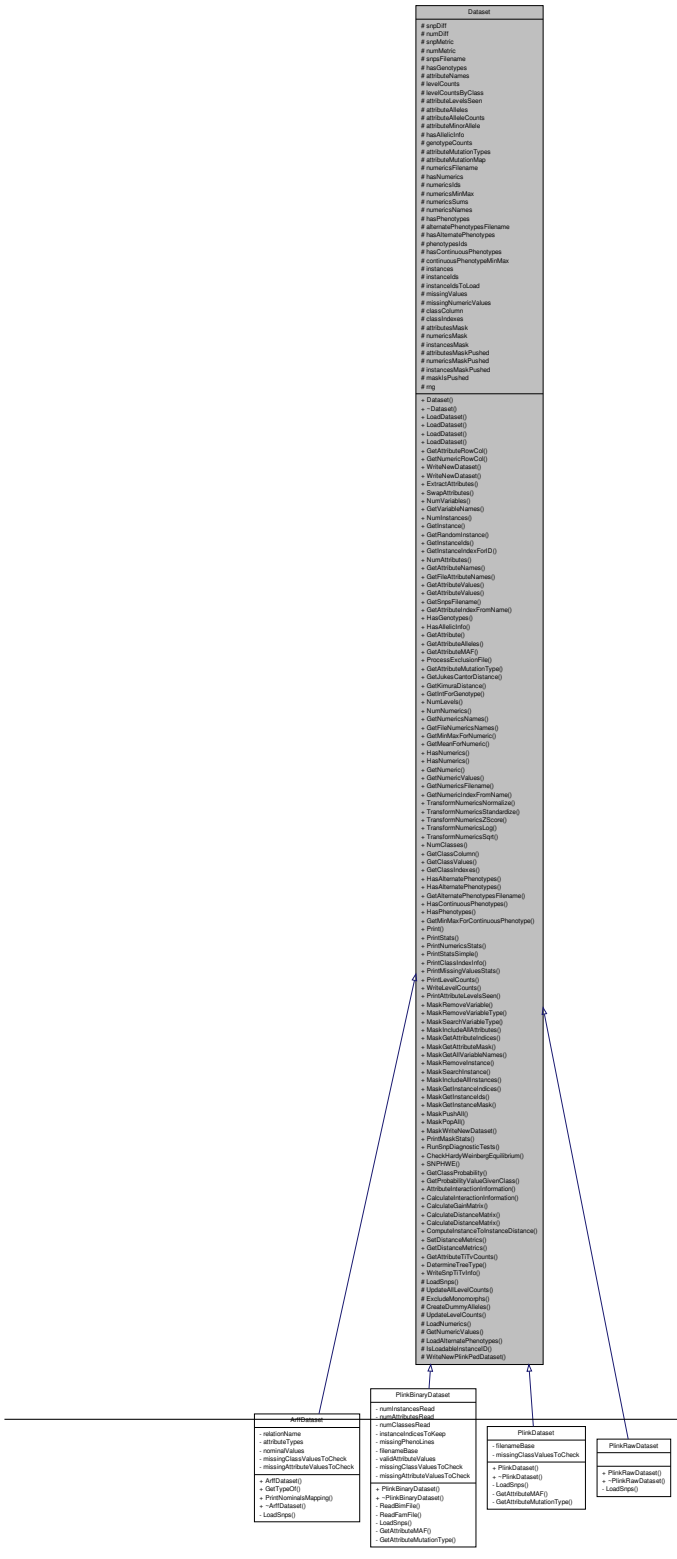
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genotypeCounts
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numericsFilename
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hasPhenotypes
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+ ProcessExclusionFile()
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+ GetJukesCantorDistance()
+ GetKimuraDistance()
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+ RunSnpDiagnosticTests()
+ CheckHardyWeinbergEquilibrium()
+ SNPHWE()
+ GetClassProbability()
+ GetProbabilityValueGivenClass()
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+ GetAttributeTiTvCounts()
+ DetermineTreeType()
+ WriteSnpTiTvInfo()
LoadSnps()
UpdateAllLevelCounts()
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CreateDummyAlleles()
UpdateLevelCounts()
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GetNumericValues()
LoadAlternatePhenotypes()
IsLoadableInstanceID()
WriteNewPlinkPedDataset()
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- relationName
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- nominalValues
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+ GetTypeOf()
+ PrintNominalsMapping()
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PlinkBinaryDataset
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- ReadBimFile()
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- GetAttributeMAF()
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UpdateAllLevelCounts()
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attributeMutationTypes
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hasNumerics
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hasPhenotypes
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+ PrintMasksStats()
+ RunSvgDiagnosticTests()
+ CheckHardyWeinbergEquilibrium()
+ SNPHWE()
+ GetClassProbability()
+ GetProbabilityValueGivenClass()
+ AttributeInteractionInformation()
+ CalculateInteractionInformation()
+ CalculateGainMatrix()
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+ ComputeInstanceToInstanceDistance()
+ SetDistanceMatrix()
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+ GetAttributeTiTvType()
+ WriteSvgTiTvVcf()
LoadSvgs()
UpdateAlleleCounts()
ExcludeMonomorphic()
CreateDummyAlleles()
UpdateLevelCounts()
LoadNumerics()
GetNumericValues()
LoadAlternatePhenotypes()
IsLoadableInstanceID()
WriteNewPrunedDataset()
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+ attributes
+ numerics
- dataset
- classLabel
- bestNeighborIdxSameClass
- bestNeighborIdxDiffClass
- bestNeighborIdx
- neighborInfluenceFactorDs
- predictedValueTau
+ DatasetInstance()
+ ~DatasetInstance()
+ GetDataset*()
+ LoadInstanceFromVector()
+ NumAttributes()
+ GetAttribute()
+ NumNumerics()
+ GetNumeric()
+ AddNumeric()
+ GetClass()
+ SetClass()
+ GetPredictedValueTau()
+ SetPredictedValueTau()
+ GetInfluenceFactorDi()
+ ClearInfluenceFactors()
+ AddInfluenceFactorDi()
+ Print()
+ SwapAttributes()
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+ PrintDistanceFarthest()
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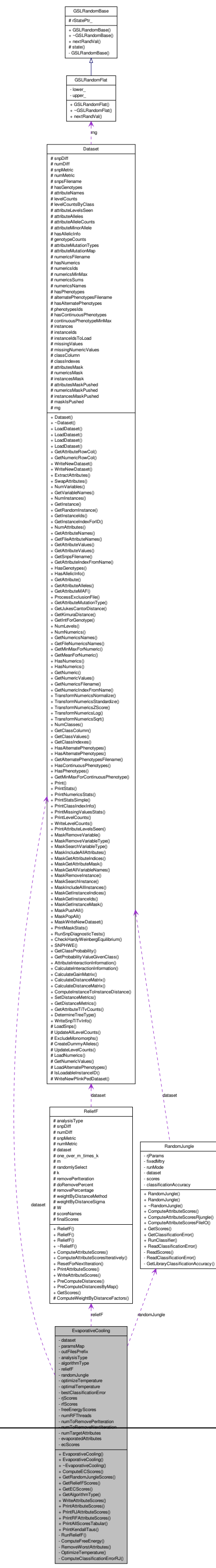
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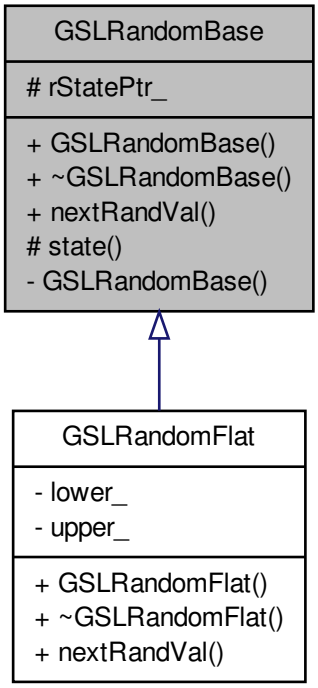
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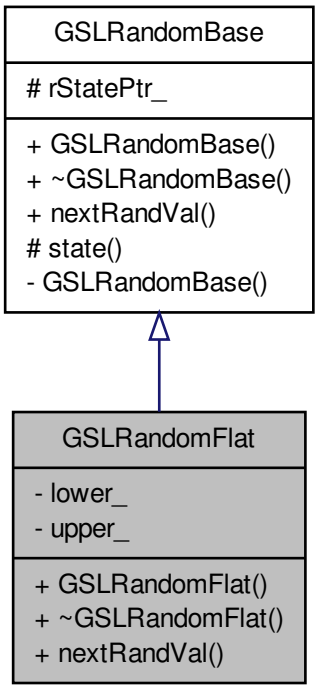
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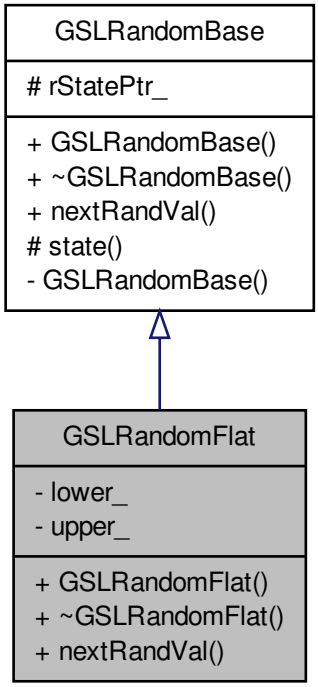
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attributeNames
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levelCountsByClass
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genotypeCounts
attributeMutationTypes
attributeMutationMap
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numericsIds
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numericsSums
numericsNames
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hasAlternatePhenotypes
phenotypesIds
hasContinuousPhenotypes
continuousPhenotypesMinMax
instances
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missingNumericValues
classColumn
classIndexes
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numericsMask
instancesMask
attributesMaskPushed
numericsMaskPushed
instancesMaskPushed
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+ GetAttributeIndexFromName()
+ HasGenotypes()
+ HasAlleleInfo()
+ GetAttribute()
+ GetAttributeAlleles()
+ GetAttributeMAF()
+ ProcessExclusionFile()
+ GetAttributeMutationType()
+ GetJukesCantorDistance()
+ GetKimuraDistance()
+ GetIntForGenotype()
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+ TransformNumericsStandardize()
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+ MaskPopAll()
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+ CheckHardyWeinbergEquilibrium()
+ SNPHWE()
+ GetClassProbability()
+ GetProbabilityValueGivenClass()
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+ CalculateInteractionInformation()
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+ CalculateDistanceMatrix()
+ CalculateDistanceMatrix()
+ ComputeInstanceToInstanceDistance()
+ SetDistanceMetrics()
+ GetDistanceMetrics()
+ GetAttributeTiTvCounts()
+ DetermineTreeType()
+ WriteSnpTiTvInfo()
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ExcludeMonomorphic()
CreateDummyAlleles()
UpdateLevelCounts()
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LoadAlternatePhenotypes()
IsLoadableInstanceID()
WriteNewPlinkPedDataset()
PlinkBinaryDataset
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- numAttributesRead
- numClassesRead
- instanceIndicesToKeep
- missingPhenoLines
- filenameBase
- validAttributeValues
- missingClassValuesToCheck
- missingAttributeValuesToCheck
+ PlinkBinaryDataset()
+ ~PlinkBinaryDataset()
- ReadBimFile()
- ReadFamFile()
- LoadSnps()
- GetAttributeMAF()
- GetAttributeMutationType()


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+ ~GSLRandomFlat()
+ nextRandVal()
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attributeMinorAllele
hasAllelicInfo
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attributeMutationTypes
attributeMutationMap
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numericsSums
numericsNames
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GetNumericValues()
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- GetAttributeMAF()
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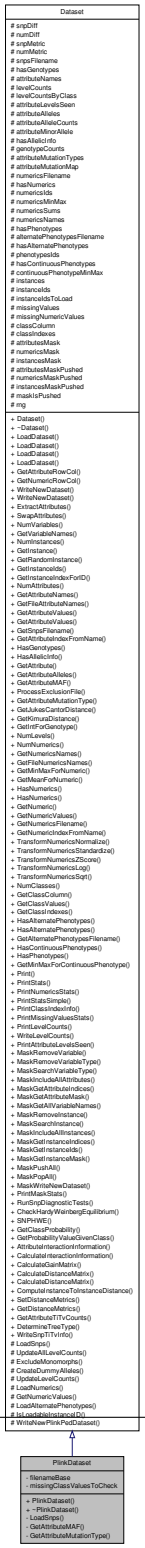
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- GetAttributeMAF()
- GetAttributeMutationType()


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+ CheckHardyWeinbergEquilibrium()
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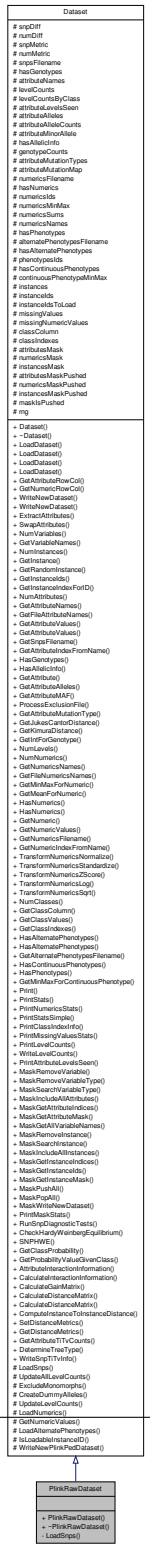
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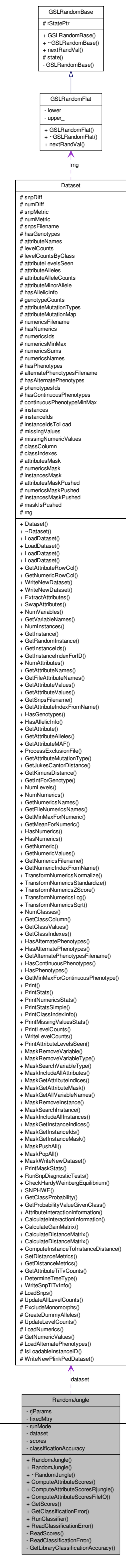

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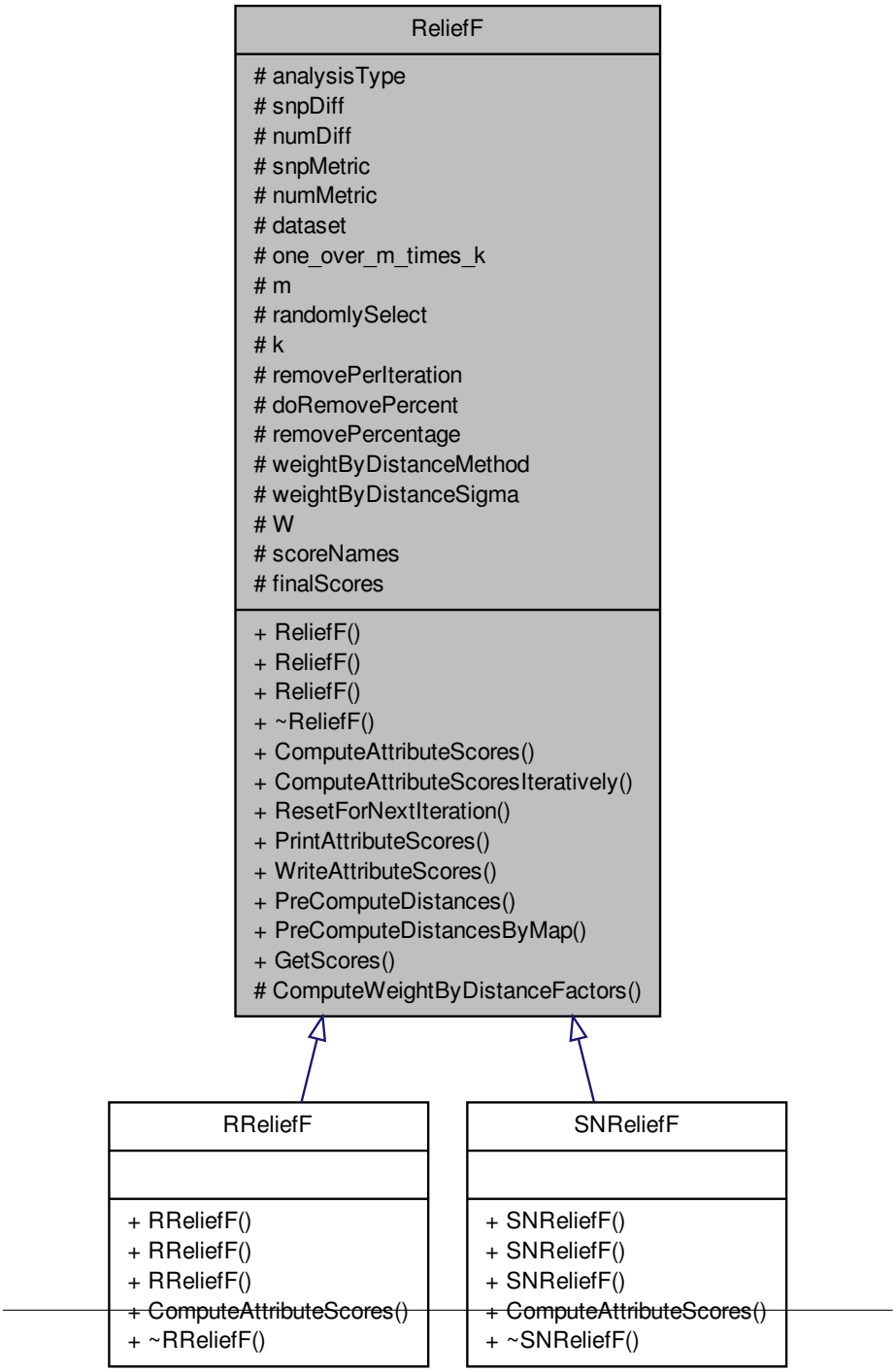
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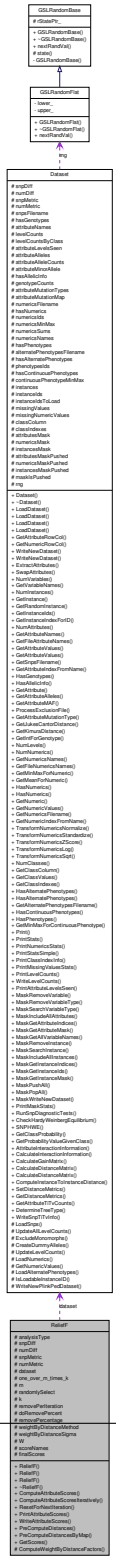
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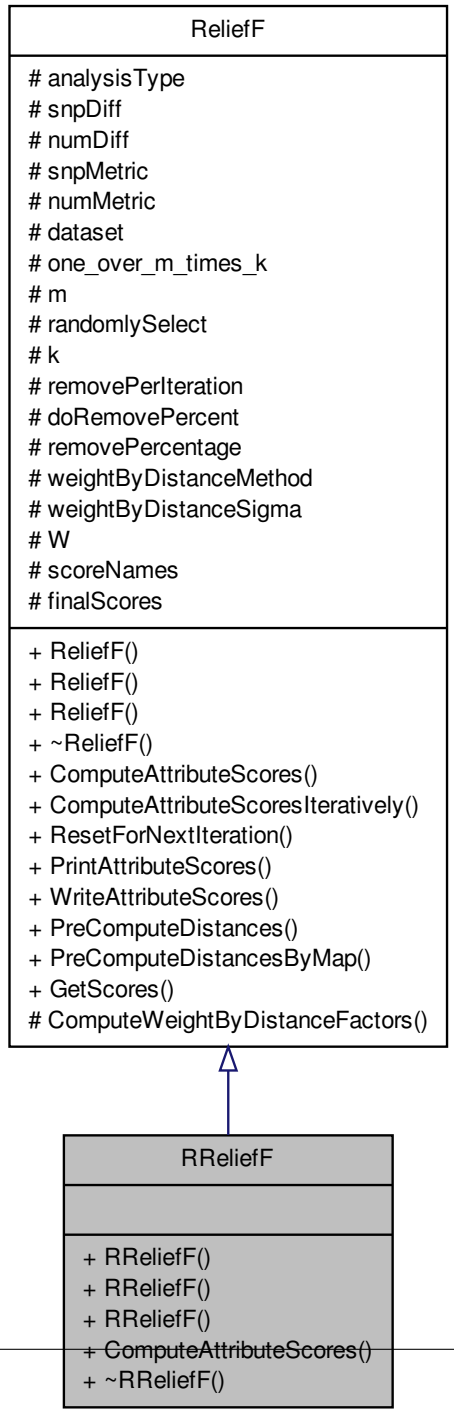
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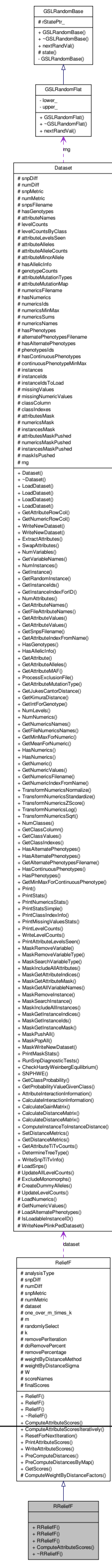

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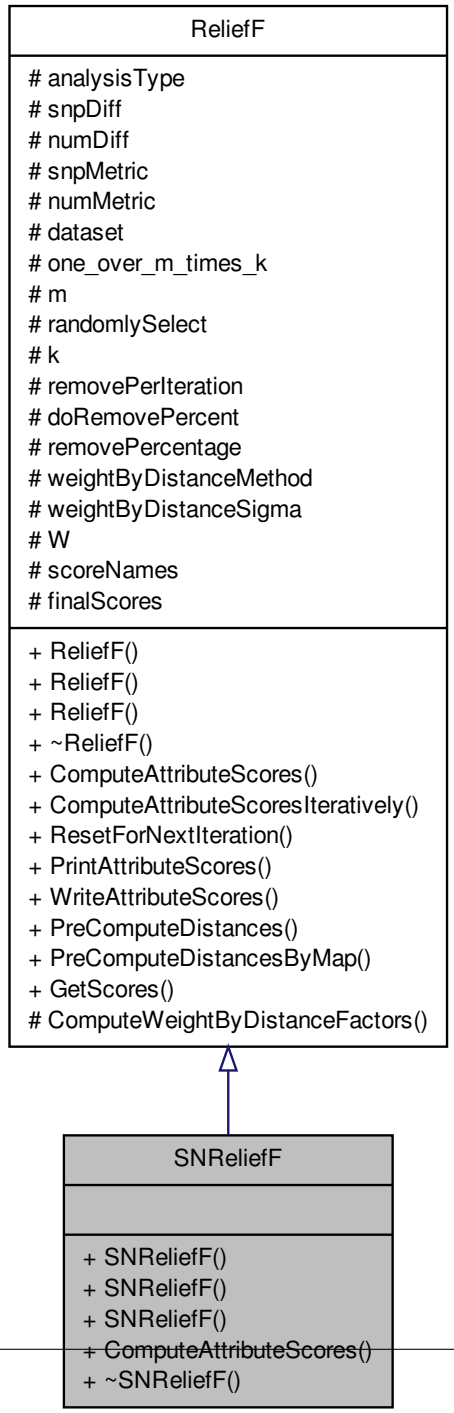
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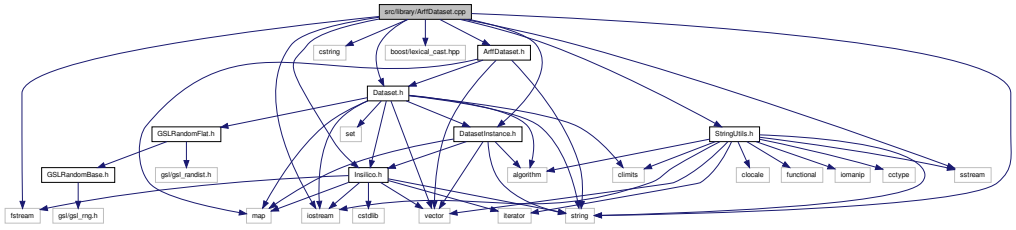
+ GetAttributeTypeCounts()
+ DetermineTreeType()
+ WriteSnpTiTvInfo()
LoadSnps()
UpdateAllLevelCounts()
ExcludeMonomorphs()
CreateDummyAlleles()
UpdateLevelCounts()
LoadNumerics()
GetNumericValues()
LoadAlternatePhenotypes()
IsLoadableInstance(0)
WriteNewRicksPrePDataset()
dataset
ReliefF
analysisType
snpsDiff
numDiff
snpsMetric
numMetric
dataset
one_over_m_times_k
m
randomlySelect
k
removePerIteration
distRemovePercent
removePercentage
weightByDistanceMethod
weightByDistanceSigma
W
scoreNames
finalScores
+ ReliefF()
+ ReliefF()
+ ReliefF()
+ ~ReliefF()
+ ComputeAttributeScores()
+ ComputeAttributeScoresIterively()
+ ResetForNextIteration()
+ PrintAttributeScores()
+ WriteAttributeScores()
+ PreComputeDistances()
+ PreComputeDistancesByMap()
+ GetScores()
ComputeWeightByDistanceFactors()
SNPReliefF
+ SNPReliefF()
+ SNPReliefF()
+ SNPReliefF()
+ ComputeAttributeScores()
+ ~SNPReliefF()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GSLRandomBase.h
gsl/gsl_randist.h
Insilico.h
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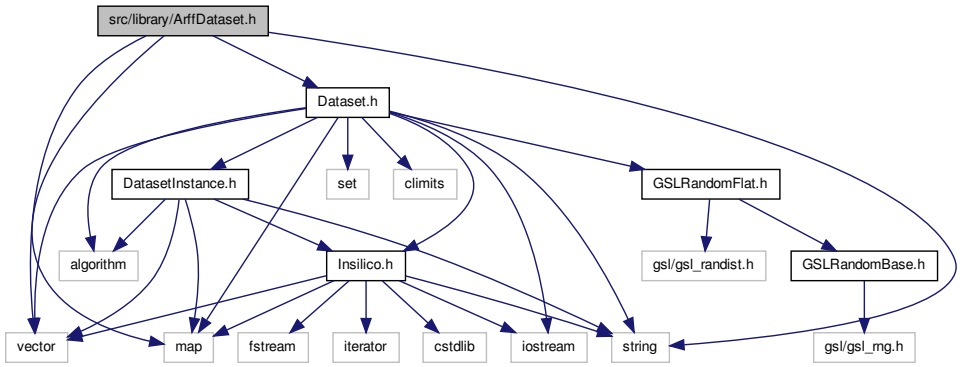
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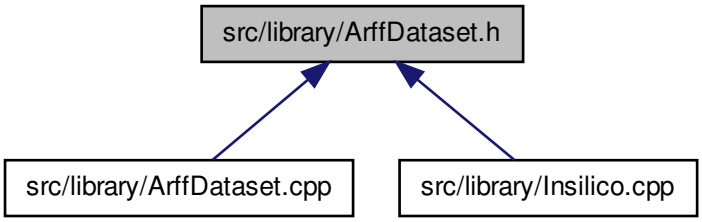
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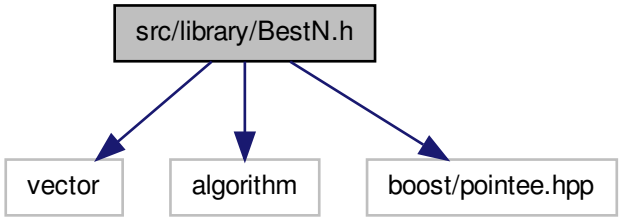
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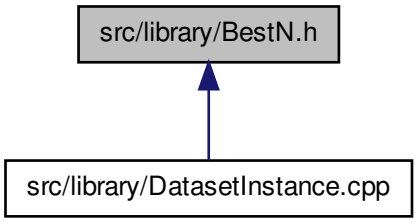
boost/pointee.hpp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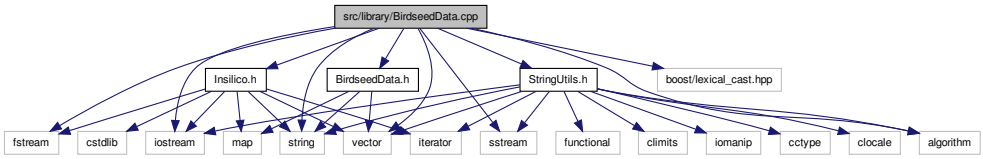
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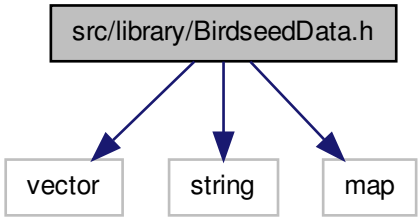
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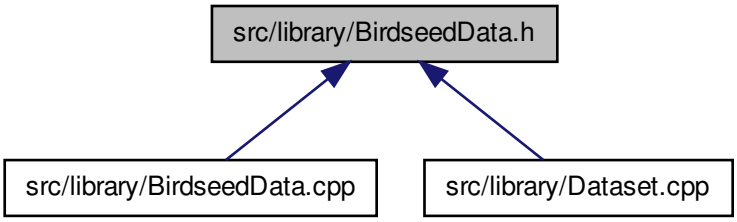
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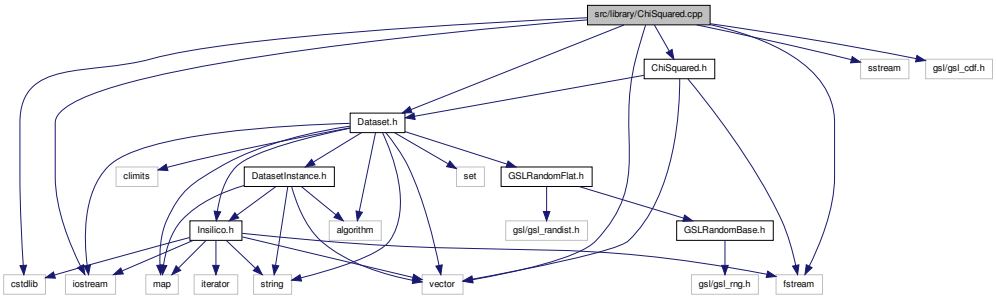
src/library/Dataset.cpp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Dataset.h
climits
DatasetInstance.h
set
GSLRandomFlat.h
Insilico.h
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GSLRandomBase.h
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iostream
map
iterator
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gsl/gsl_rng.h
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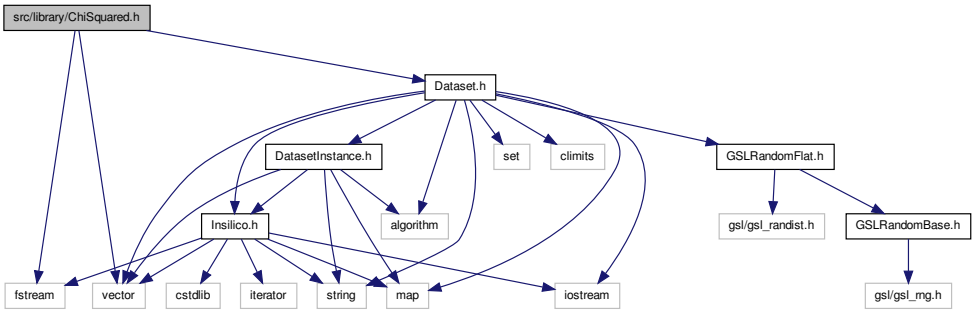
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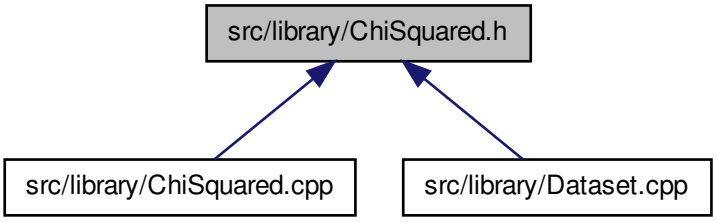
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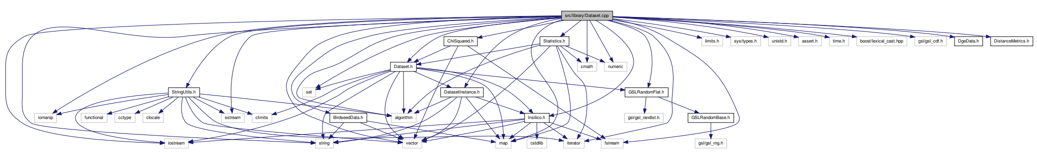
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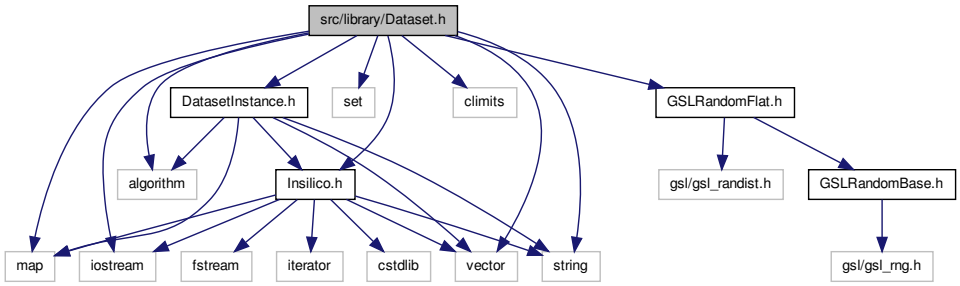
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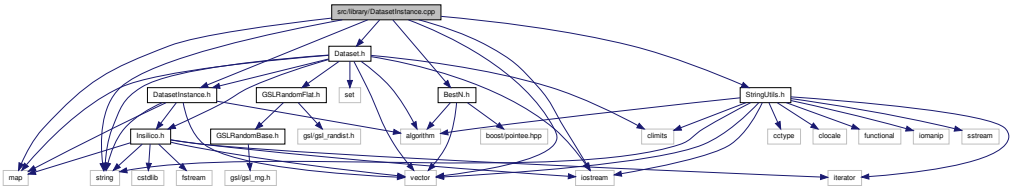
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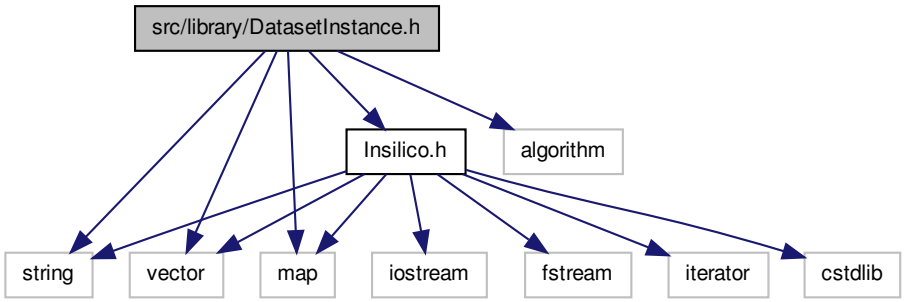
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iterator
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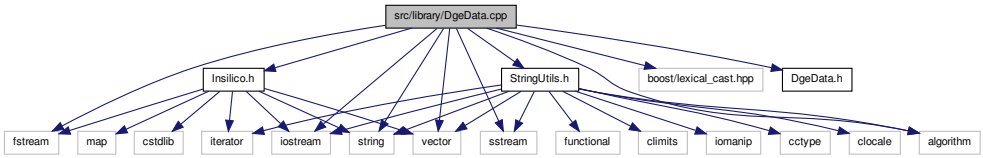
src/library/DgeData.cpp
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boost/lexical_cast.hpp
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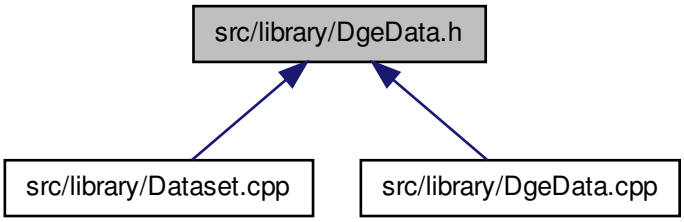
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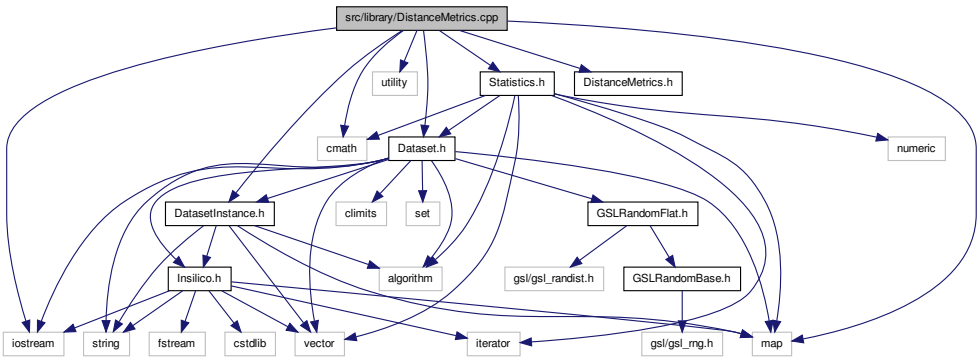
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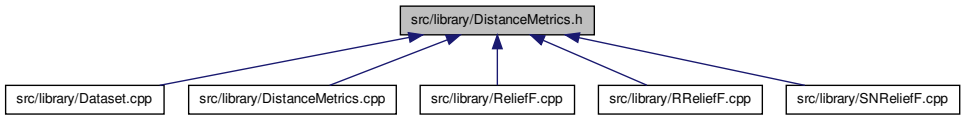
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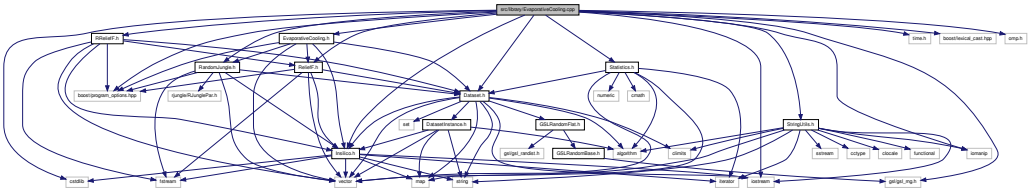
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RandomJungle.h
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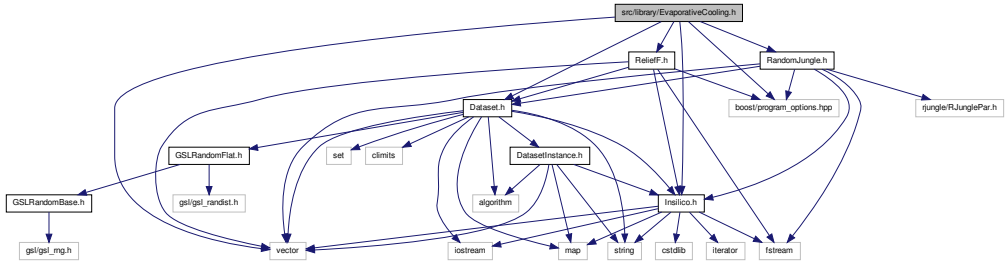
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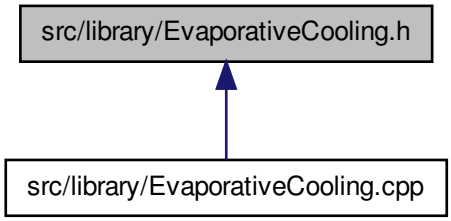
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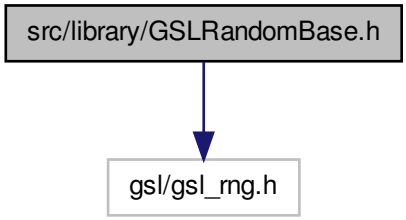
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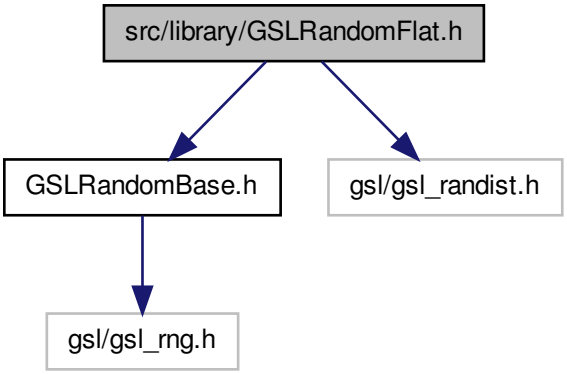
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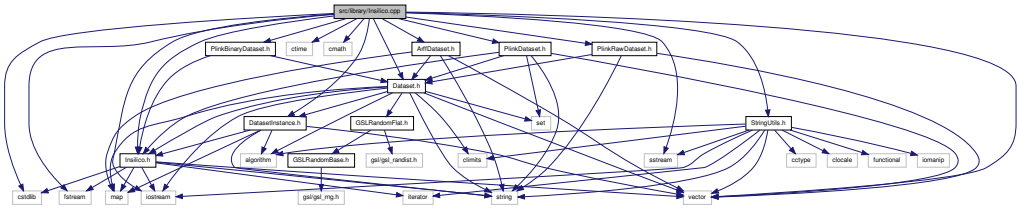
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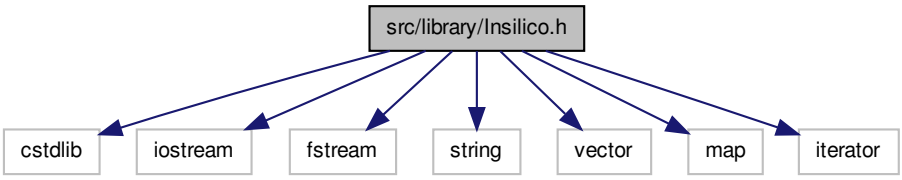
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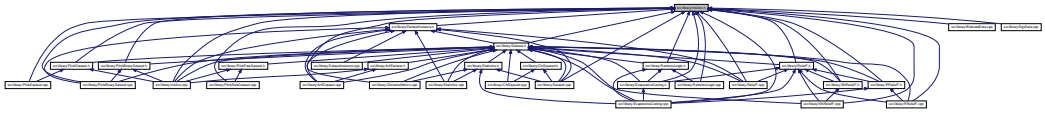

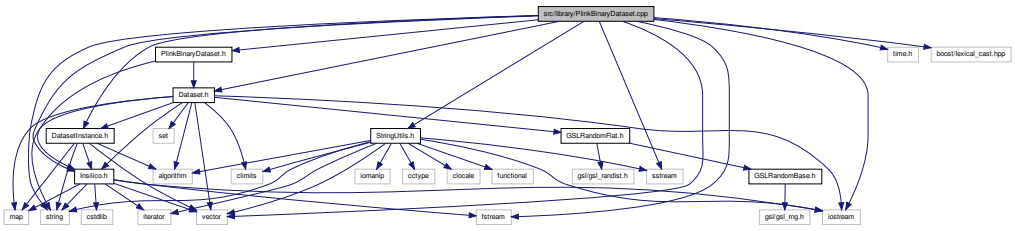
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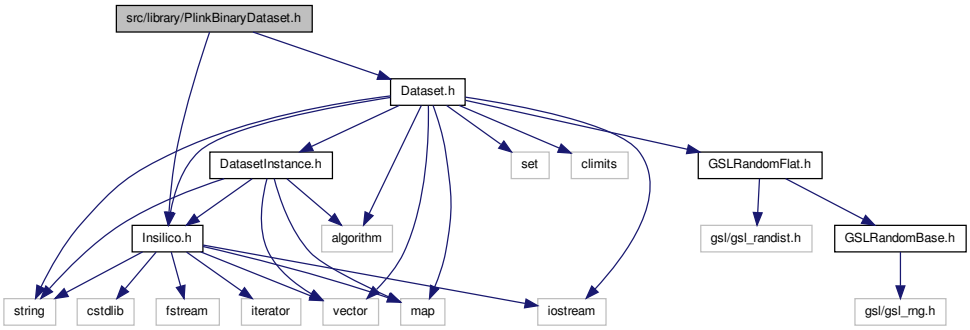
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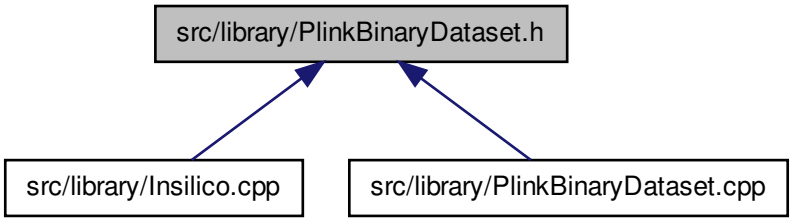
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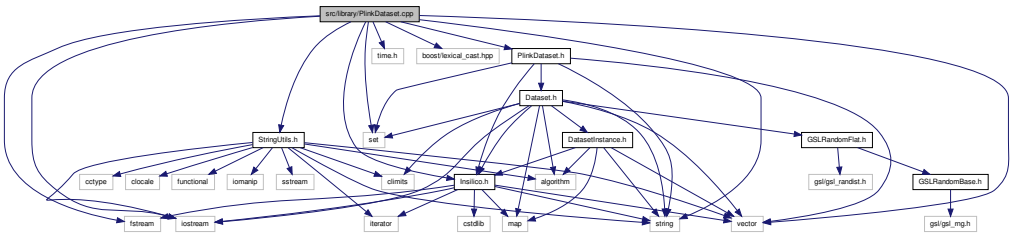
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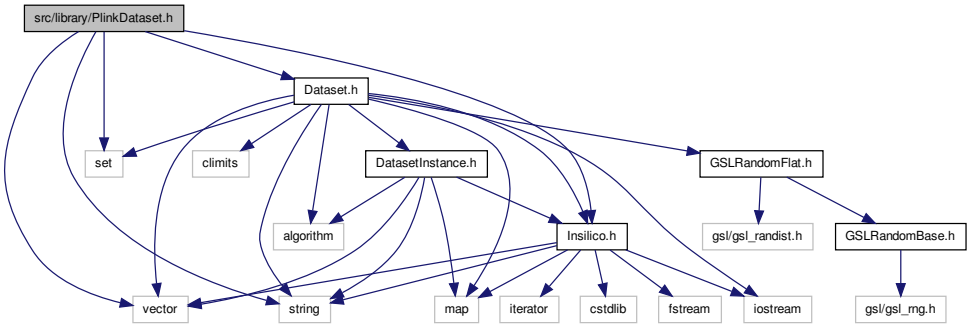
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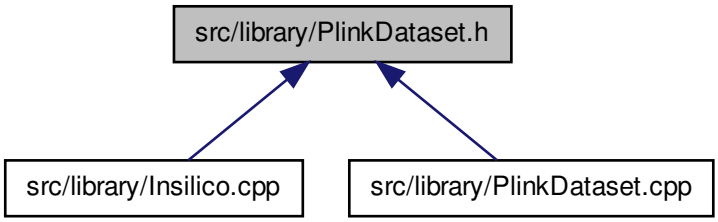
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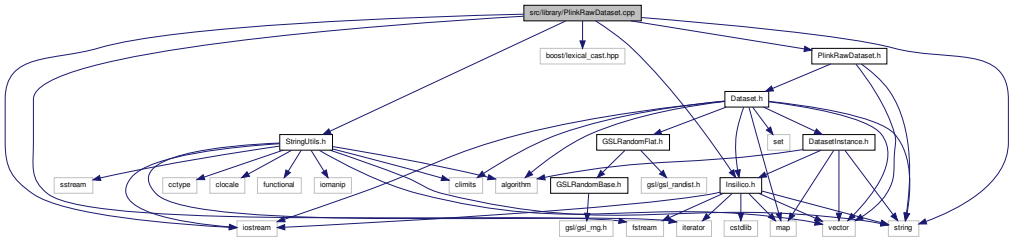
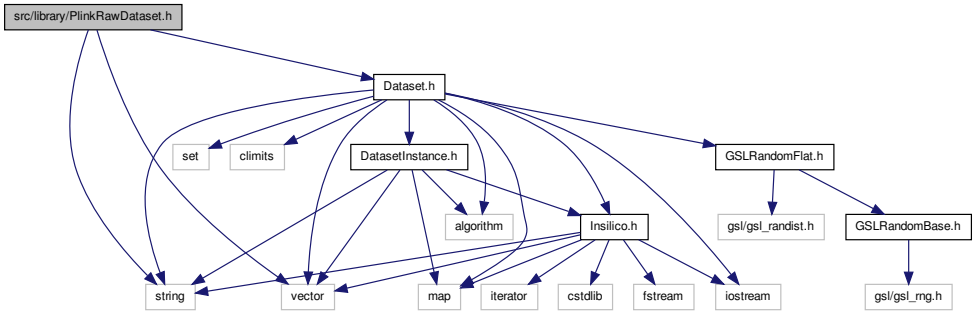

src/library/PlinkRawDataset.cpp
boost/lexical_cast.hpp
PlinkRawDataset.h
Dataset.h
StringUtils.h
GSLRandomFlat.h
set
DatasetInstance.h
sstream
cctype
clocale
functional
iomanip
climits
algorithm
GSLRandomBase.h
gsl/gsl_randist.h
lnsilico.h
iostream
gsl/gsl_rng.h
fstream
iterator
cstdlib
map
vector
string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Dataset.h
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DatasetInstance.h
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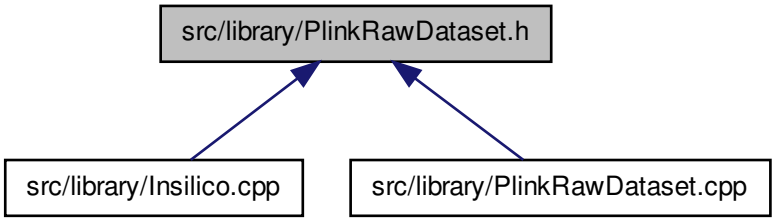
gsl/gsl_rng.h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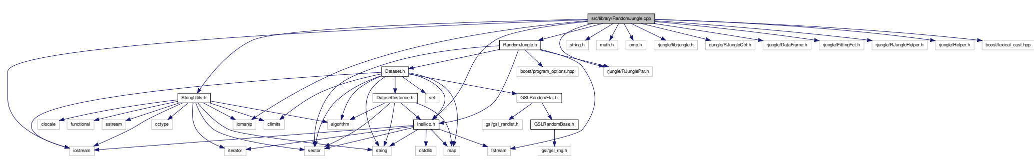
src/library/Insilico.cpp
src/library/PlinkRawDataset.cpp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RandomJungle.h
string.h
math.h
omp.h
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rjungle/RJungleCtrl.h
rjungle/DataFrame.h
rjungle/FittingFct.h
rjungle/RJungleHelper.h
rjungle/Helper.h
boost/lexical_cast.hpp
Dataset.h
boost/program_options.hpp
rjungle/RJunglePar.h
StringUtils.h
DatasetInstance.h
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GSLRandomFlat.h
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iomanip
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algorithm
Insilico.h
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iterator
vector
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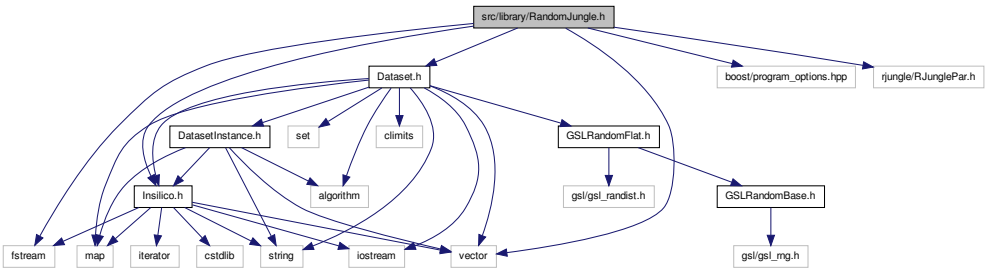
cstdlib
map
fstream
gsl/gsl_rng.h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Dataset.h
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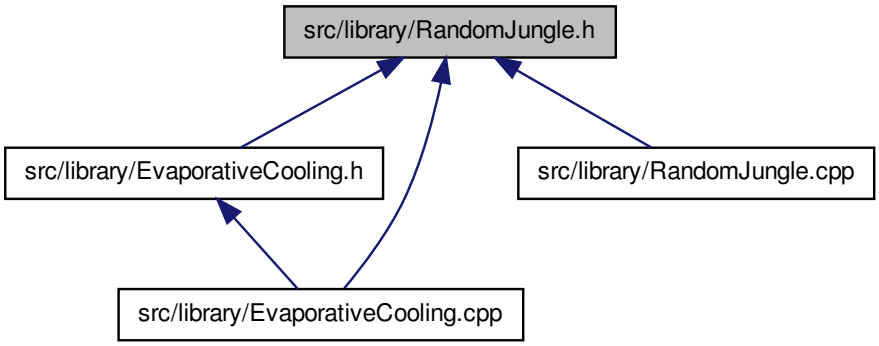
gsl/gsl_rng.h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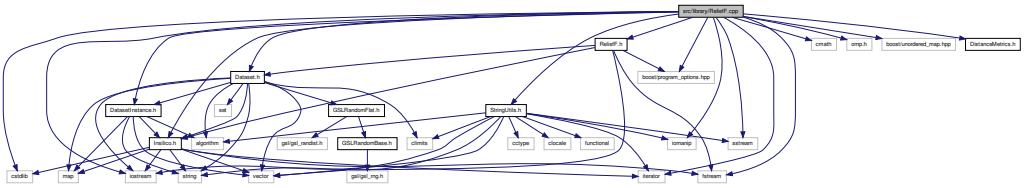
src/library/EvaporativeCooling.h
src/library/RandomJungle.cpp
src/library/EvaporativeCooling.cpp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boost/program_options.hpp
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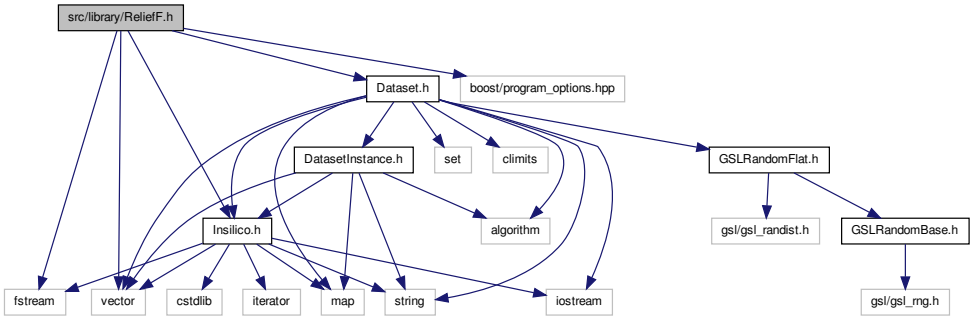
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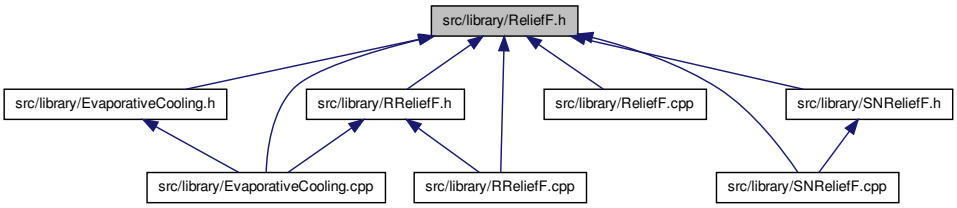
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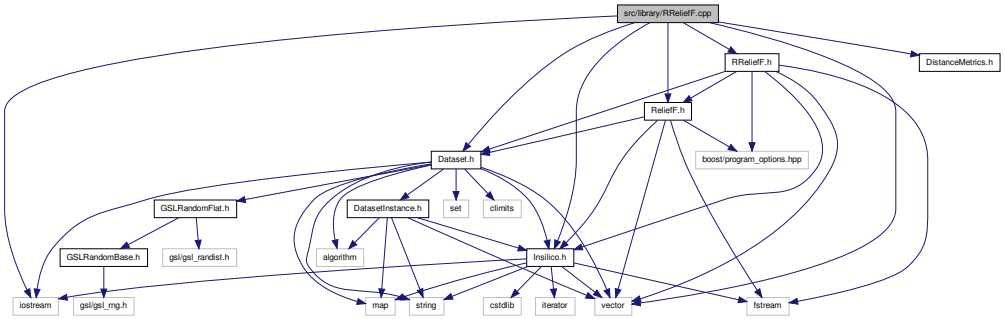
src/library/EvaporativeCooling.h
src/library/RReliefF.h
src/library/ReliefF.cpp
src/library/SNReliefF.h
src/library/EvaporativeCooling.cpp
src/library/RReliefF.cpp
src/library/SNReliefF.cpp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GSLRandomFlat.h
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iostream
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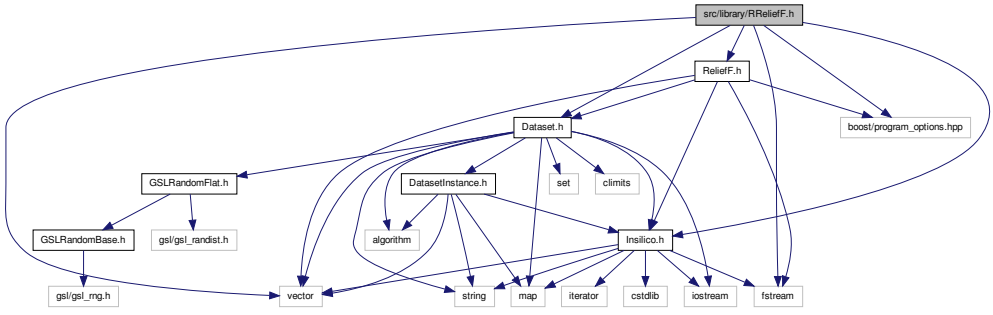
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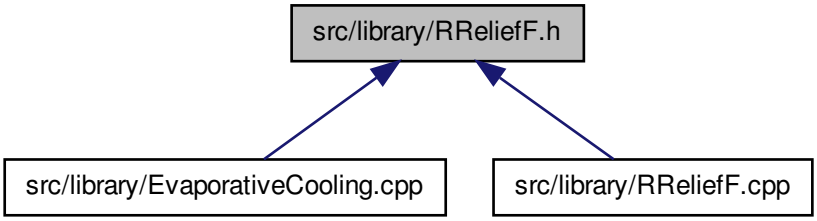
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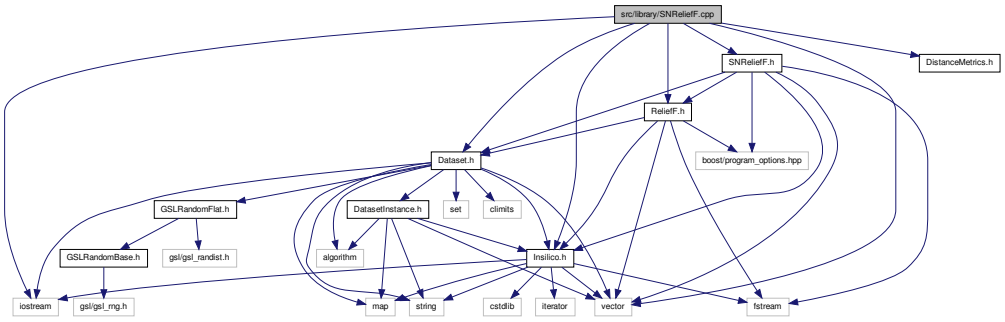
src/library/EvaporativeCooling.cpp
src/library/RReliefF.cpp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ReliefF.h
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boost/program_options.hpp
GSLRandomFlat.h
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GSLRandomBase.h
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gsl/gsl_rng.h
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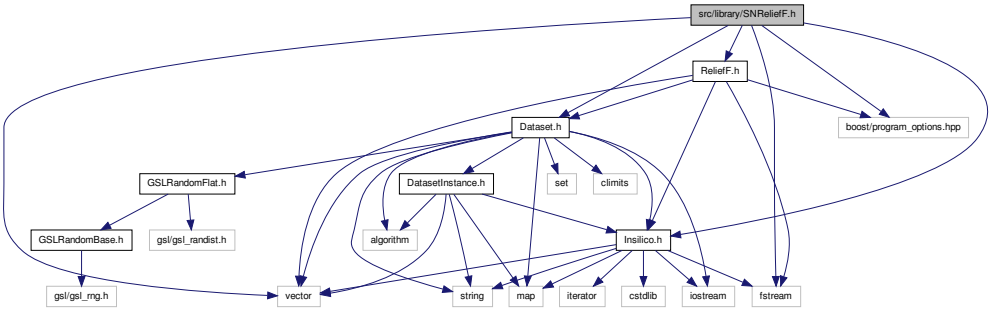
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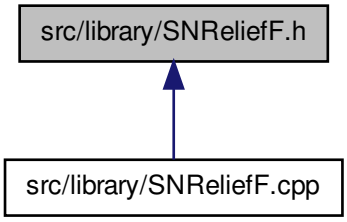
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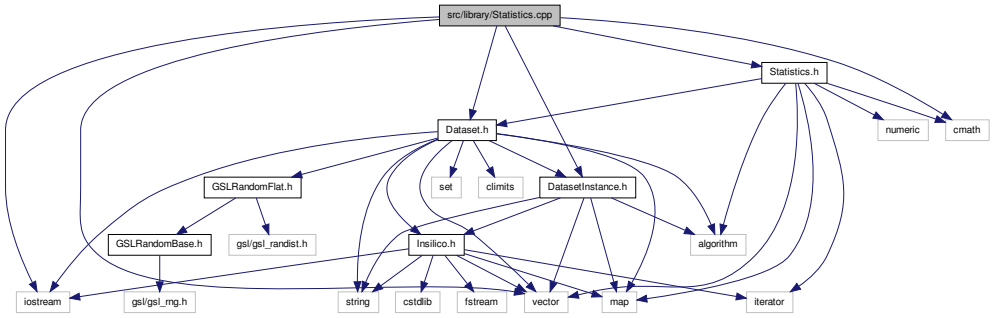
src/library/Statistics.cpp
Statistics.h
Dataset.h
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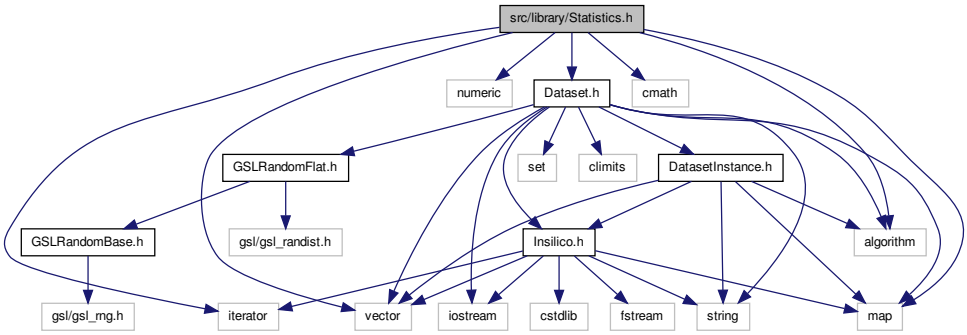
src/library/Statistics.h
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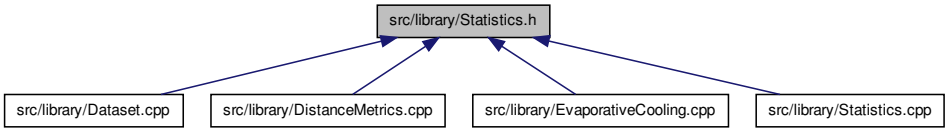
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src/library/Dataset.cpp
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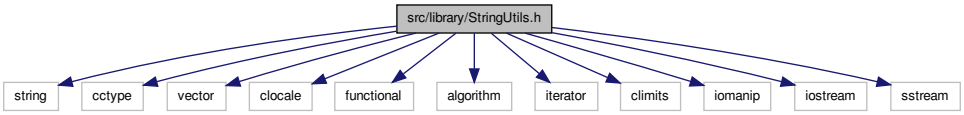
src/library/StringUtils.h
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