Defined packages and functions to be loaded are:

- OMRITools`GeneralTools` with functions:

{ApplyCrop, AutoCropData, BSplineCurveFit, CheckExtension, ClearTemporaryVariables, CompilebleFunctions, CropData, CropInit, CropOutput, CropPadding, CutData, Data2DToVector, Data3DToVector, DataToVector, DecomposeAffineMatrix, DecomposeScaleMatrix, DevideNoZero, DynamicPartition, ExpNoZero, ExtractDemoData, FileSelect, FindCrop, FindMaxDimensions, GetAssetLocation, GridData, GridData3D, GyromagneticRatio, LapFilter, LLeastSquares, LogNoZero, MADNoZero, MakeIntFunction, MeanNoZero, MedFilter, MedianNoZero, MemoryUsage, NNLeastSquares, OutputWeights, PadDirection, PadToDimensions, PadValue, QMRIToolsFuncPrint, QMRIToolsFunctions, QMRIToolsPackages, QuaternionToRotationMatrix, QuaternionVectorToRotationMatrix, RescaleData, ReverseCrop, ReverseDimensions, RMSNoZero, RotateDimensionsLeft, RotateDimensionsRight, RotationMatrixToQuaternion, RotationMatrixToQuaternionVector, SaveImage, SplineKnotsNumber, SplineRegularization, Squeeze, StdFilter, StichData, SumOfSquares, TensMat, TensVec, VectorToData}

- OMRITools`MaskingTools` with functions:

{GetMaskData, GetMaskOnly, GetMaskOutput, GrowMask, HomoginizeData, Mask, MaskClosing, MaskComponents,
MaskData, MaskDilation, MaskFiltKernel, MaskSmoothing, MeanSignal, MergeSegmentations, NormalizeData, NormalizeMeanData,
RemoveMaskOverlaps, RescaleSegmentation, ROIMask, SegmentMask, SmoothMask, SmoothSegmentation, SplitSegmentations, UseMask}

- QMRITools`NiftiTools` with functions:

{CompressNii, CompressNiiFiles, CorrectNiiOrientation, DcmToNii, DeleteOutputFolder, ExportBmat, ExportBval, ExportBvec, ExportNii, ExtractNiiFiles, FlipBvec, GetNiiOrientation, ImportBmat, ImportBval, ImportBvalvec, ImportBvec, ImportExploreDTItens, ImportNii, ImportNiiDiff, ImportNiiDix, ImportNiiT1, ImportNiiT2, MakeNiiOrentationQ, MakeNiiOrentationS, NiiDataType, NiiLegacy, NiiMethod, NiiOffset, NiiScaling, NiiSliceCode, RotateGradients, UseSubfolders, UseVersion}

- QMRITools`ElastixTools` with functions:

{AffineDirections, BsplineDirections, BsplineSpacing, DeleteTempDirectory, FindTransform, HistogramBins, HistogramBinsA, InterpolationOrderReg, InterpolationOrderRegA, Iterations, IterationsA, MethodReg, MethodRegA, NumberSamples, NumberSamplesA, OutputImage, OutputTransformation, PCAComponents, PrintTempDirectory, ReadTransformParameters, RegisterCardiacData, RegisterData, RegisterDataSplit, RegisterDataTransform, RegisterDataTransformSplit, RegisterDiffusionData, RegisterDiffusionDataSplit, RegistrationTarget, Resolutions, ResolutionsA, SplitMethod, TempDirectory, TransformData, UseGPU, \$debugElastix}

- QMRITools`PlottingTools` with functions:

{DropSlices, GetSliceData, GetSlicePositions, GradientPlot, ImageLegend, ImageOrientation, ListSpherePlot, MakeCheckPlot, MakeSliceImages, NormalizeIVIM, PeakNumber, PlotColor, PlotContour, PlotCorrection, PlotData, PlotData3D, PlotDefGrid, PlotDuty, PlotIVIM, PlotMoments, PlotSequence, PlotSpace, PositiveZ, SphereColor, SphereSize}

- OMRITools`DixonTools` with functions:

{DixonAmplitudes, DixonBipolar, DixonClipFraction, DixonFieldStrength, DixonFilterInput, DixonFilterOutput,
DixonFilterSize, DixonFrequencies, DixonIterations, DixonMaskThreshhold, DixonNucleus, DixonPrecessions, DixonReconstruct,
DixonTollerance, DixonToPercent, MakeGroups, MonitorUnwrap, SimulateDixonSignal, Unwrap, UnwrapDimension, UnwrapSplit, UnwrapThresh}

- OMRITools`IVIMTools` with functions:

{BayesianIVIMFit2, BayesianIVIMFit3, ChainSteps, CorrectPar, CorrectParMap, FConvert, FConverti, FilterMaps, FilterSize, FilterType, FitConstrains, FixPseudoDiff, FixPseudoDiffSD, FracCorrect, HistogramPar, IVIMCalc, IVIMComponents, IVIMConstrained, IVIMConstrains, IVIMCorrectData, IVIMFixed, IVIMFunction, IVIMResiduals, IVIMTensFit, MonitorIVIMCalc, OutputSamples, ThetaConv, ThetaConvi, UpdateStep}

{AnisoFilterData, AnisoFilterSteps, AnisoFilterTensor, AnisoItterations, AnisoKappa, AnisoKernel, AnisoStepTime,
AnisoWeightType, DeNoise, DenoiseCSIdata, DenoiseDynamicSpectraData, DeNoiseIterations, DeNoiseKernel, DeNoiseMonitor, NNDeNoise,
NNThreshhold, PCAClipping, PCADeNoise, PCADeNoiseFit, PCAKernel, PCANoiseSigma, PCAOutput, PCATollerance, PCAWeighting, WeightMapCalc}

- QMRITools`CardiacTools` with functions:

{AxesMethod, BackgroundValue, BloodMaskRange, BullPlotMethod, BullseyePlot, CalculateWallMap, CardiacCoordinateSystem, CardiacSegment, CentralAxes, CreateHeart, CutOffMethod, DistanceMeasure, DropSamples, ECVCalc, ExcludeSlices, GetMaskSegmentPoints, GetSegmentLines, GetSegmentSlices, GridLineSpacing, HelixAngleCalc, LCMMethod, LineStep, LinesToSegmentIndex, LineThreshold, MakeECVBloodMask, MakeLineImage, MakeMaskImage, MaskHelix, MaskToLines, MaskWallMap, OutputCheckImage, PlotSegmentMask, PlotSegments, RadialSample, RadialSamples, RowSize, SegmentAngle, SegmentLinesToMask, SegmentsPerSlice, ShowOutliers, ShowPlot, SmoothHelix, StartPoints, StartSlices, TextNumberForm, TextOffset, TextSize, TransmuralPlot}

- QMRITools`RelaxometryTools` with functions:

{CalibrateEPGT2Fit, CreateT2Dictionary, DictB1Range, DictionaryMinSearch, DictT2fRange, DictT2fValue, DictT2IncludeWater, DictT2Range, EPGCalibrate, EPGFatShift, EPGFitFat, EPGFitPoints, EPGMethod, EPGMethodCal, EPGRelaxPars, EPGSignal, EPGSmoothB1, EPGT2Fit, MonitorEPGFit, NonLinearEPGFit, OutputCalibration, ShiftPulseProfile, T1Fit, T1rhoFit, T2Fit, TriExponentialT2Fit, WaterFatShift, WaterFatShiftDirection}

- QMRITools`GradientTools` with functions:

{Bmatrix, BmatrixCalc, BmatrixConv, BmatrixInv, BmatrixRot, BmatrixToggle, CalculateMoments, ConditionCalc, ConditionNumberCalc, ConvertGrads, CorrectBmatrix, CorrectGradients, EnergyCalc, FinalGrads, FindOrder, FlipAxes, FlipGrad, FullGrad, FullSphere, GenerateGradients, GenerateGradientsGUI, GetGradientScanOrder, GetSliceNormal, GetSliceNormalDir, GradBmatrix, GradSeq, GradType, ImportGradObj, OrderSpan, OutputPlot, OutputType, OverPlusCalc, PhaseEncoding, Runs, Steps, StepSizeI, SwitchAxes, UniqueBvalPosition, UnitMulti, UseGrad, VisualOpt}

- OMRITools`TensorTools` with functions:

{ADCCalc, AngleCalc, AngleMap, ColorFAPlot, ConcatenateDiffusionData, Correct, Deriv, Distribution, DriftCorrect, ECalc, EigensysCalc, EigenvalCalc, EigenvecCalc, FACalc, FilterShape, FlipGradientOrientation, FlipTensorOrientation, FullOutput, MeanRes, MonitorCalc, NormalizeSignal, ParameterCalc, Reject, RejectMap, RemoveIsoImages, ResidualCalc, RobustFit, RobustFitParameters, RotationCorrect, SigmaCalc, SortDiffusionData, TensorCalc, TensorCorrect, WestinMeasures}

- QMRITools`JcouplingTools` with functions:

{CenterFrequency, FieldStrength, GetSpinSystem, Linewidth, LinewidthShape, MakeSpinSystem, ReadoutBandwith,
ReadoutMethod, ReadoutOutput, ReadoutPhase, ReadoutSamples, SequencePulseAcquire, SequenceSpaceEcho, SequenceSpinEcho,
SequenceSteam, SequenceTSE, SimAddPhase, SimEvolve, SimHamiltonian, SimNucleus, SimReadout, SimRotate, SimSignal, SimSpoil, SysTable}

- QMRITools`SpectroTools` with functions:

{ApodizationFunction, ApodizeEcho, ApodizeFid, ApodizePadEcho, ApodizePadFid, ApodizePadSpectra, ApodizeSpectra, BasisSequence, ChangeDwellTimeFid, CompareFidFitPlot, CompareSpectraFitPlot, CorrectTEFid, CorrectTESpec, CSIInterface, ExportSparSdat, FindSpectraPpmShift, FineTuneFit, FitLineShape, FitSpectra, FitSpectraResultTable, GetGyro, GetPpmRange, GetSpectraBasisFunctions, GetTimePpmRange, GetTimeRange, ImportSparSdat, InitializeFit, MakeSpectraResultPlot, PaddingFactor, PadEcho, PadFid, PadSpectra, PhaseCorrectSpectra, PhaseShiftSpectra, PlotCSIData, PlotFid, PlotSpectra, ReadjMRUI, ReadoutType, ShiftSpectra, SparID, SparName, SparOrientation, SpectraBandwith, SpectraFieldStrength, SpectraFitResult, SpectraNucleus, SpectraOutputPlots, SpectraPpmShift, SpectraSamples, SpectraSpacing, SplineSpacingFactor, TimeShiftEcho, TimeShiftFid, TimeShiftFidV}

- QMRITools`ReconstructionTools` with functions:

{AcquisitionMethod, CoilCombine, CoilSamples, CoilWeightedRecon, CoilWeightedReconCSI, DeconvolutionMethod, DeconvolveCSIdata, EchoShiftData, FourierKspace2D, FourierKspace3D, FourierKspaceCSI, FourierRescaleData, FourierShift, FourierShifted, HammingFilter, HammingFilterCSI, HammingFilterData, InverseFourierShift, InverseFourierShifted, MakeHammingFilter, MakeSense, MeanType, NoiseCorrelation, NoiseCovariance, NormalizeOutputSpectra, NormalizeSpectra, OrderKspace, OutputSense, ReadListData, RescaleRecon, SagitalTranspose, SenseRescale, ShiftedFourier, ShiftedInverseFourier, TotalType, WienerRegularization}

- QMRITools`TractographyTools` with functions:

```
{CombineROIs, FiberAngle, FiberLengthRange, FiberTractography, FilterTracts, FindTensorPermutation, FittingOrder, FitTract,
MakeColor, MaxSeedPoints, MaxTracts, PartTracts, PlotTracts, SeedDensityMap, SelectTractInVol, SelectTractPartInVol, SelectTracts,
SelectTractTroughPlane, SelectTractTroughVol, StepSize, StopThreshhold, TensorFilps, TensorPermutations, TracMonitor, TractDensityMap}
   - OMRITools`VisteTools` with functions:
{BinaryType, DatRead, DatWrite, DTItoolExp, DTItoolExpFile, DTItoolExpInd, DTItoolExpTens, ExportVol, ImportDTI, ImportVol, LoadFiberTracts}
   - QMRITools`ProcessingTools` with functions:
{B1EqualPower, B1FilterData, B1MapCalc, B1Masking, B1MaxPower, B1Output, B1Scaling, B1ShimMethod, B1Shimming, ColorValue, CombineB1,
CorrectJoinSetMotion, DataTransformation, DatTot, DatTotXLS, ErrorPlot, FiberDensityMap, FiberLengths, FindOutliers, FitData, FitFunction,
FitOutput, GetMaskMeans, Hist, Hist2, InvertDataset, JoinSets, JoinSetSplit, MaskCompartment, MeanMethod, MeanRange, MeanStd, MedCouple,
 MotionCorrectSets, NormalizeOverlap, NormalizeSets, NumberTableForm, OutlierIncludeZero, OutlierIterations, OutlierMethod, OutlierOutput,
OutlierRange, OutputSNR, PaddOverlap, ParameterFit, ParameterFit2, ReferenceB1, ReverseData, ReverseSets, RotateData, RotateTensor, Scaling,
 SeedDensity, SetupDataStructure, SmartMask, SmartMaskOutput, SmartMethod, SmoothSNR, SNRCalc, SNRMapCalc, SplitSets, Strictness, TableMethod}
   - OMRITools`SimulationTools` with functions:
{AddNoise, BlochSeries, CalculateGfactor, CreateDiffData, FatFieldStrength, GESignal, GetPulseProfile, GfactorSimulation, GOutput, GRegularization,
MagnetizationVector, NoiseSize, NoiseType, PlotSimulation, PlotSimulationAngle, PlotSimulationAngleHist, PlotSimulationHist, PlotSimulationVec, Pulses,
 ReportFits, Signal, SimAngleParameters, SimParameters, SimulateDualTR, SimulateSliceEPG, SliceRange, SliceRangeSamples, SortVecs, Tensor, TensOutput}
   – QMRITools`PhysiologyTools` with functions:
{AlignRespLog, ImportPhyslog, ImportRespirect, OutputMethod, PlotPhyslog, PlotRespiract, SampleStep}
   - QMRITools`CoilTools` with functions:
{CoilArrayPlot, CoilSNRCalc, CoilSurfaceVoxelSize, FindCoilPosition, LoadCoilSetup, LoadCoilTarget, MakeCoilLayout, MakeNoisePlots, MakeWeightMask, OutputCoilSurface}
   – QMRITools`TaggingTools` with functions:
{AnnalyzeTagging, CalculateDispacementParameters, HistoryWeighting, MonitorTagging}
   - QMRITools`ImportTools` with functions:
{BmatrixOut, BvalRead, ConvertDcm, GradRead, ReadBrukerDiff, ReadBvalue, ReadDicom,
ReadDicomDiff, ReadDicomDir, ReadDicomDirDiff, ReadGradients, ReadVoxSize, RotateGradient, ScaleCorrect, ShiftPar
  ______
Removing all local and global definitions of:
   OMRITools`GeneralTools`
   – QMRITools`MaskingTools`
   OMRITools`NiftiTools`
   – QMRITools`ElastixTools`
   – QMRITools`PlottingTools`
```

OMRITools`DixonTools` - OMRITools`IVIMTools` – QMRITools`DenoiseTools` OMRITools`CardiacTools`

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- QMRITools`GradientTools`
          - QMRITools`TensorTools`
          - QMRITools`JcouplingTools`
          QMRITools`SpectroTools`
          - QMRITools`ReconstructionTools`
          QMRITools`TractographyTools`
          - QMRITools`VisteTools`
          – QMRITools`ProcessingTools`
          – QMRITools`SimulationTools`
          - QMRITools`PhysiologyTools`
          - QMRITools`CoilTools`
          - QMRITools`TaggingTools`
          - QMRITools`ImportTools`
       Loading and protecting all definitions of:
          QMRITools`GeneralTools`
          - QMRITools`MaskingTools`
          - QMRITools`NiftiTools`
          - QMRITools`ElastixTools`
          - QMRITools`PlottingTools`
          - QMRITools`DixonTools`
          - QMRITools`IVIMTools`
          QMRITools`DenoiseTools`
          - QMRITools`CardiacTools`
          QMRITools`RelaxometryTools`
          - QMRITools`GradientTools`
          - QMRITools`TensorTools`
          - QMRITools`JcouplingTools`
          QMRITools`SpectroTools`
          - QMRITools`ReconstructionTools`
          QMRITools`TractographyTools`
          - QMRITools`VisteTools`
```

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QMRITools`ProcessingTools`
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- QMRITools`SimulationTools`
- QMRITools`PhysiologyTools`
- QMRITools`CoilTools`
- QMRITools`TaggingTools`
- QMRITools`ImportTools`

Column@QMRIToolsPackages[]

In[13]:= Out[13]=

CardiacTools

CoilTools

DenoiseTools

DixonTools

ElastixTools

GeneralTools

GradientTools

ImportTools

IVIMTools

JcouplingTools

MaskingTools

NiftiTools

PhysiologyTools

PlottingTools

ProcessingTools

ReconstructionTools

RelaxometryTools

SimulationTools

SpectroTools

TaggingTools

TensorTools

TractographyTools

VisteTools

[14]:= QMRIToolsFunctions[100]

Functions

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Anglecalc ErnorPot 1VPFunction ReadOctomitrDiff VectorTodata AngleMap EcQuédices 1VPNessiduals ReadFoadments WeightPapCalc AnisofilterData ExploZero JoinSets Readj#RUI WestinWeasures AnisofilterData ExprorBeat Lapfilter Read Listabata Sdebuglastix AnisofilterData ExprorBeat Lapfilter Read Listabata Sdebuglastix AnisofilterData ExportBeat Limited ReadVoxize ReadVoxize Apodizeful ExportBeat Limited ReadVoxize ReadVoxize Apodizeful ExportBeat Limited ReadVoxize ReadVoxize Apodizeful ExportBeat Limited ReadVoxize RegisterCardiaCabata Apodizeful ExportBeat Limited ReadVoxize RegisterCardiaCabata Apodizeful ExportBeat Limited ReadVoxize RegisterCardiaCabata Apodizeful ExportBeat Limited RegisterDataForm ReadVoxize RegisterDataForm ReadVoxize RegisterDataForm ReadVoxize RegisterDataForm RegisterDataFo					•
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8 All-	Functions.nb.			
- 1,	Functions.nb. AcquisitionMethod	FlipGrad	PCAOutput	UseMask
	AffineDirections	FullOutput	PCATollerance	UseSubfolders
	AnisoFilterSteps	FullSphere	PCAWeighting	UseVersion
	AnisoItterations	GetMaskOnly	PeakNumber	VisualOpt
	AnisoKappa	GetMaskOutput	PhaseEncoding	WaterFatShift
	AnisoKernel	GOutput	PlotColor	WaterFatShiftDirection
	AnisoStepTime	GradType	PlotLabel	WienerRegularization
	AnisoWeightType	GRegularization	PlotLabels	WindowTitle
	ApodizationFunction	GridLines	PlotRange	
	AspectRatio	GridLineSpacing	PlotSpace	
	AxesLabel	HammingFilter	PlotStyle	
	AxesMethod	HistogramBins	PositiveZ	
	B1EqualPower	HistogramBinsA	PrintTempDirectory	
	B1FilterData	HistoryWeighting	QMRITools`CardiacTools`Private`ReverseDirection	
	B1Masking	ImageLegend	QMRITools`CardiacTools`Private`ReversePoints	
	B1MaxPower	ImageOrientation	QMRITools`ReconstructionTools`Private`ReconFilter	
	B1Output	ImageResolution	RadialSamples	
	B1Scaling	ImageSize	ReadoutBandwith	
	B1ShimMethod	InitializeFit	ReadoutMethod	
	BackgroundValue	InterpolationOrder	ReadoutOutput	
	BasisSequence	InterpolationOrderReg	ReadoutPhase	
	BinaryType	InterpolationOrderRegA	ReadoutSamples	
	BloodMaskRange	Iterations	ReadoutType	
	BmatrixOut	IterationsA	ReferenceB1	
	BsplineDirections	IVIMComponents	RegistrationTarget	
	BsplineSpacing	IVIMConstrained	Reject	
	BullPlotMethod	IVIMConstrains	RejectMap	
	CenterFrequency	IVIMFixed	ReportFits	
	ChainSteps	IVIMTensFit	RescaleRecon	
	CoilArrayPlot	JoinSetSplit	Resolutions	
	CoilSamples	LCMMethod	ResolutionsA	
	CoilSurfaceVoxelSize	LineThreshold	ReverseData	
	ColorFunction	Linewidth	ReverseSets	
	ColorValue	LinewidthShape	RobustFit	
	CompressNii	MagnetizationVector	RobustFitParameters	
	ConditionCalc	MakeCheckPlot	RotateGradient	
	ContourStyle	MaskClosing	RotateGradients	
	ConvertDcm	MaskCompartment	RotationCorrect	
	CorrectPar	MaskComponents	RowSize	
	CropInit	MaskDilation	Runs	
	CropOutput	MaskFiltKernel	SampleStep	
	CropPadding	MaskSmoothing	ScaleCorrect	
	CutOffMethod	MaskWallMap	Scaling	
	DeconvolutionMethod	MaxSeedPoints	SeedDensity	
	DeleteOutputFolder	MaxTracts	SenseRescale	
	DeleteTempDirectory	MeanMethod	ShowOutliers	
	DeNoiseIterations	MeanRes	ShowPlot	
	DeNoiseKernel	Method	SimNucleus	
	DeNoiseMonitor	MethodReg	SliceRange	
		MethodRegA	SliceRangeSamples	
	DictB1Range DictT2fRange	MonitorCalc	SmartMaskOutput	
	DICCIZTRANGE	Monitorcaic	- · · · · ·	

CardiacTools

Functions

BullseyePlot GetSegmentSlices PlotSegments CalculateWallMap HelixAngleCalc RadialSample SegmentAngle CardiacCoordinateSystem LineStep LinesToSegmentIndex SegmentLinesToMask CardiacSegment SegmentsPerSlice CentralAxes MakeECVBloodMask TransmuralPlot CreateHeart MakeLineImage ECVCalc MakeMaskImage

ExcludeSlices MaskHelix
GetMaskSegmentPoints MaskToLines
GetSegmentLines PlotSegmentMask

Options

AxesMethod LCMMethod QMRITools`CardiacTools`Private`ReversePoints BackgroundValue LineThreshold RowSize BloodMaskRange MaskWallMap ShowOutliers BullPlotMethod ShowPlot Method ColorFunction OutputCheckImage SmoothHelix PlotLabel StartPoints CutOffMethod DistanceMeasure PlotRange StartSlices PlotStyle TextNumberForm DropSamples TextOffset GridLineSpacing RadialSamples ImageSize QMRITools`CardiacTools`Private`ReverseDirection TextSize

CoilTools

Functions

CoilSNRCalc FindCoilPosition LoadCoilSetup LoadCoilTarget MakeCoilLayout

MakeNoisePlots

MakeWeightMask

Options

CoilArrayPlot CoilSurfaceVoxelSize ColorFunction ImageSize OutputCoilSurface PlotRange

DenoiseTools

Functions

AnisoFilterData AnisoFilterTensor DeNoise DenoiseCSIdata DenoiseDynamicSpectraData NNDeNoise **PCADeNoise** PCADeNoiseFit WeightMapCalc

Options

AnisoFilterSteps PCAClipping AnisoItterations **PCAKernel** AnisoKappa PCANoiseSigma AnisoKernel PCAOutput AnisoStepTime PCATollerance AnisoWeightType PCAWeighting DeNoiseIterations

DeNoiseKernel DeNoiseMonitor NNThreshhold

DixonTools

Functions

DixonReconstruct
DixonToPercent
MakeGroups
SimulateDixonSignal
Unwrap
UnwrapSplit

OptionsDixonAmplitudes

DixonBipolar
DixonClipFraction
DixonFieldStrength
DixonFilterInput
DixonFilterOutput
DixonFilterSize
DixonFrequencies
DixonIterations

DixonMaskThreshhold

DixonNucleus
DixonPrecessions
DixonTollerance
MonitorUnwrap
UnwrapDimension
UnwrapThresh

ElastixTools

Functions

ReadTransformParameters
RegisterCardiacData
RegisterData
RegisterDataSplit
RegisterDataTransform
RegisterDataTransformSplit
RegisterDiffusionData
RegisterDiffusionDataSplit
TransformData
\$debugElastix

Options

Iterations

AffineDirections
BsplineDirections
BsplineSpacing
DeleteTempDirectory
FindTransform
HistogramBins
HistogramBinsA
InterpolationOrderReg
InterpolationOrderRegA

IterationsA
MethodReg
MethodRegA
NumberSamples
NumberSamplesA
OutputImage

OutputTransformation PCAComponents PrintTempDirectory RegistrationTarget Resolutions ResolutionsA SplitMethod TempDirectory UseGPU

GeneralTools

Functions

ApplyCrop AutoCropData BSplineCurveFit CheckExtension ClearTemporaryVariables

CompilebleFunctions CropData CutData Data2DToVector

Data3DToVector

DataToVector

DecomposeAffineMatrix DecomposeScaleMatrix

DevideNoZero DynamicPartition ExpNoZero

ExtractDemoData FileSelect FindCrop

FindMaxDimensions

GetAssetLocation GridData GridData3D

GyromagneticRatio LapFilter LLeastSquares LogNoZero MADNoZero

MakeIntFunction MeanNoZero

MedFilter MedianNoZero MemoryUsage NNLeastSquares PadToDimensions OMRIToolsFuncPrint QMRIToolsFunctions

QMRIToolsPackages

QuaternionToRotationMatrix OuaternionVectorToRotationMatrix RescaleData ReverseCrop ReverseDimensions

RMSNoZero RotateDimensionsLeft

RotateDimensionsRight RotationMatrixToQuaternion

RotationMatrixToQuaternionVector

SaveImage Squeeze

StdFilter StichData SumOfSquares TensMat TensVec

VectorToData

Options

CropInit PadValue CropOutput SplineDegree CropPadding SplineKnotsNumber FileType SplineRegularization

WindowTitle

ImageResolution

ImageSize

InterpolationOrder OutputWeights

Padding PadDirection

GradientTools

Functions

BmatrixCorrectGradientsGradBmatrixBmatrixCalcEnergyCalcGradSeqBmatrixConvFinalGradsImportGradObj

BmatrixConv FinalGrads ImportGradODJ

BmatrixInv FindOrder OverPlusCalc

BmatrixRot FullGrad UniqueBvalPosition

BmatrixToggle GenerateGradients
CalculateMoments GenerateGradientsGUI
ConditionNumberCalc GetGradientScanOrder

ConvertGrads GetSliceNormal
CorrectBmatrix GetSliceNormalDir

Options

ConditionCalc PhaseEncoding

FlipAxes Runs
FlipGrad Steps
FullSphere StepSizeI
GradType SwitchAxes
Method UnitMulti
MethodReg UseGrad
OrderSpan VisualOpt

OutputPlot OutputType

ImportTools

Functions

BvalRead ShiftPar

GradRead

ReadBrukerDiff

ReadBvalue

ReadDicom

ReadDicomDiff

ReadDicomDir

ReadDicomDirDiff

ReadGradients

ReadVoxSize

Options

BmatrixOut

ConvertDcm

RotateGradient

ScaleCorrect

IVIMTools

Functions

BayesianIVIMFit2 BayesianIVIMFit3 CorrectParMap IVIMResiduals ThetaConv ThetaConvi

FConverti FConverti FracCorrect HistogramPar IVIMCalc

IVIMCorrectData
IVIMFunction

Options

FilterMaps

ChainSteps CorrectPar

IVIMFixed IVIMTensFit

IVIMConstrains

FilterSize

ize Method

FilterType MonitorIVIMCalc
FitConstrains OutputSamples
FixPseudoDiff Parallelize
FixPseudoDiffSD UpdateStep

FixPseudoDiffSD IVIMComponents

IVIMComponents
IVIMConstrained

JcouplingTools

Functions

GetSpinSystem SimReadout
MakeSpinSystem SimRotate
SequencePulseAcquire SimSignal
SequenceSpaceEcho SimSpoil
SequenceSpinEcho SysTable

SequenceSteam
SequenceTSE
SimAddPhase
SimEvolve
SimHamiltonian

Options

CenterFrequency
FieldStrength
Linewidth
LinewidthShape
ReadoutBandwith
ReadoutMethod
ReadoutOutput
ReadoutPhase

ReadoutSamples SimNucleus

${\tt MaskingTools}$

Functions

GetMaskData RescaleSegmentation

GrowMask ROIMask HomoginizeData SegmentMask Mask SmoothMask

MaskData SmoothSegmentation MeanSignal SplitSegmentations

MergeSegmentations NormalizeData NormalizeMeanData RemoveMaskOverlaps

Options

GetMaskOnly GetMaskOutput MaskClosing MaskComponents MaskDilation MaskFiltKernel MaskSmoothing UseMask

NiftiTools

Functions

CorrectNiiOrientation ImportBvalvec DcmToNii ImportBvec

ExportBmat ImportExploreDTItens

ExportBval ImportNii
ExportBvec ImportNiiDiff
ExportNii ImportNiiDix
ExtractNiiFiles ImportNiiT1
GetNiiOrientation ImportNiiT2

Options

CompressNii PositiveZ
DeleteOutputFolder RotateGradients
FlipBvec UseSubfolders
Method UseVersion

NiiDataType NiiLegacy NiiMethod NiiOffset NiiScaling NiiSliceCode

PhysiologyTools

Functions

AlignRespLog ImportPhyslog ImportRespirect PlotPhyslog PlotRespiract

Options

OutputMethod SampleStep

${\bf Plotting Tools}$

Functions

GetSliceData PlotDuty
GetSlicePositions PlotIVIM
GradientPlot PlotMoments
ListSpherePlot PlotSequence

MakeSliceImages
PlotContour
PlotCorrection
PlotData
PlotData3D

Options

PlotDefGrid

ColorFunction PlotColor
ContourStyle PlotRange
DropSlices PlotSpace
ImageLegend PositiveZ
ImageOrientation SphereColor
ImageSize SphereSize

MakeCheckPlot

Method

NormalizeIVIM PeakNumber

ProcessingTools

Functions

B1MapCalc FindOutliers NumberTableForm
B1Shimming FitData ParameterFit
CombineB1 GetMaskMeans ParameterFit2
CorrectJoinSetMotion Hist RotateData
DataTransformation Hist2 RotateTensor

DatTot InvertDataset SetupDataStructure
DatTotXLS JoinSets SmartMask

ErrorPlot MeanRange SNRCalc
FiberDensityMap MeanStd SNRMapCalc
FiberLengths MedCouple SplitSets

Options

AxesLabel FitOutput ReverseSets OutlierIncludeZero B1EqualPower ImageSize OutlierIterations Scaling B1FilterData InterpolationOrder OutlierMethod SeedDensity B1Masking JoinSetSplit OutlierOutput SmartMaskOutput B1MaxPower MaskCompartment OutlierRange SmartMethod MeanMethod B10utput OutputSNR SmoothSNR Method PaddOverlap B1Scaling Strictness B1ShimMethod MotionCorrectSets PlotLabel TableAlignments ColorValue NormalizeOverlap ReferenceB1 TableDepth FitFunction NormalizeSets ReverseData TableDirections

TableHeadings

TableMethod

TableSpacing

ReconstructionTools

Functions

CoilCombine HammingFilterCSI
CoilWeightedRecon HammingFilterData
CoilWeightedReconCSI InverseFourierShift
DeconvolveCSIdata InverseFourierShifted
FourierKspace2D MakeHammingFilter

FourierKspace3D MakeSense

FourierKspaceCSI MeanType

FourierShift NoiseCovariance
FourierShifted NormalizeSpectra

OrderKspace ReadListData SagitalTranspose ShiftedFourier ShiftedInverseFourier

Shirtedinver.serour.i

TotalType

Options

AcquisitionMethod CoilSamples

DeconvolutionMethod

EchoShiftData HammingFilter

Method

NormalizeOutputSpectra

OutputSense

 ${\tt QMRITools`ReconstructionTools`Private`ReconFilter}$

RescaleRecon

SenseRescale

WienerRegularization

RelaxometryTools

Functions

CalibrateEPGT2Fit

TriExponentialT2Fit

CreateT2Dictionary
DictionaryMinSearch

EPGSignal EPGT2Fit

NonLinearEPGFit ShiftPulseProfile

T1Fit T1rhoFit T2Fit

Options

DictB1Range EPGMethodCal
DictT2fRange EPGRelaxPars
DictT2fValue EPGSmoothB1

DictT2IncludeWater Method

DictT2Range MonitorEPGFit
EPGCalibrate OutputCalibration
EPGFatShift WaterFatShift

EPGFitFat WaterFatShiftDirection

EPGFitPoints EPGMethod

SimulationTools

Functions

AddNoise PlotSimulationHist BlochSeries PlotSimulationVec

CalculateGfactor Pulses CreateDiffData Signal

GESignal SimAngleParameters

GetPulseProfile SimParameters
GfactorSimulation SimulateDualTR
PlotSimulation SimulateSliceEPG

PlotSimulationAngle Tensor

PlotSimulationAngleHist

Options

FatFieldStrength SliceRangeSamples

GOutput SortVecs
GRegularization TensOutput

MagnetizationVector

NoiseSize NoiseType PlotRange Reject ReportFits SliceRange

Functions

ApodizeEcho
ApodizeFid
ApodizePadEcho
ApodizePadFid
ApodizePadSpectra
ApodizeSpectra
ChangeDwellTimeFid
CompareFidFitPlot

ApodizeSpectra FitSpect
ChangeDwellTimeFid GetGyro
CompareFidFitPlot GetPpmRa
CompareSpectraFitPlot GetSpect
CorrectTEFid GetTimeF

CorrectTESpec
CSIInterface
ExportSparSdat
FindSpectraPpmShift
FitSpectra
FitSpectraResultTable

GetPpmRange GetSpectraBasisFunctions GetTimePpmRange GetTimeRange
ImportSparSdat
MakeSpectraResultPlot
PadEcho
PadFid
PadSpectra
PhaseCorrectSpectra
PhaseShiftSpectra

PlotCSIData

PlotFid

PlotSpectra
ReadjMRUI
ShiftSpectra
SpectraFitResult
TimeShiftEcho
TimeShiftFid
TimeShiftFid

Options

ApodizationFunction AspectRatio BasisSequence CenterFrequency FineTuneFit FitLineShape GridLines GridLineSpacing ImageSize

InitializeFit

PaddingFactor
PlotColor
PlotLabel
PlotLabels
PlotRange
ReadoutType
SparID
SparName
SparOrientation

Method

SpectraBandwith
SpectraFieldStrength
SpectraNucleus
SpectraOutputPlots
SpectraPpmShift
SpectraSamples
SpectraSpacing
SplineSpacingFactor

TaggingTools

Functions

AnnalyzeTagging CalculateDispacementParameters

Options

HistoryWeighting MonitorTagging

TensorTools

Functions

ADCCalc EigenvalCalc
AngleCalc EigenvecCalc
AngleMap FACalc

ColorFAPlot FlipGradientOrientation
ConcatenateDiffusionData FlipTensorOrientation

Correct ParameterCalc
Deriv RemoveIsoImages
DriftCorrect ResidualCalc
ECalc SigmaCalc

EigensysCalc SortDiffusionData

Options

Distribution RobustFit

FilterShape RobustFitParameters
FullOutput RotationCorrect

MeanRes UseMask

Method MonitorCalc NormalizeSignal Parallelize Reject

RejectMap

TensorCalc TensorCorrect WestinMeasures

TractographyTools

Functions

CombineROIs SelectTractPartInVol

FiberTractography SelectTracts

FilterTracts SelectTractTroughPlane
FindTensorPermutation SelectTractTroughVol
FitTract TractDensityMap

MakeColor PartTracts PlotTracts SeedDensityMap SelectTractInVol

Options

FiberAngle TensorFilps

FiberLengthRange TensorPermutations

FittingOrder TracMonitor

ImageSize

InterpolationOrder

MaxSeedPoints

MaxTracts

Method

StepSize

StopThreshhold

VisteTools

Functions

DatRead

DatWrite

DTItoolExp

DTItoolExpFile

DTItoolExpInd

DTItoolExpTens

ExportVol

ImportDTI

ImportVol

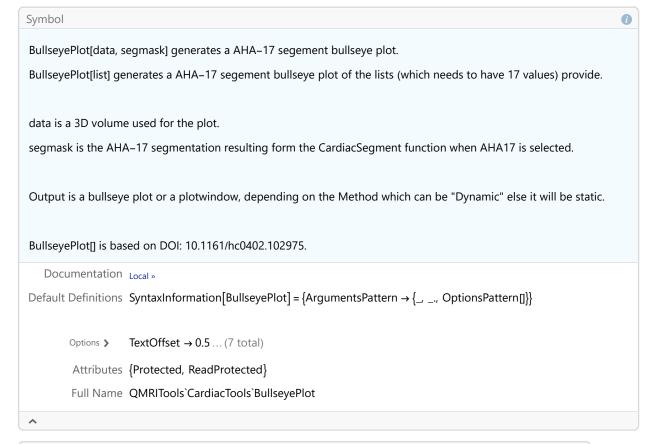
LoadFiberTracts

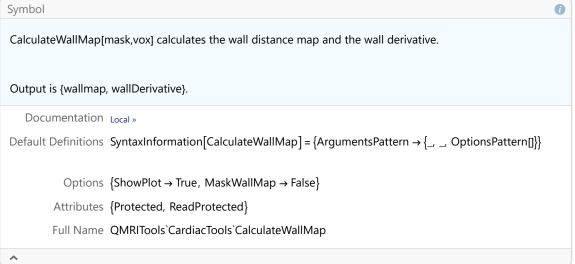
Options

BinaryType

CardiacTools

Functions





```
CardiacCoordinateSystem[mask, vox] creates the cardiac coordinate system within the mask and is used in HelixAngleCalc.

Output is a set of vectors {radvecn, norvecc, cirvec}, being the radial, normal and circular axes of each voxel respectivley.

If the option showPlot is true the output is {{radvecn, norvecc, cirvec}, plots}.

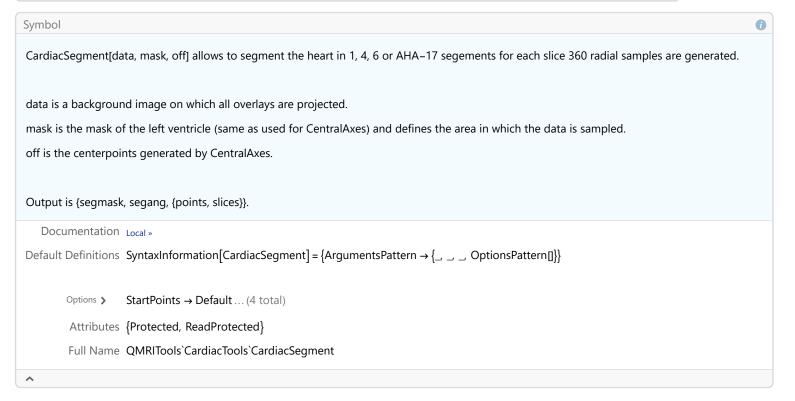
Documentation Local »

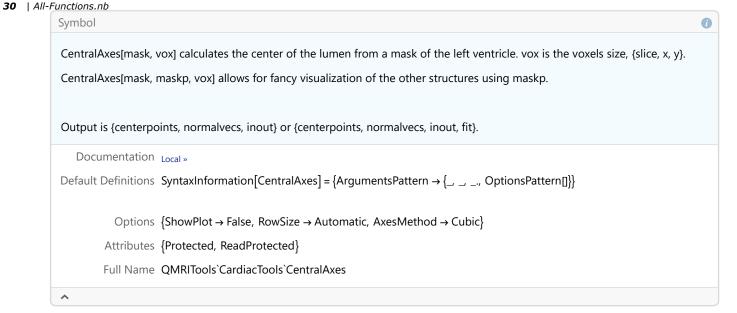
Default Definitions SyntaxInformation[CardiacCoordinateSystem] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}}

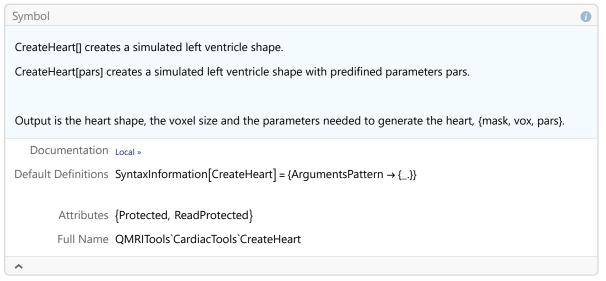
Options {ShowPlot → False, LCMMethod → WallMap, AxesMethod → Quadratic}

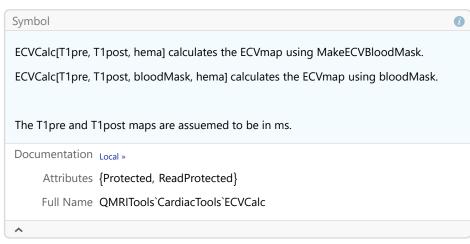
Attributes {Protected, ReadProtected}

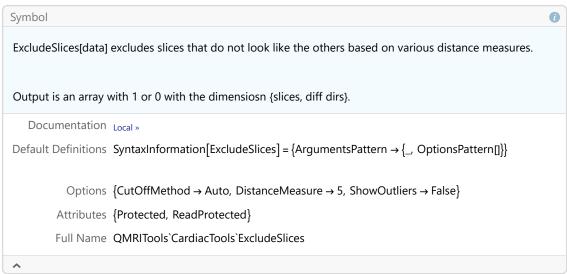
Full Name QMRITools CardiacTools CardiacCoordinateSystem
```

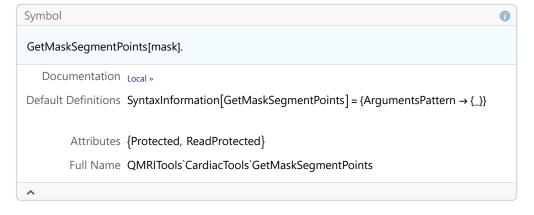


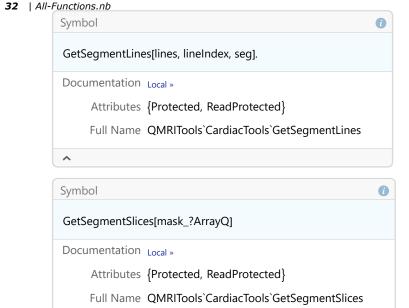












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HelixAngleCalc[eigenvectors, mask, vox] calculates the helix angle matrix of cardiac data using only a left ventricle mask.

HelixAngleCalc[eigenvectors, mask, maskp, vox] calculates the helix angle matrix of cardiac data using only a left ventricle mask, and a maskp for visualization.

HelixAngleCalc[eigenvectors, mask, centerpoint, vec, inout, vox] calculates the helix angle matrix of cardiac data using only a left ventricle mask.

HelixAngleCalc[eigenvectors, mask, maskp, centerpoint, vec, inout, vox] calculates the helix angle matrix of cardiac data using a left vantricle mask and a maskp for visualization.

eigenvectors are the tensor eigenvectors calculated with EigenvecCalc.

mask is a mask of the left ventricle.

maskp is a mask used for visualization.

vox is the voxels size, {slice, x, y}.

The following values are calculated automaticlay Using CentralAxes but can also be provided as an input.

centerpoint is the center of each slice calculated with CentralAxes.

inout is the inner and outer radius calcualted with CentralAxes.

vec is the vector describin the central axes of the heart, calculated with CentralAxes.

Output is het fiber angle matrix FAM = {9, slice, x, y} or {FAM, plot}.

The angles are in degrees.

HelixAngleCalc[] is based on DOI: 10.1186/1532-429X-17-S1-P15.

Documentation Local »

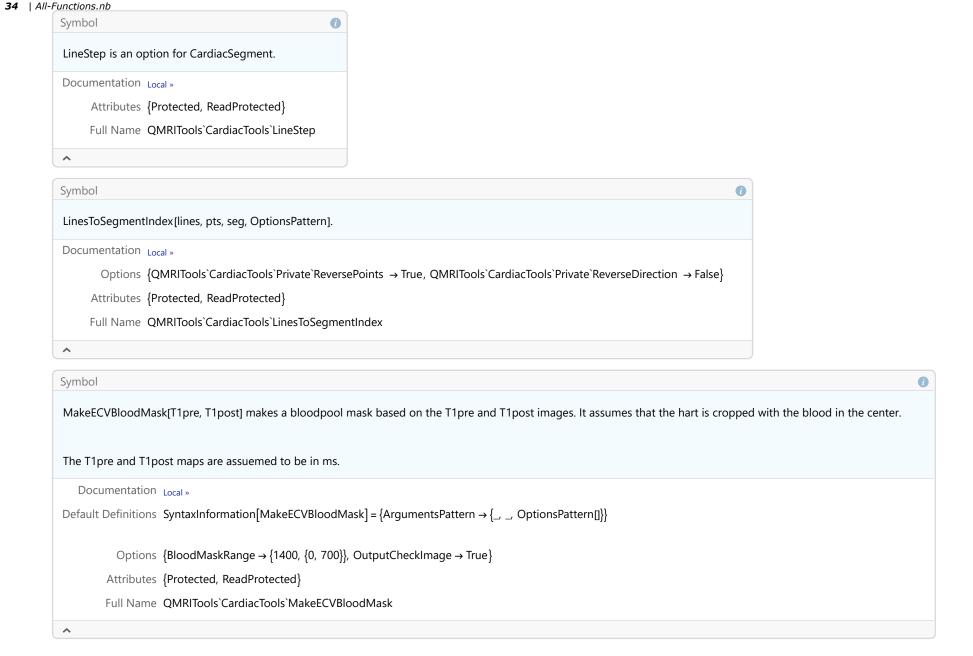
Default Definitions SyntaxInformation[HelixAngleCalc] = {ArgumentsPattern → {_, _, _, _, OptionsPattern[]}}

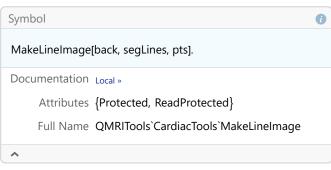
Options {ShowPlot → True, LCMMethod → WallMap, AxesMethod → Quadratic}

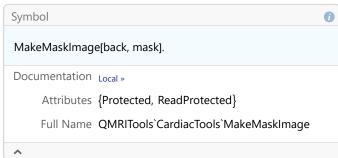
Attributes {Protected, ReadProtected}

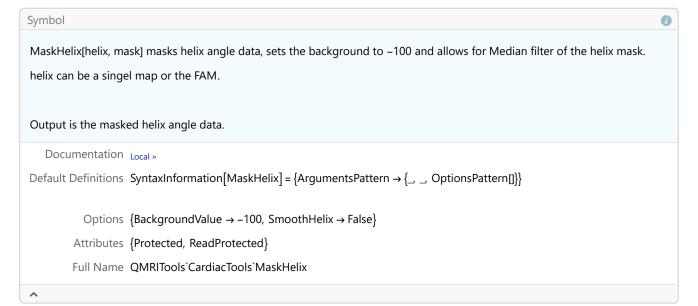
Full Name QMRITools`CardiacTools`HelixAngleCalc

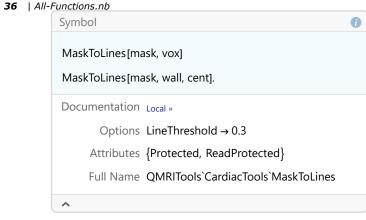
^

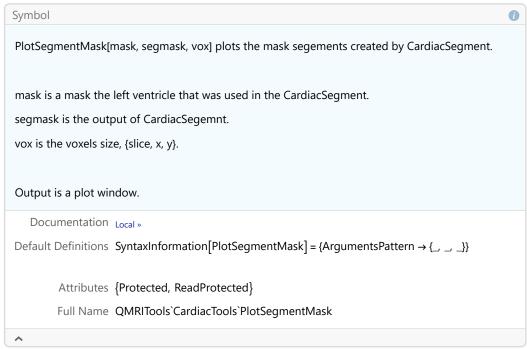












Symbol

RadialSample[mask, data, segang] radialy samples the provided parametermap data.

The mask should be a mask of the left ventricle that was used in the CardiacSegment. segang is the output of the cardaic SegmentFunction.

Output is {points, vals} which are orderd as indicated by the user.

Documentation Local »

Default Definitions SyntaxInformation[RadialSample] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}}

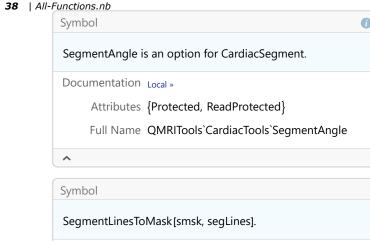
Options {RadialSamples \rightarrow 10, DropSamples \rightarrow 0}

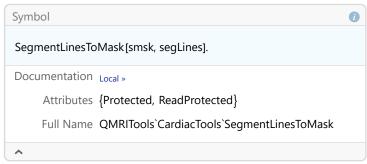
Attributes {Protected, ReadProtected}

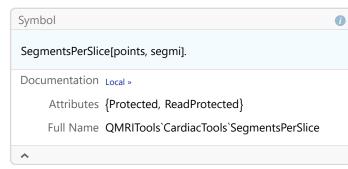
Full Name QMRITools`CardiacTools`RadialSample

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All-Functions.nb | 37







```
TransmuralPlot[data] plots transmural profiles of the data which are created by RadialSample.

data can be a single profile or a list of profiles. In the second case the mean and standardeviations are plotted.

Output is a plot of the transmural profile.

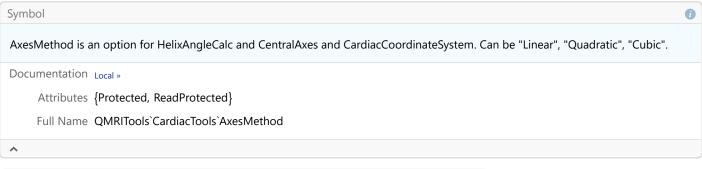
Documentation Local >>

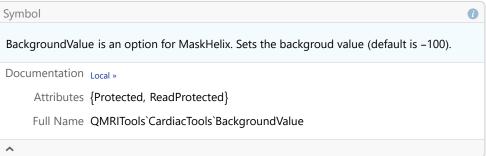
Default Definitions SyntaxInformation[TransmuralPlot] = {ArgumentsPattern → {_, OptionsPattern[]}}

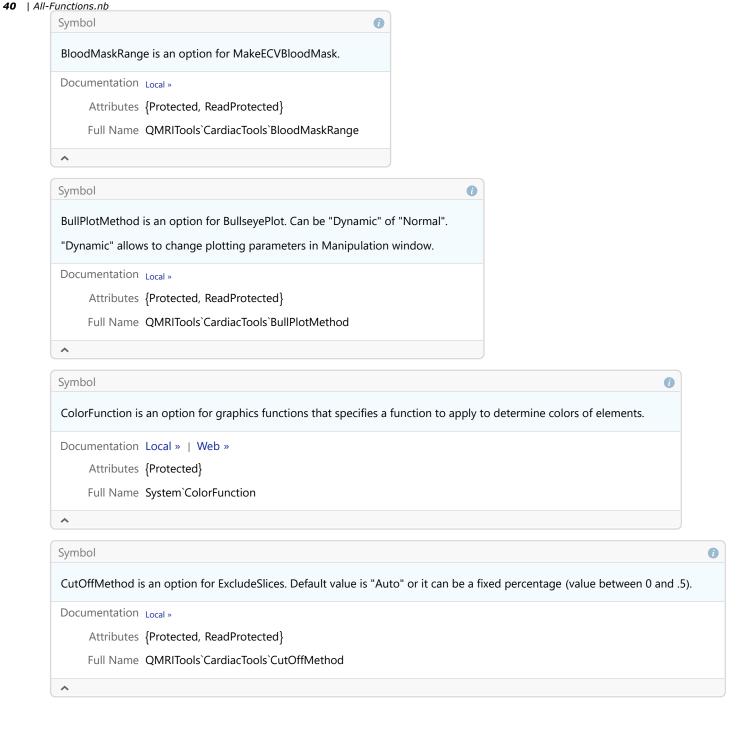
Options > GridLineSpacing → 10 ... (6 total)

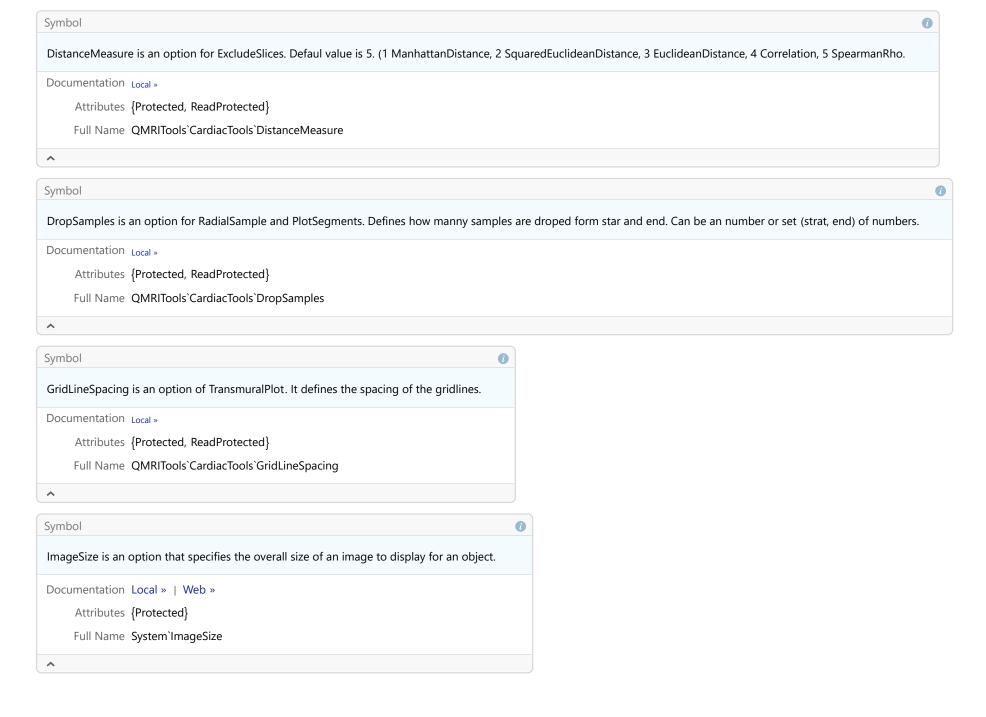
Attributes {Protected, ReadProtected}

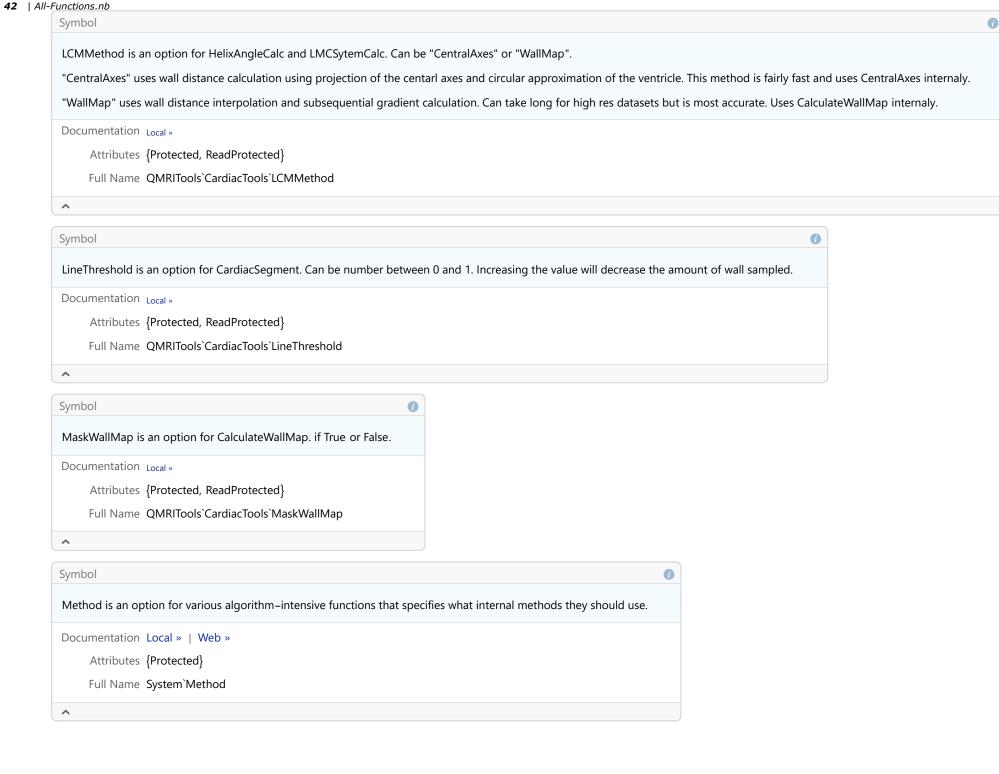
Full Name QMRITools`CardiacTools`TransmuralPlot
```

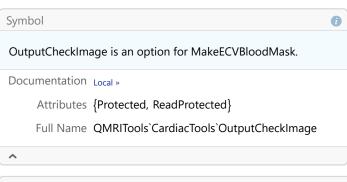




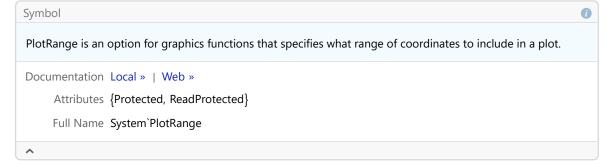


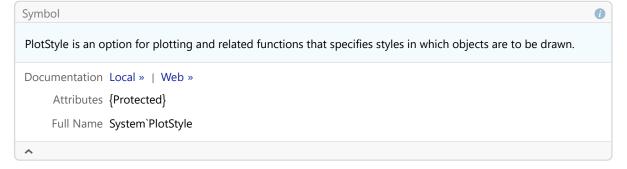


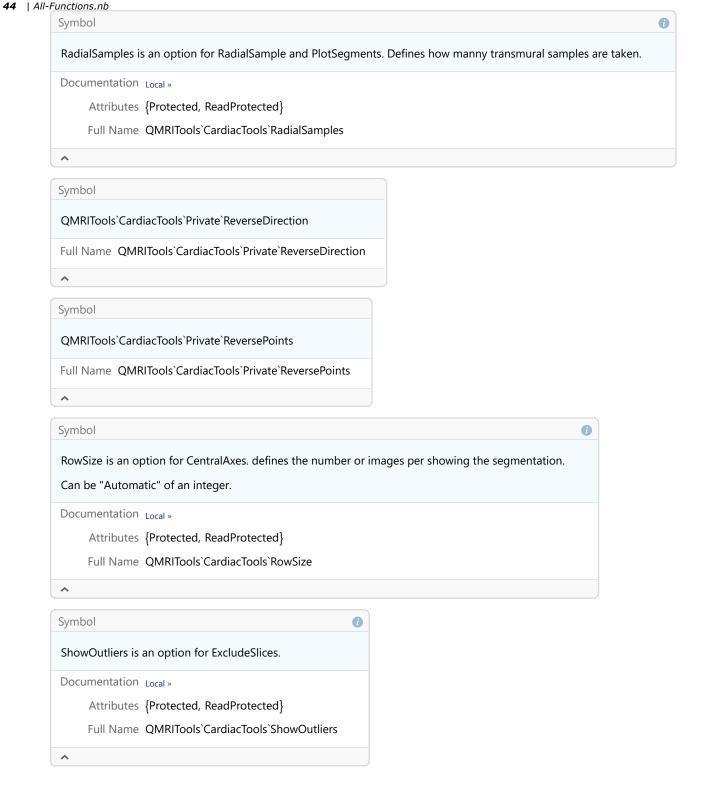


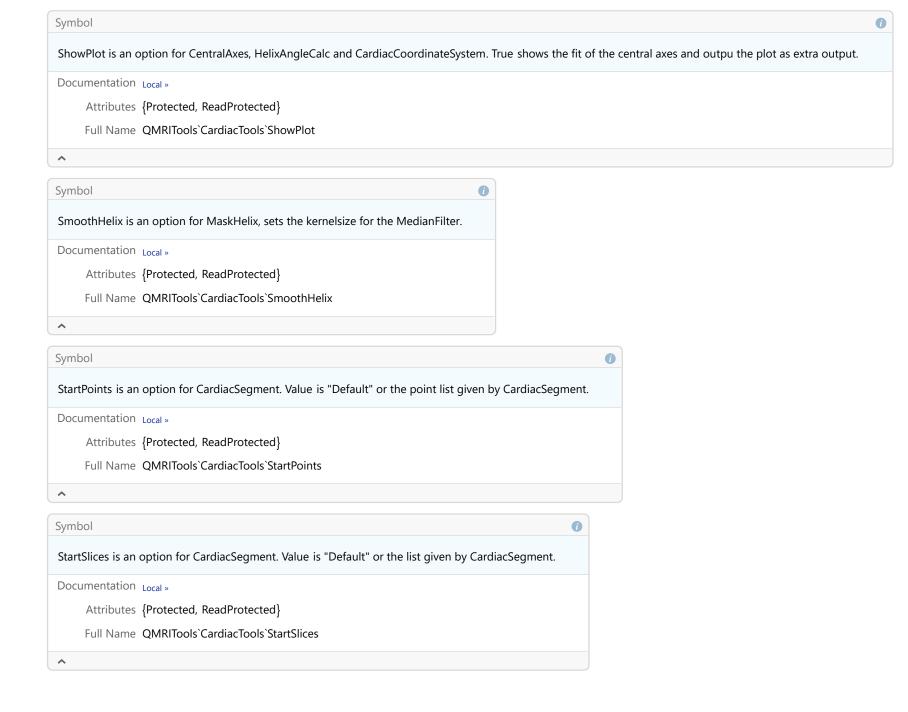


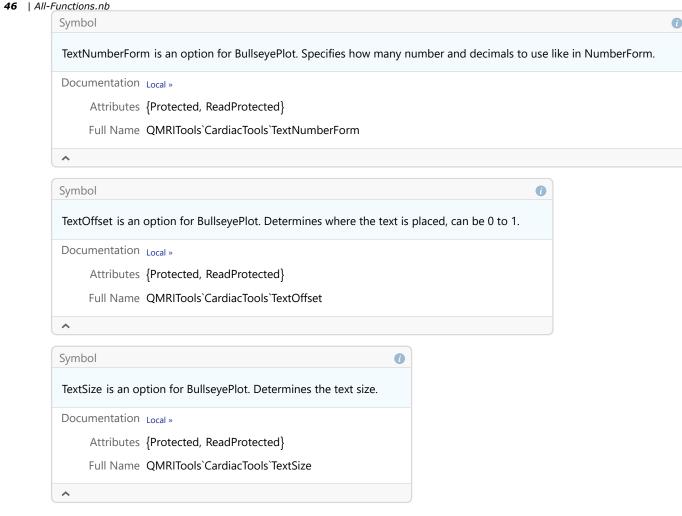








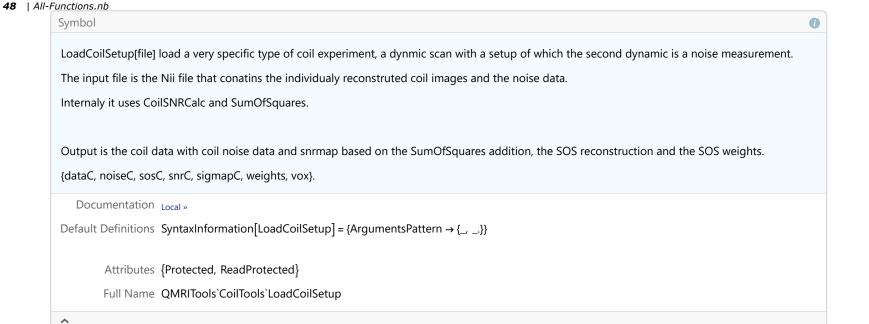


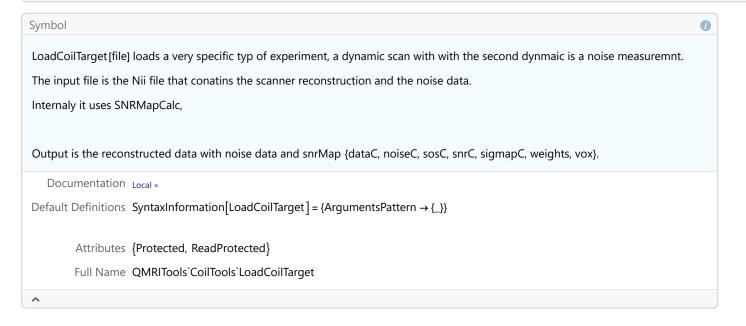


CoilTools

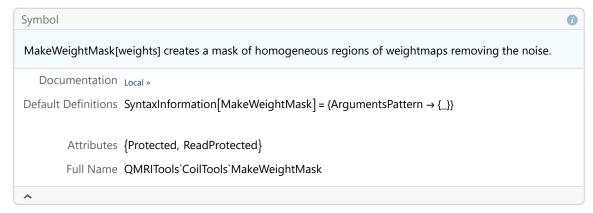
^

FindCoilPosition[weights] finds the coil posision by locating the highest intensity location in the coil weight map, which can be obtianed by LoadCoilSetup or SumOfSquares. Internally it uses MakeWeightMask to remove the noise of the weightmasks. FindCoilPosition[weights, mask] limits the search region to the provided mask. Documentation Local > Default Definitions SyntaxInformation[FindCoilPosition] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}} Options {OutputCoilSurface → False, CoilSurfaceVoxelSize → {1, 1, 1}} Attributes {Protected, ReadProtected} Full Name QMRITools'CoilTools'FindCoilPosition

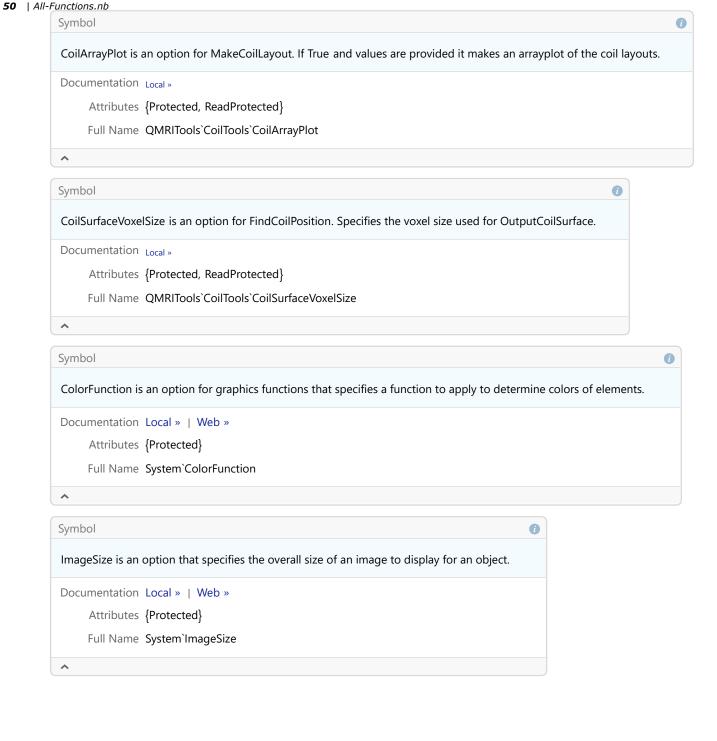




```
Symbol
MakeCoilLayout[{name, size, number}] makes a coil grid with label name, partioned in size rows and with label number.
MakeCoilLayout[{name, size, number}, val] makes a coil grid with label name, partioned in size rows and with label the val at location number.
MakeCoilLayout[{coils..}] same but for multile coils grids. Each coil grid is defined as {name, size, number}.
MakeCoilLayout[{coils..}, val] savem but for multiple coil grids.
Documentation Local »
                PlotRange → Automatic ... (4 total)
     Options >
     Attributes {Protected, ReadProtected}
     Full Name QMRITools`CoilTools`MakeCoilLayout
^
Symbol
MakeNoisePlots[noise] returns a grid of plots of the noise per channel
MakeNoisePlots[noise, {met, prt}] met can be "Grid" with prt a number or Automatic. Else all plots will be returend as a list of plots.
MakeNoisePlots[noise, {met, prt}, sub] sub defines how much the noise is subsampled, default is 40 (every 40th sample is used in plot).
   Documentation Local »
Default Definitions SyntaxInformation[MakeNoisePlots] = {ArgumentsPattern → {_, __, OptionsPattern[]}}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'CoilTools'MakeNoisePlots
```



^



```
OutputCoilSurface is an option for FindCoilPosition. If set true it will also output a SurfacePlot of the coil location volume.

Documentation Local »

Attributes {Protected, ReadProtected}

Full Name QMRITools CoilTools OutputCoilSurface

Symbol

PlotRange is an option for graphics functions that specifies what range of coordinates to include in a plot.

Documentation Local » | Web »

Attributes {Protected, ReadProtected}

Full Name System PlotRange
```

DenoiseTools

```
AnisoFilterData[data] Filter the diffusion tensor data using an anisotropic filter based on the strucure tensor of the data.

Output is the smoothed data.

AnisoFilterData[] is based on DOI: 10.1016/j.jbiomech.2021.110540.

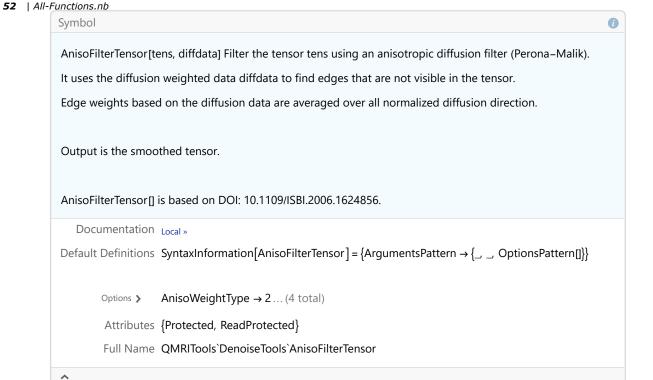
Documentation Local >>

Default Definitions SyntaxInformation[AnisoFilterData] = {ArgumentsPattern → {_, OptionsPattern[]}}

Options {AnisoStepTime → 0.35, AnisoItterations → 3, AnisoKernel → {0.05, 0.1}}

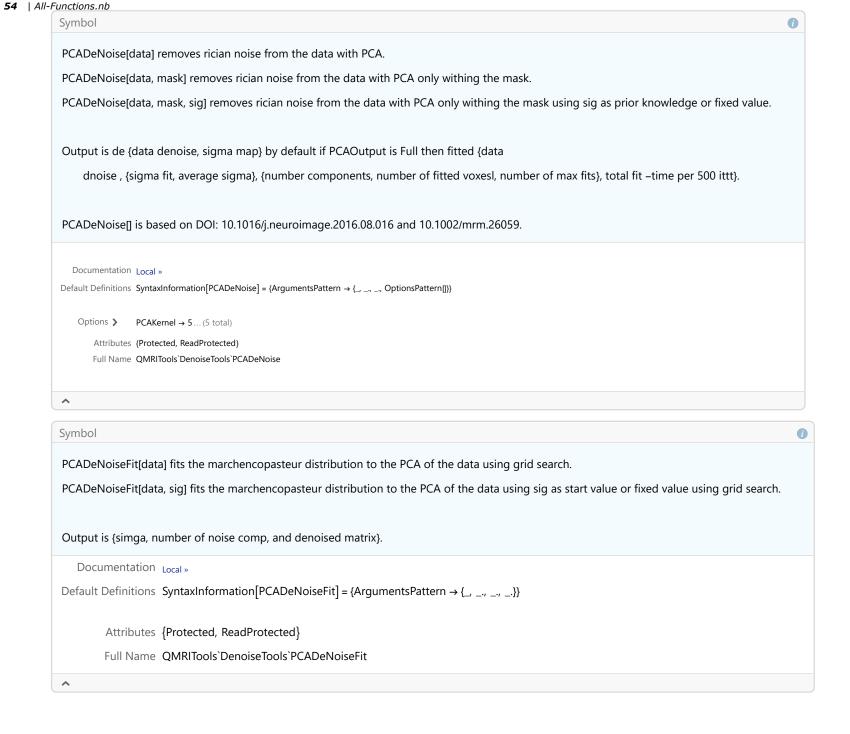
Attributes {Protected, ReadProtected}

Full Name QMRITools`DenoiseTools`AnisoFilterData
```



DeNoise[data,sigma,filtersize] removes Rician noise with standard deviation "sigma" from the given dataset using a kernel with size "filtersize" a gaussian kernel. DeNoise[data,sigma,filtersize, Kernel->"kerneltype"] removes Rician noise with standard deviation "sigma" from the given dataset using a kernel with size "filtersize" and type "kerneltype". Output is data denoised. DeNoise[] is based on DOI: 10.1109/TMI.2008.920609. Documentation Local. Default Definitions SyntaxInformation[DeNoise] = {ArgumentsPattern → {__ _ _ _ _ OptionsPattern[]}} Options {DeNoiseKernel → Gaussian, DeNoiseMonitor → False, DeNoiseIterations → 1} Attributes {Protected, ReadProtected}} Full Name QMRITools'DenoiseTools'DeNoise

```
Symbol
DenoiseCSIdata[spectra] perfroms PCA denoising of the complex values spectra, data has to be 3D and the spectral dimensions is last, {x,y,z,spectra}.
   Documentation Local »
Default Definitions SyntaxInformation[DenoiseCSIdata] = {ArgumentsPattern → {_, OptionsPattern[]}}
          Options {PCAKernel → 5, PCANoiseSigma → Corners}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'DenoiseTools'DenoiseCSIdata
^
Symbol
                                                                                                                                                                        0
DenoiseDynamicSpectraData[spectra] perfroms PCA denoising of the complex values spectra, The data is given as a list of dynamicly acquired spectra {dynamic ,spectra}.
   Documentation Local »
Default Definitions SyntaxInformation[DenoiseDynamicSpectraData] = {ArgumentsPattern \rightarrow \{\_\}}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'DenoiseTools'DenoiseDynamicSpectraData
^
Symbol
NNDeNoise[data] removes rician noise from the data using self supravized neural net.
NNDeNoise[data, mask] removes rician noise from the data with PCA using self supravized neural net withing the mask.
PCADeNoise[] is based on DOI:10.48550/arXiv.2011.01355.
   Documentation Local »
Default Definitions SyntaxInformation[NNDeNoise] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}}
          Options NNThreshhold \rightarrow 2
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'DenoiseTools'NNDeNoise
\wedge
```



```
WeightMapCalc[diffdata] calculates a weight map which is used in AnisoFilterTensor.

Output is a weight map of the diffdata which is high in isotropic regions and low at edges.

Documentation Local »

Default Definitions SyntaxInformation[WeightMapCalc] = {ArgumentsPattern → {_, OptionsPattern[]}}

Options {AnisoWeightType → 2, AnisoKappa → 10.}

Attributes {Protected, ReadProtected}

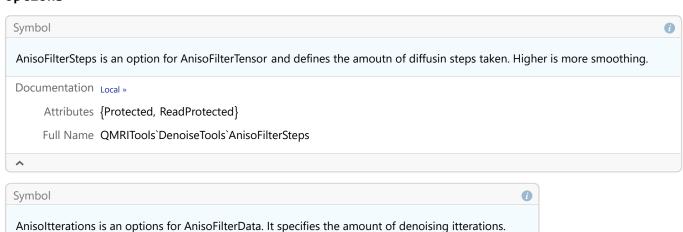
Full Name QMRITools`DenoiseTools`WeightMapCalc
```

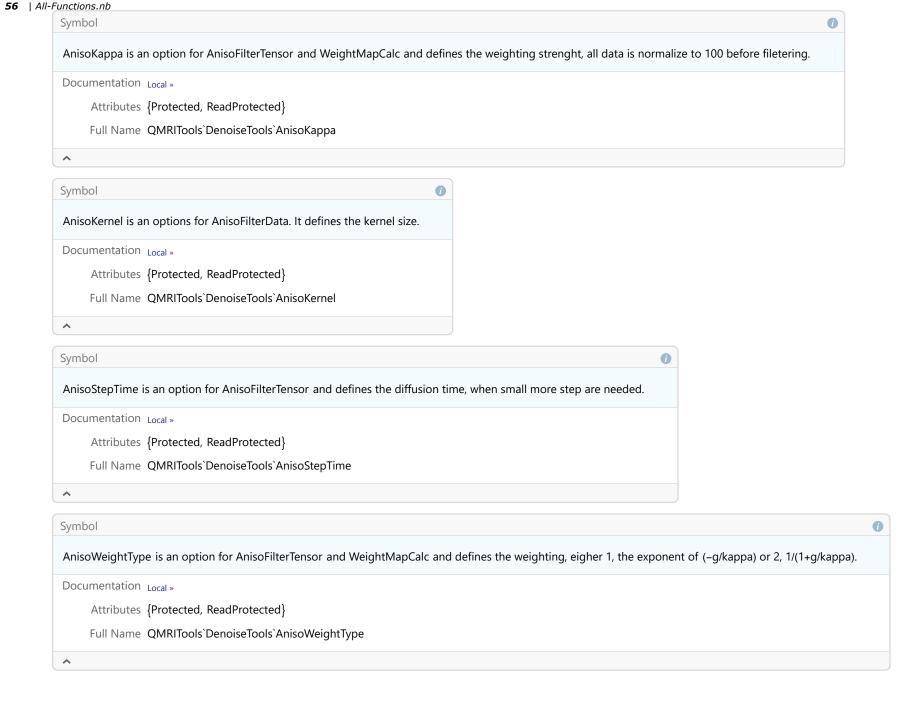
Documentation Local »

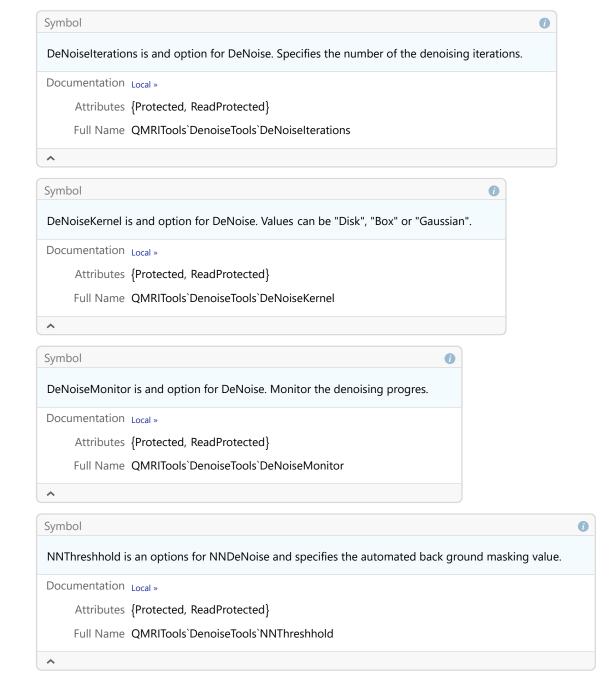
 \wedge

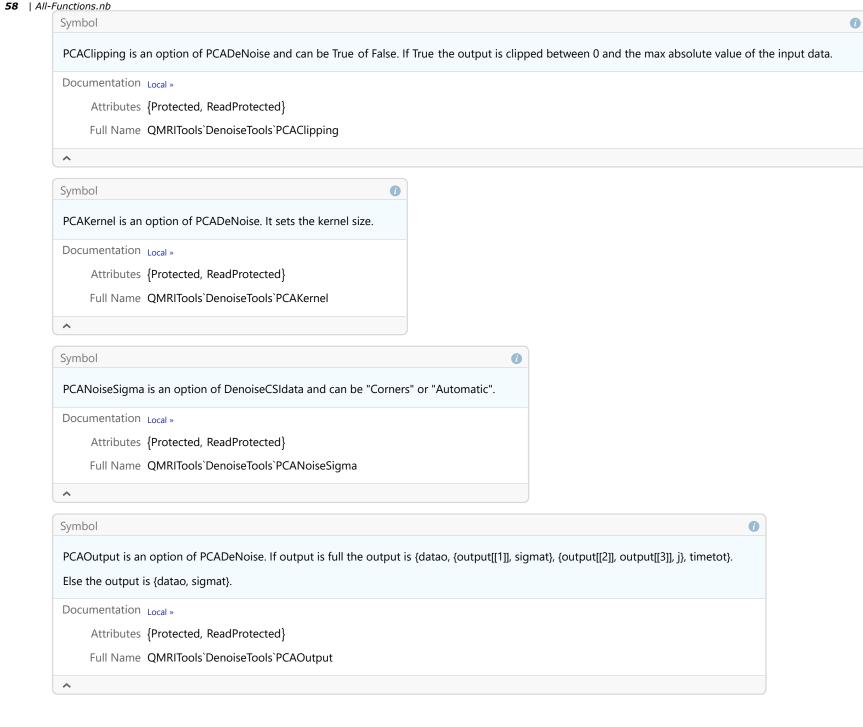
Attributes {Protected, ReadProtected}

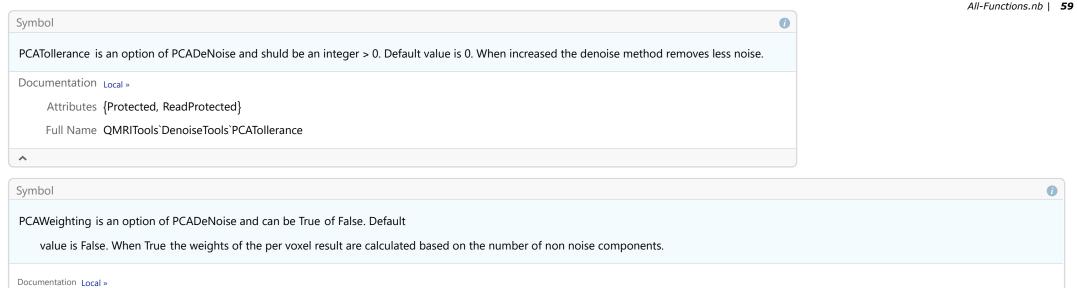
Full Name QMRITools`DenoiseTools`AnisoItterations











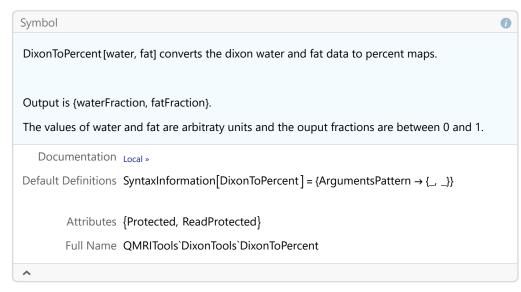
DixonTools

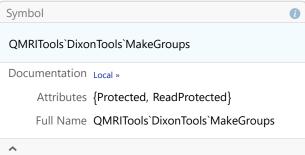
Attributes {Protected, ReadProtected}

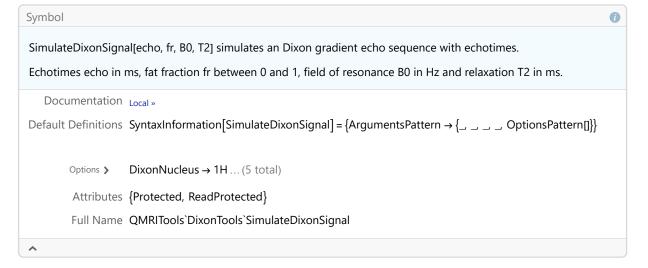
Full Name QMRITools`DenoiseTools`PCAWeighting

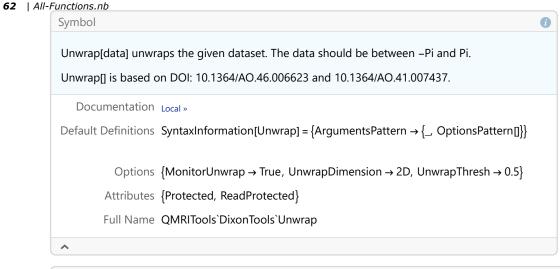
60 | All-Functions.nb Symbol DixonReconstruct[real, imag, echo] reconstruxt Dixon data with initital guess b0 = 0 and T2star = 0. DixonReconstruct[real, imag, echo, b0] reconstructs Dixon data with intitial guess T2star = 0. DixonReconstruct[real, imag, echo, b0, t2] reconstructs Dixon data. real is the real data in radials. imag is the imaginary data in radians. B0 can be estimated from two phase images using Unwrap. T2 can be estimated from multiple echos using T2fit. Output is {{watF,fatF},{watSig,fatSig},{inphase,outphase},{B0,T2star},itterations}. The fractions are between 0 and 1, the B0 field map is in Hz and the T2start map is in ms. DixonReconstruct[] is based on DOI: 10.1002/mrm.20624 and 10.1002/mrm.21737 (10.1002/nbm.3766). Documentation Local » Default Definitions SyntaxInformation[DixonReconstruct] = {ArgumentsPattern → {_, _, _, _, OptionsPattern[]}} DixonPrecessions \rightarrow -1 ... (13 total) Attributes {Protected, ReadProtected} Full Name QMRITools`DixonTools`DixonReconstruct

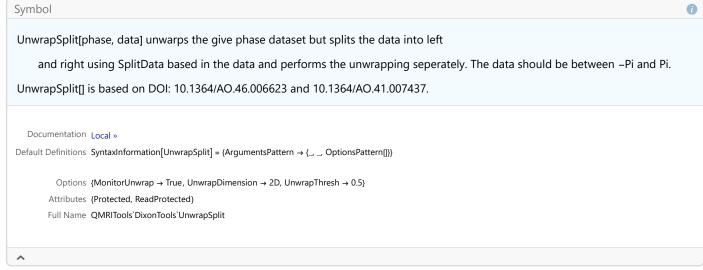
^

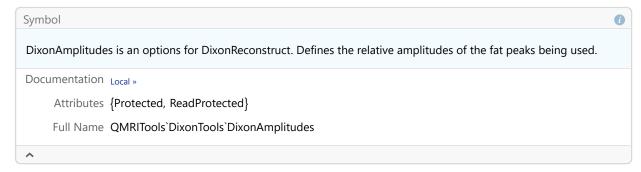


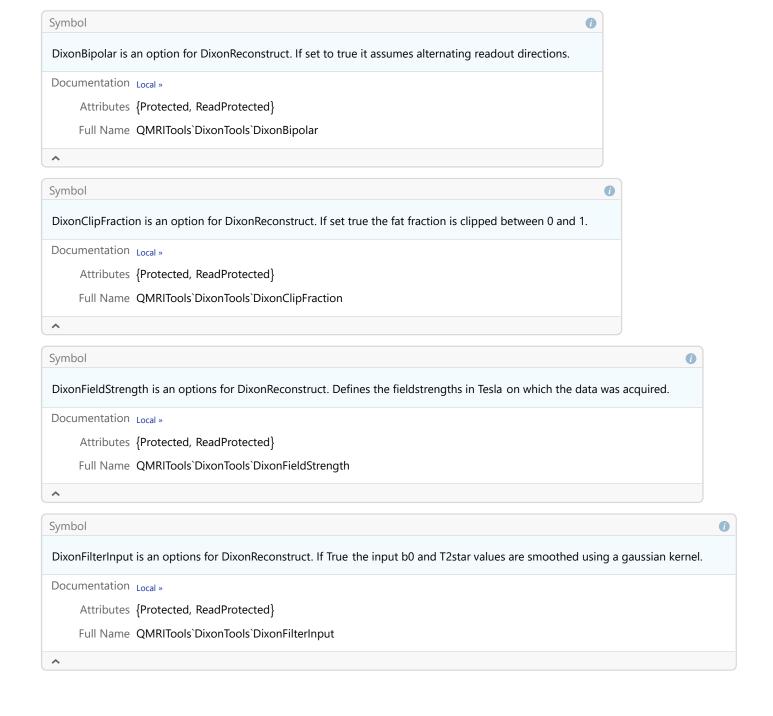


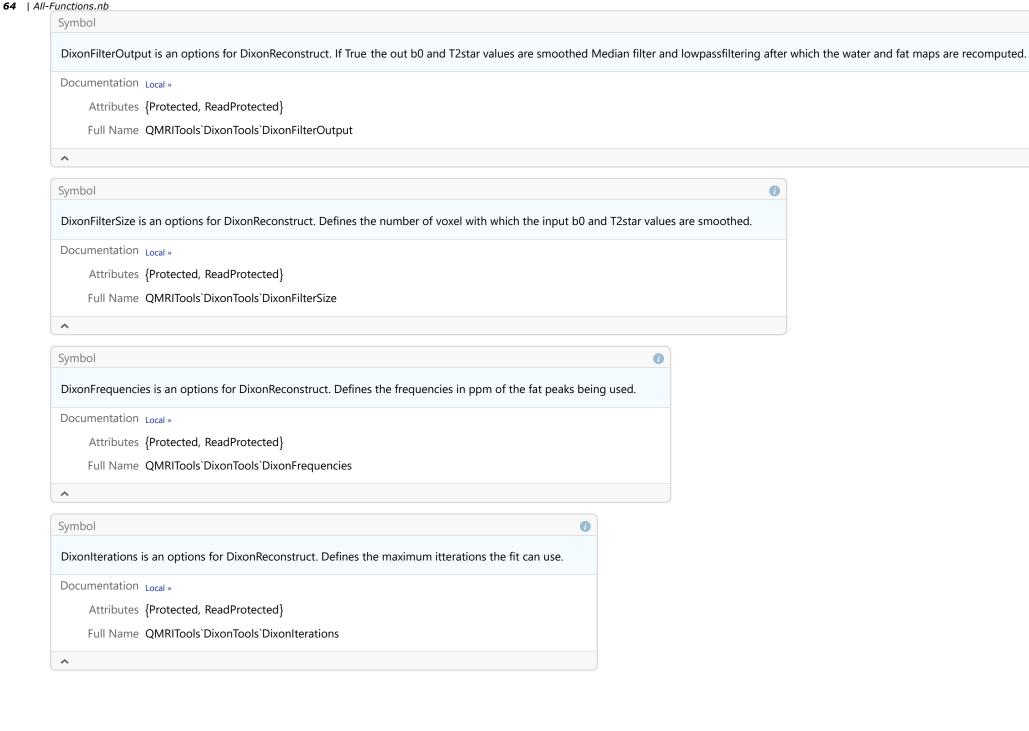


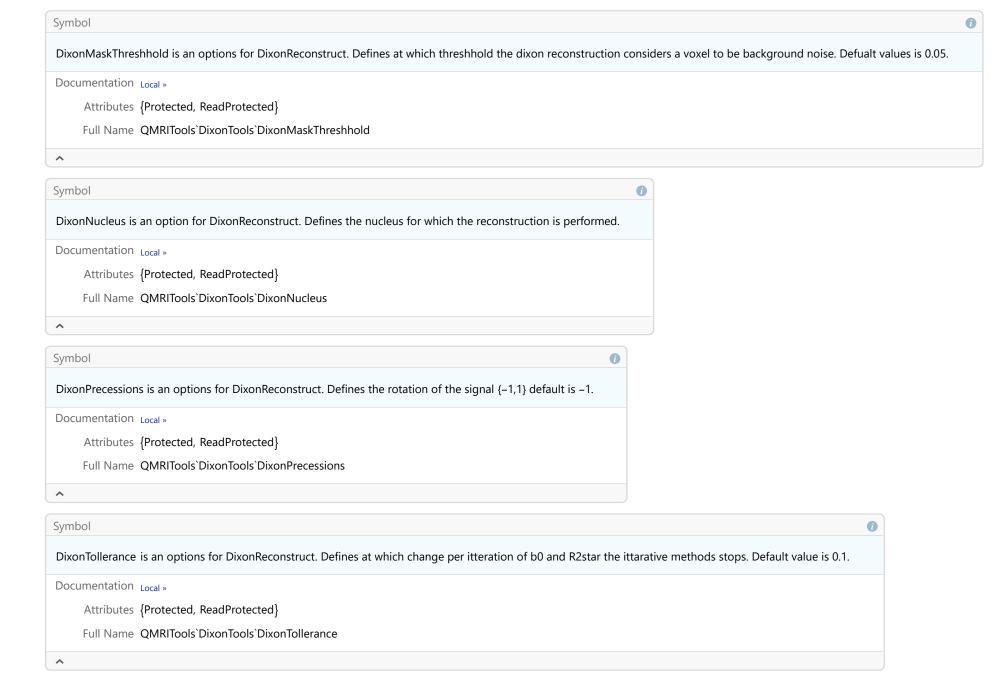


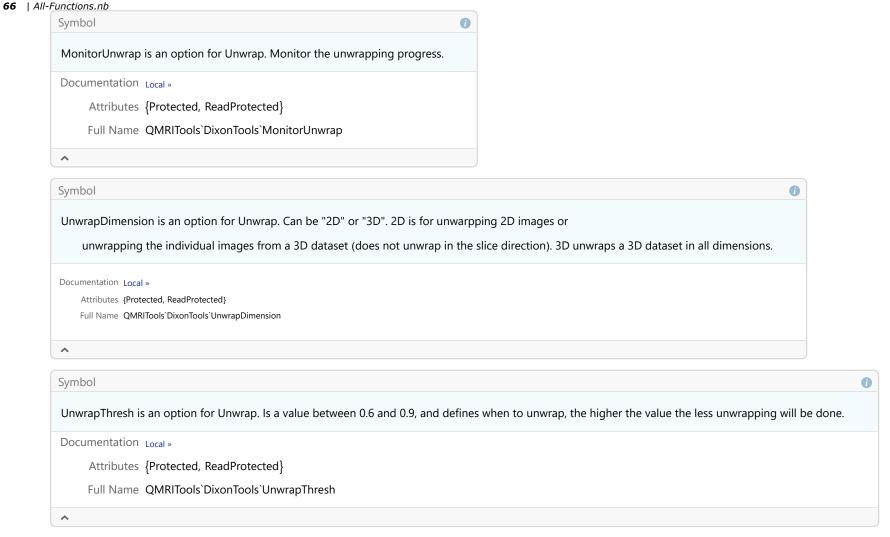




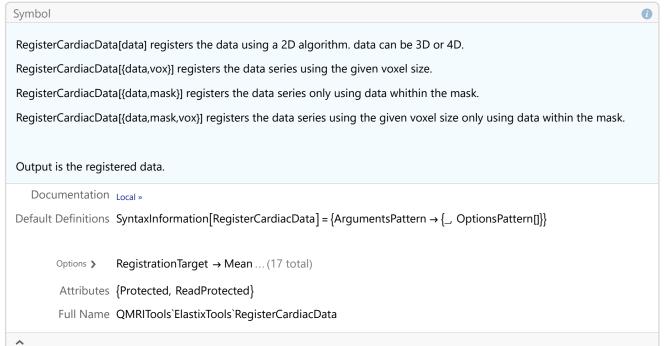








ElastixTools



Symbol

RegisterData[data] registers the data series. If data is 3D it performs multiple 2D registration, if data is 4D it performs multiple 3D registration. The target is the first image or volume in the series.

RegisterData[{data, vox}] registers the data series using the given voxel size.

RegisterData[{data, mask}] registers the data series only using data whithin the mask.

RegisterData[{data, mask, vox}] registers the data series using the given voxel size only using data within the mask.

68 | All-Functions.nb

RegisterData[target, moving] registers the moving data to the target data. target can be 2D or 3D. moving can be the same of one dimension higher than the target.

RegisterData[{target, mask, vox},{moving, mask, vox}] registers the data using the given voxel size only using data within the mask.

RegisterData[{target, vox}, moving] registers the data using the given voxel size.

RegisterData[target, {moving, vox}] registers the data using the given voxel size.

RegisterData[{target, vox}, {moving, vox}] registers the data using the given voxel size.

RegisterData[{target, mask}, moving] registers the data series only using data whithin the mask.

RegisterData[target, {moving, mask}] registers the data series only using data whithin the mask.

RegisterData[{target, mask}, moving] registers the data series only using data whithin the mask.

RegisterData[{target, mask}, {moving, mask}] registers the data series only using data whithin the mask.

RegisterData[target, {moving, mask, vox}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, mask}, {moving, mask, vox}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, vox}, {moving, mask, vox}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, mask, vox}, moving] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, mask, vox}, {moving, mask}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, mask, vox}, {moving, vox}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, mask}, {moving, vox}] registers the data series using the given voxel size only using data within the mask.

RegisterData[{target, vox}, {moving, mask}] registers the data series using the given voxel size only using data within the mask.

Output is the registered data with the dimensions of the moving data.

If OutputTransformation is True it also outputs the translation, rotation scale and skew of all images or volumes.

RegisterData[] is based on DOI: 10.1109/TMI.2009.2035616 and 10.3389/fninf.2013.00050.

```
Documentation Local »
```

Default Definitions SyntaxInformation[RegisterData] = $\{ArgumentsPattern \rightarrow \{_, _, OptionsPattern[]\}\}$

```
Options \Rightarrow Iterations \Rightarrow 250 ... (16 total)
```

Attributes {Protected, ReadProtected}

Full Name QMRITools`ElastixTools`RegisterData

Symbol

^

RegisterDataTransform[target, moving, {moving2nd, vox}] performs the registration exactly as RegisterData. target and moving are the inputs for Registerdata, which can be {data,mask,vox}.

After the registeration is done the moving2nd data is deformed according to the output of the registration of moving.

moving2nd can have the same dimensions of moving or one dimension higher (e.g. 3D and 3D or 3D and 4D).

Output is {registered moving, deformed moving2nd}.

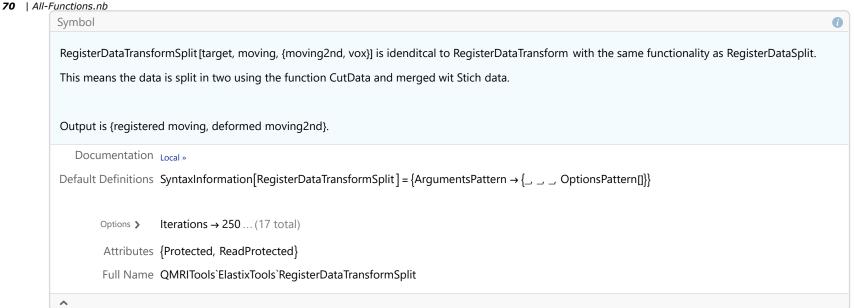
Documentation Local »

Default Definitions SyntaxInformation[RegisterDataTransform] = {ArgumentsPattern \rightarrow {_, _, _, OptionsPattern[]}}

Options > Iterations \rightarrow 250 ... (16 total)

Attributes {Protected, ReadProtected}

Full Name QMRITools`ElastixTools`RegisterDataTransform



RegisterDiffusionData[{dtidata, vox}] registers a diffusion dataset. dtidata should be 4D {slice, diff, x, y}. vox is the voxelsize of the data. RegisterDiffusionData[{dtidata, dtimask, vox}] registers the data series using the given voxel size only using data within the mask. RegisterDiffusionData[{dtidata, vox}, {anatdata, voxa}] registers a diffusion dataset. The diffusion data is also registered to the anatdata. RegisterDiffusionData[{dtidata, dtimask, vox}, {anatdata, voxa}] registers the data series using the given voxel size only using data within the mask.

RegisterDiffusionData[{dtidata,vox}, {anatdata, anatmask, voxa}] registers the data series using the given voxel size only using data within the mask.

RegisterDiffusionData[{dtidata, dtimask, vox}, {anatdata, anatmask, voxa}] registers the data series using the given voxel size only using data within the mask.

Output is the registered dtidata and, if anatdata is given, the registered dtidata in

anatomical space. If OutputTransformation is True it also outputs the translation, rotation scale and skew of all images or volumes.

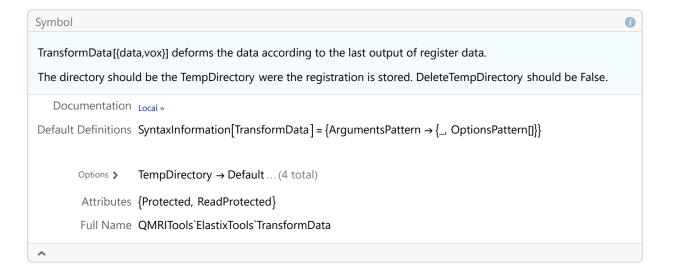
```
Documentation Local »

Default Definitions SyntaxInformation[RegisterDiffusionData] = {ArgumentsPattern → {...., OptionsPattern[]}}

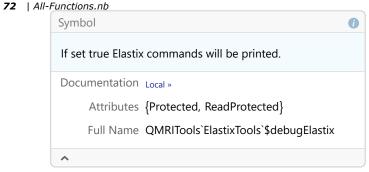
Options > Iterations → 250 ... (23 total)

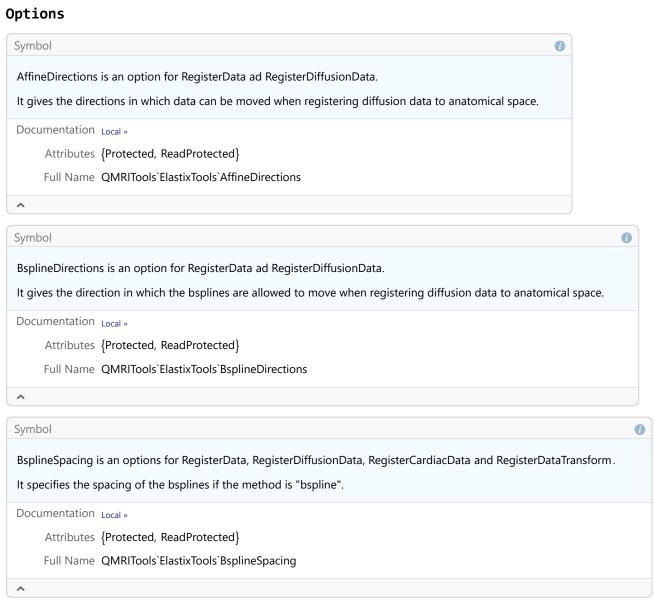
Attributes {Protected, ReadProtected}}

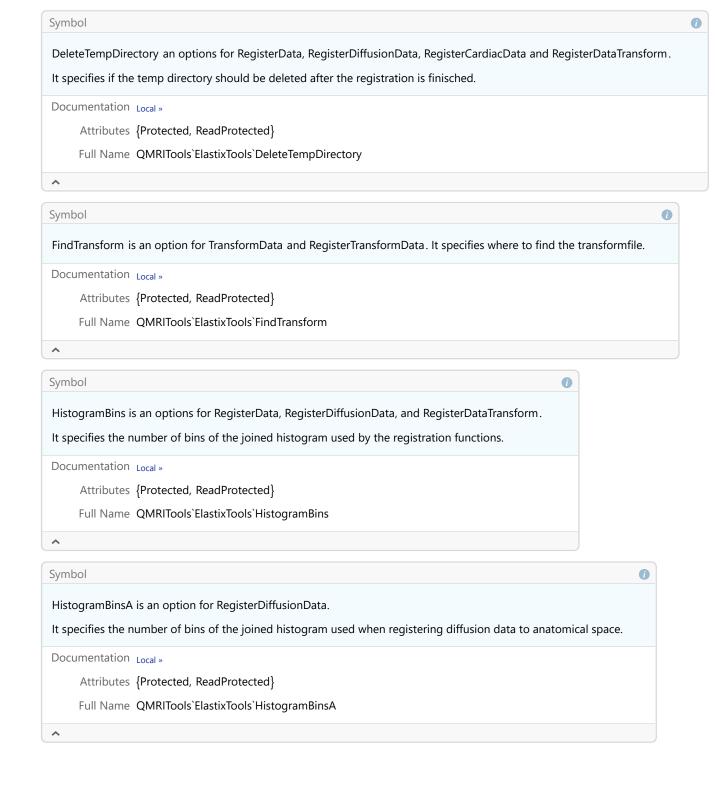
Full Name QMRITools`ElastixTools`RegisterDiffusionData
```

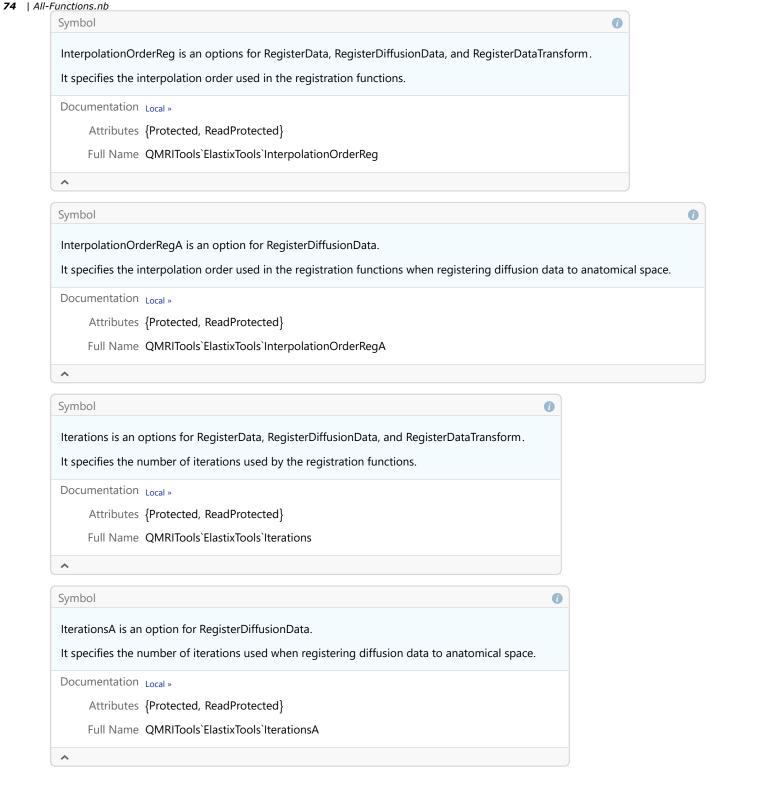


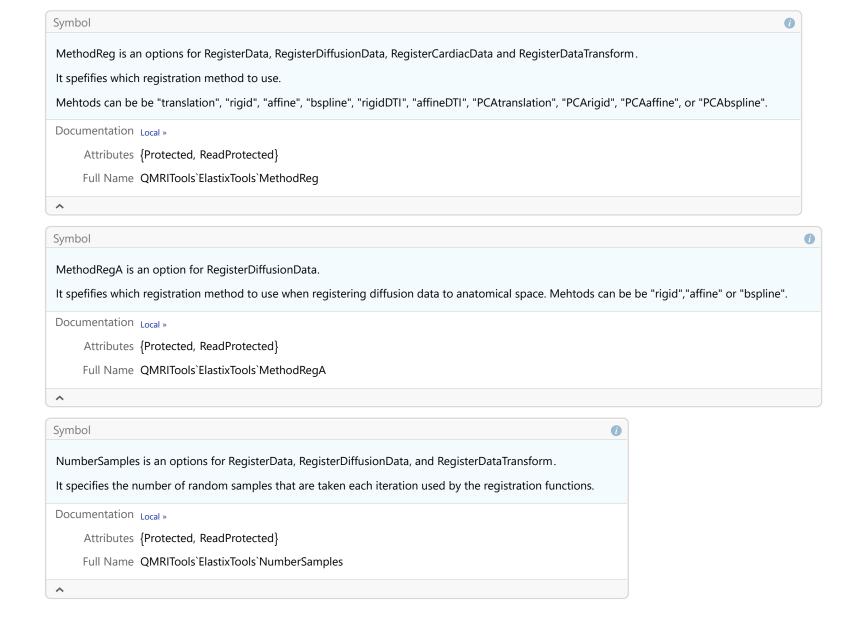
^

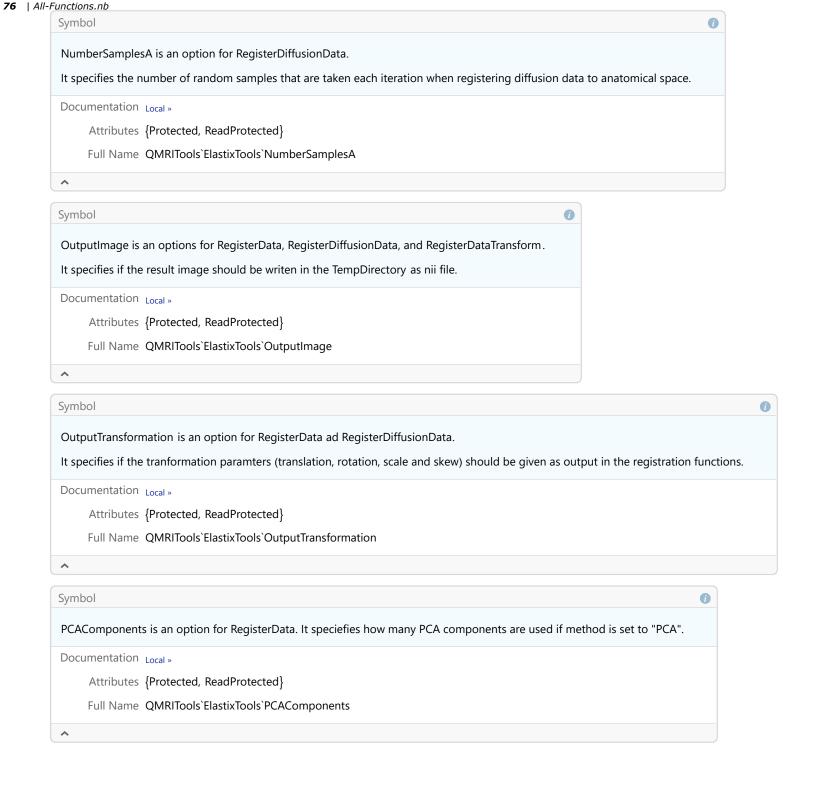


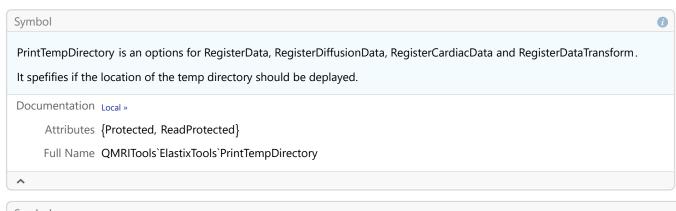


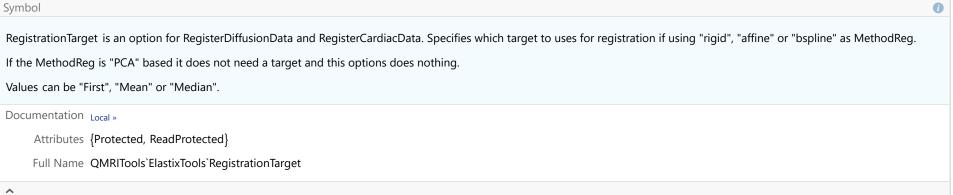


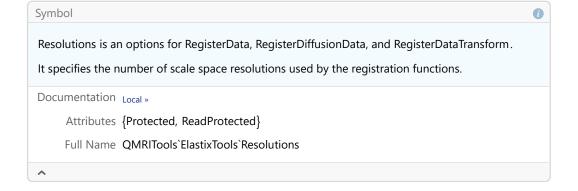


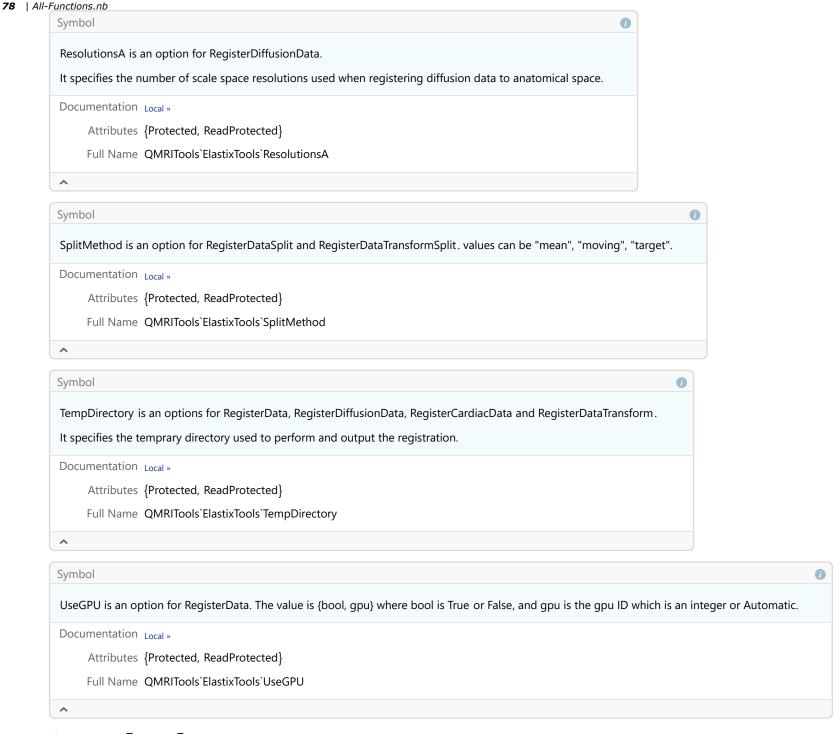












GeneralTools

Functions

```
ApplyCrop[data,crop] aplies the corpped region obtained form CropData to the data.

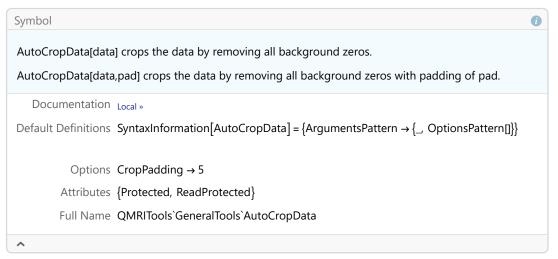
ApplyCrop[data,crop,{voxorig,voxnew}] aplies the corpped region obtained form CropData to the data.

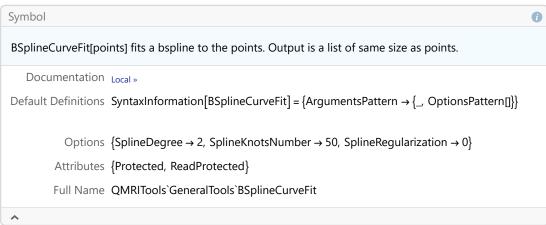
Documentation Local >>

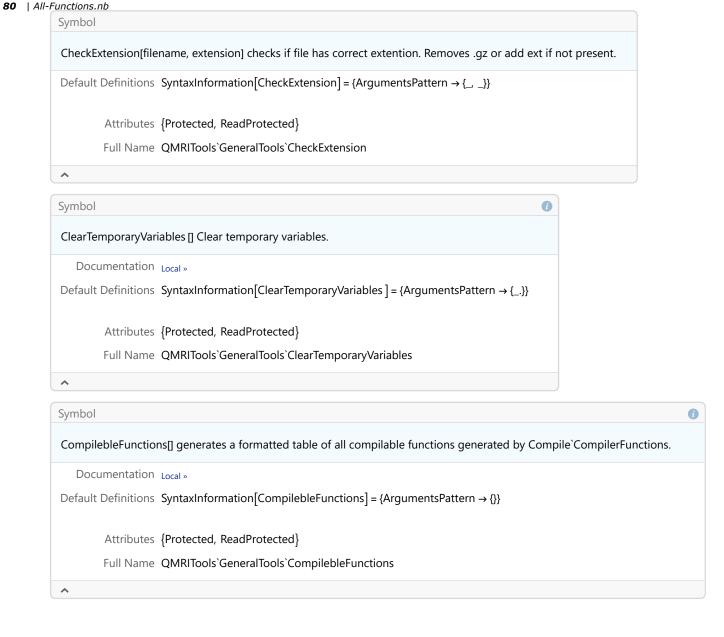
Default Definitions SyntaxInformation[ApplyCrop] = {ArgumentsPattern → {__ __ __}}}

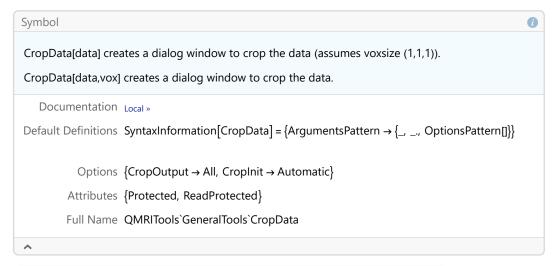
Attributes {Protected, ReadProtected}

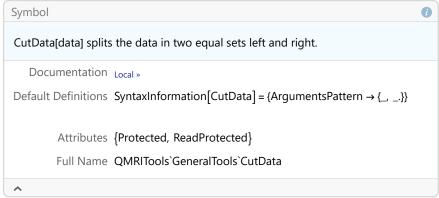
Full Name QMRITools`GeneralTools`ApplyCrop
```

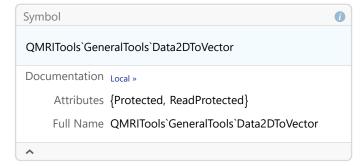


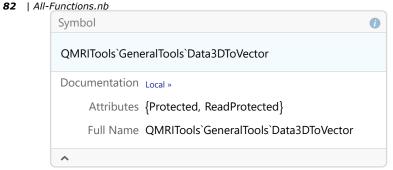


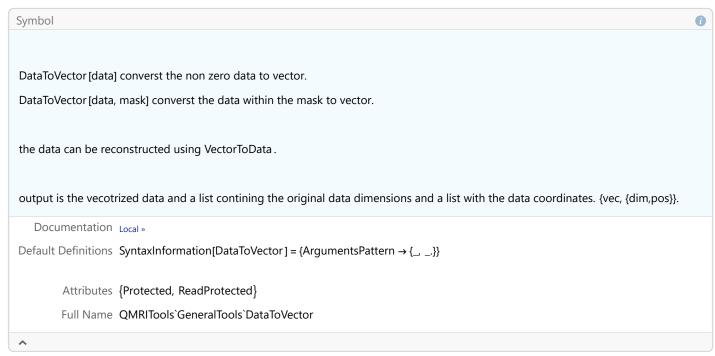


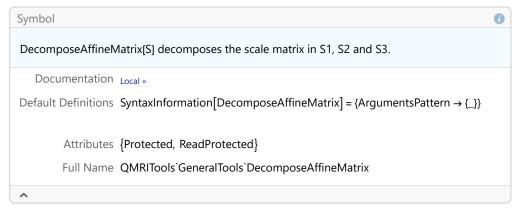


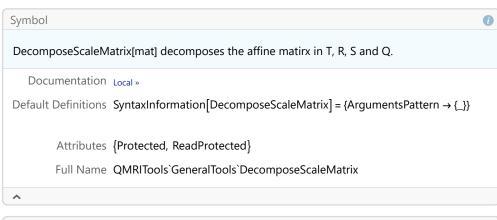


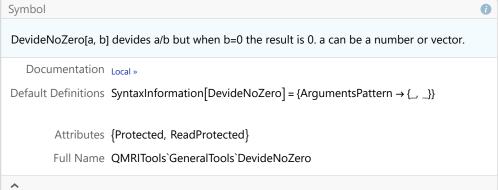


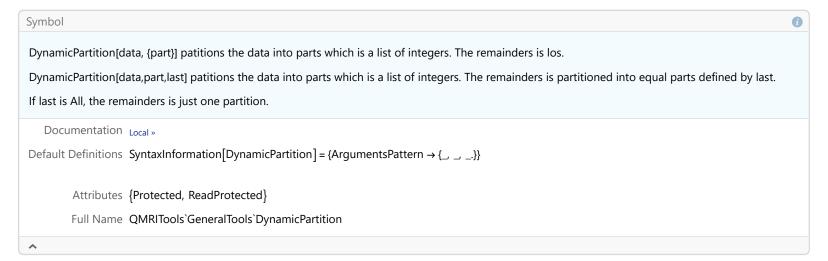


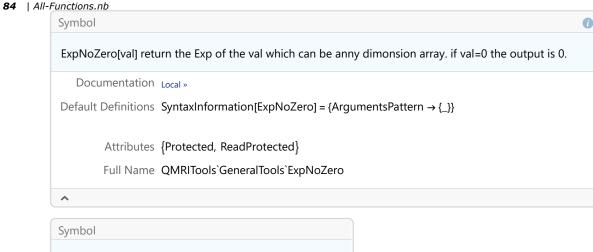


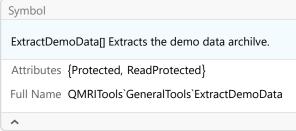


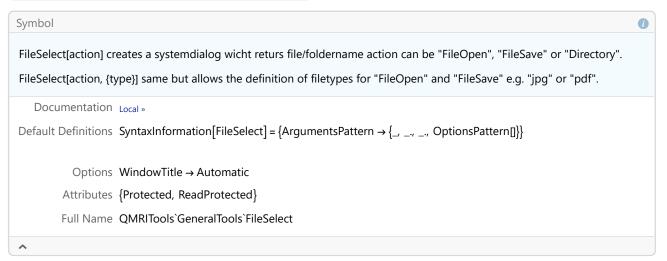


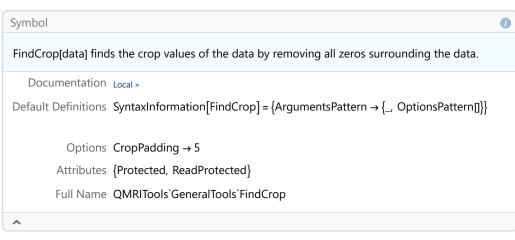


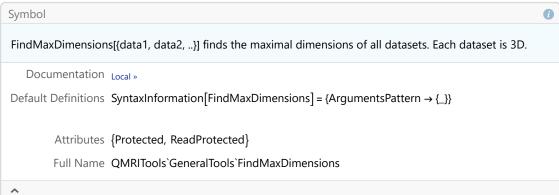


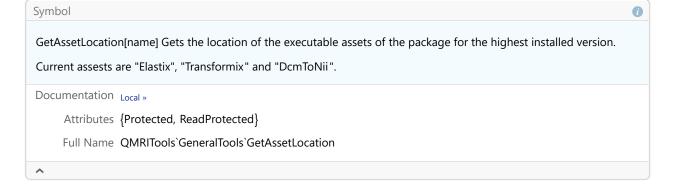


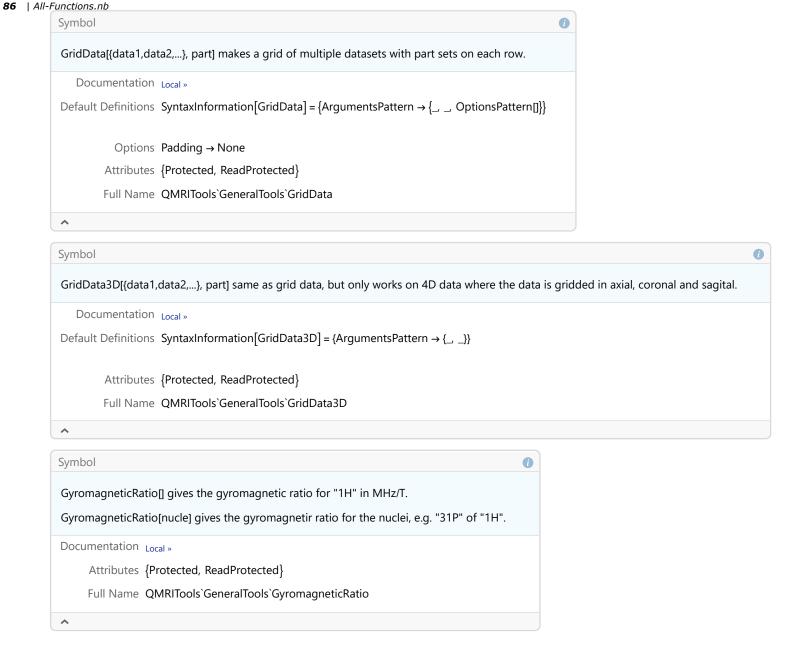


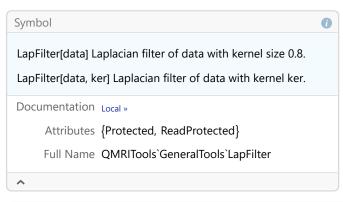


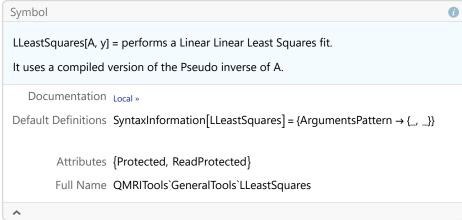


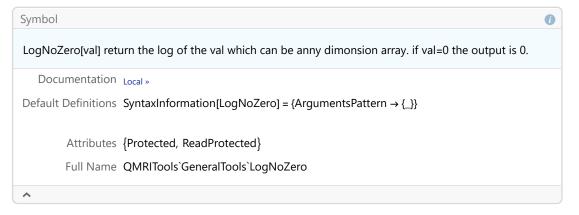


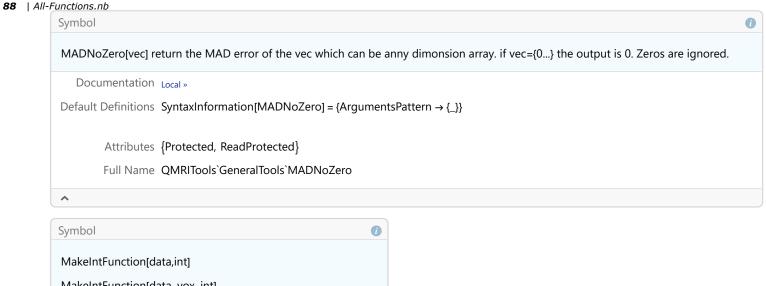


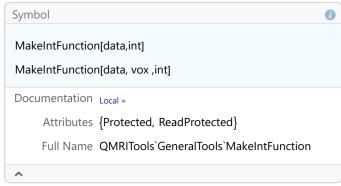


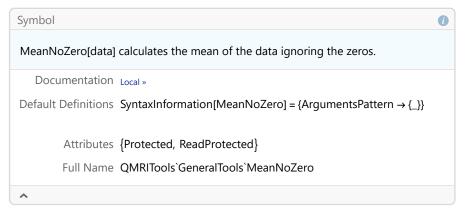


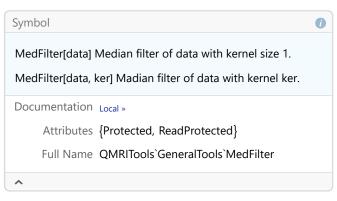


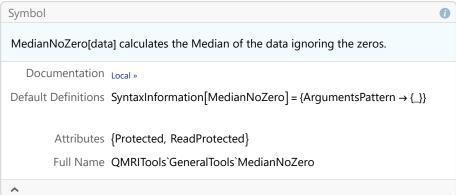


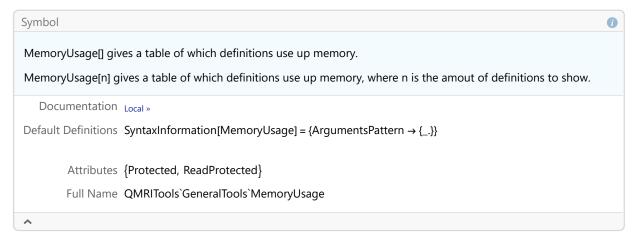


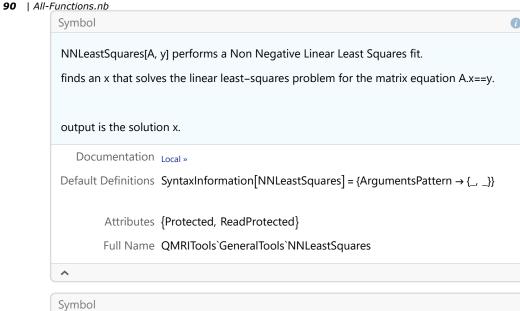


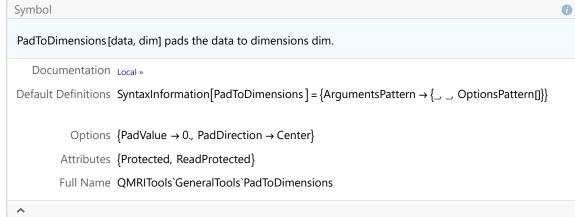


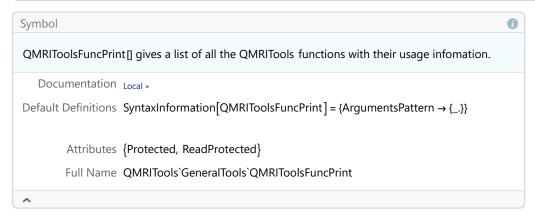


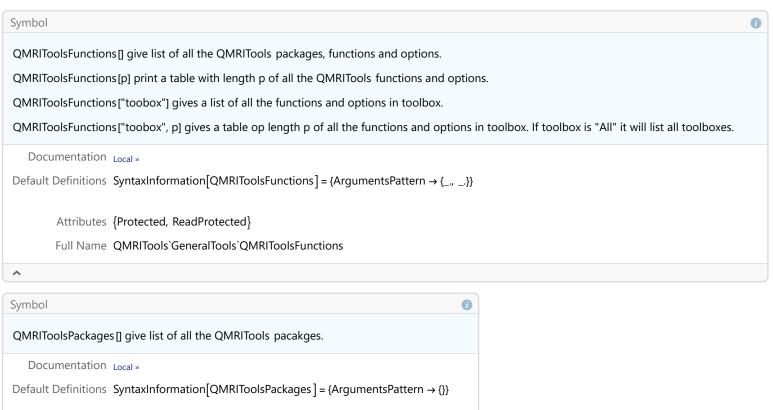


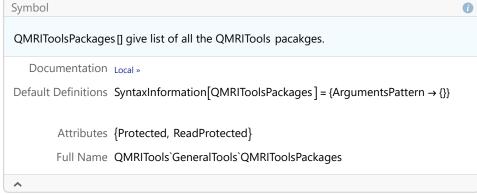


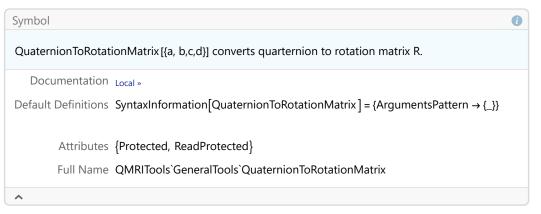


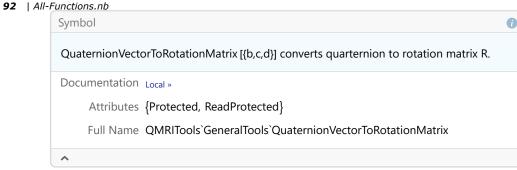


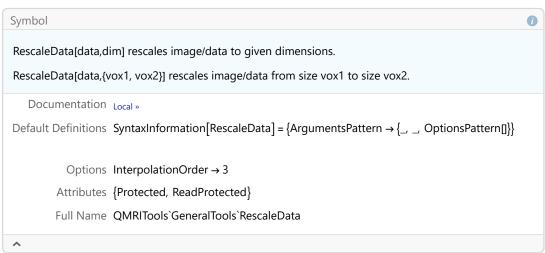


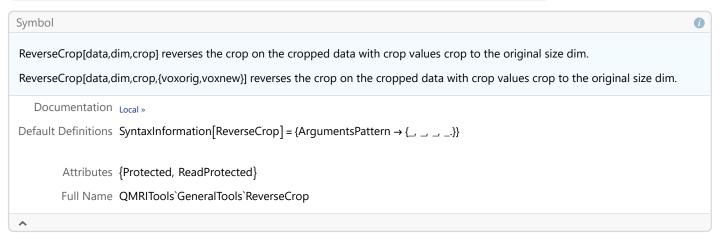


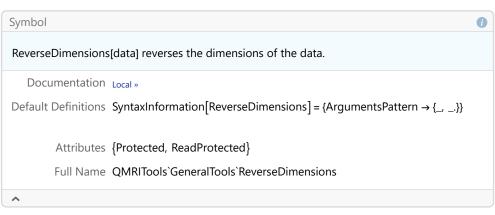


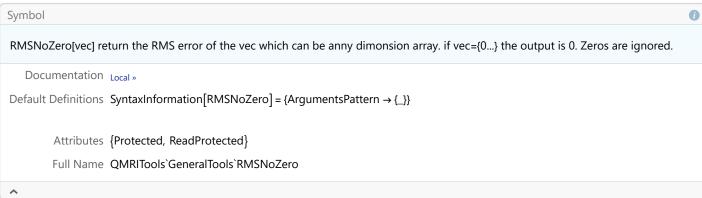


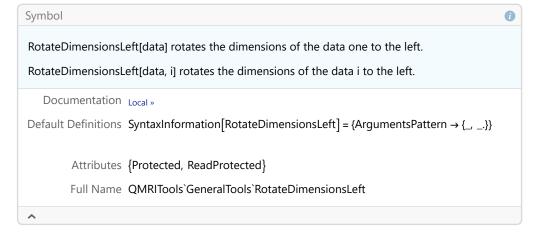


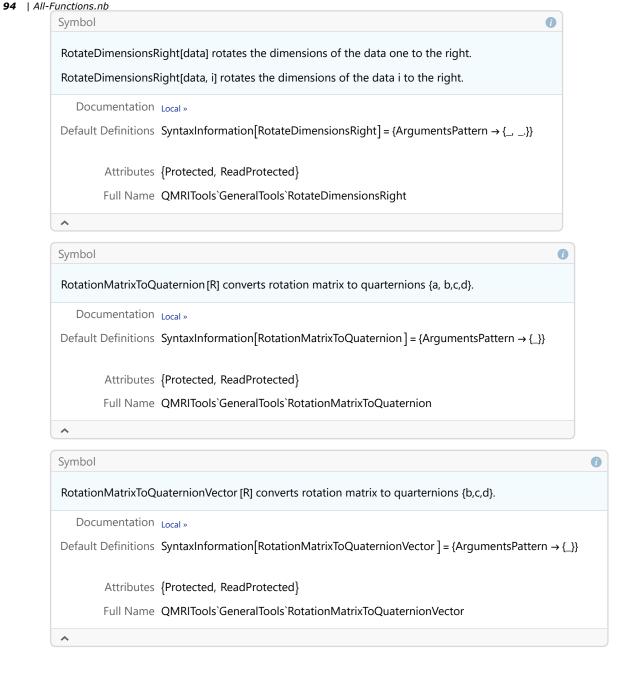












```
SaveImage[image] exports graph to image, ImageSize, FileType and ImageResolution can be given as options.

SaveImage[image, "filename"] exports graph to image with "filname", ImageSize, FileType and ImageResolution can be given as options.

Documentation Local »

Default Definitions SyntaxInformation[SaveImage] = {ArgumentsPattern → {\_____, OptionsPattern[]}}

Options {ImageSize → 6000, FileType → .jpg, ImageResolution → 300}

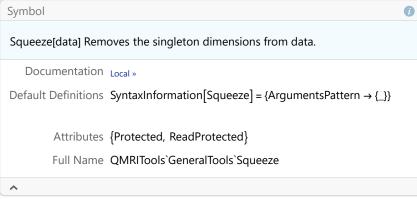
Attributes {Protected, ReadProtected}

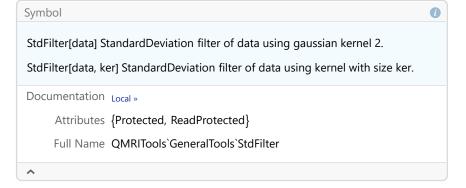
Full Name QMRITools'GeneralTools'SaveImage

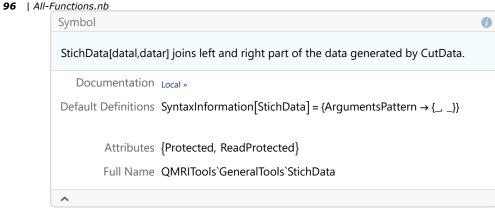
Symbol

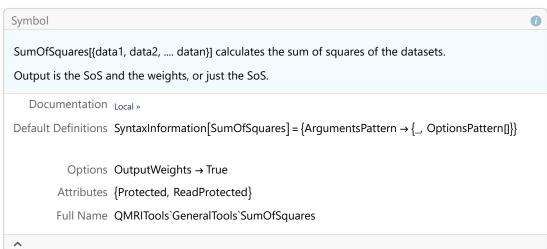
Squeeze[data] Removes the singleton dimensions from data.

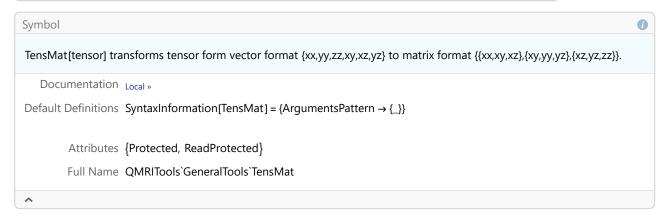
Documentation Local »
```

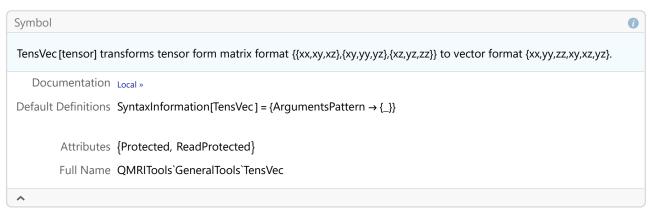


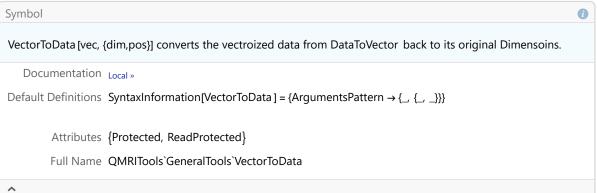




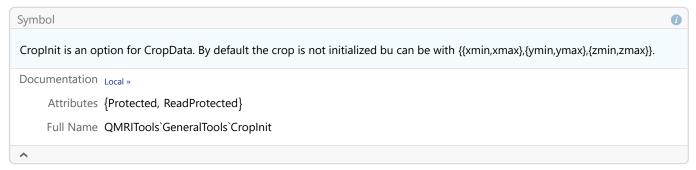




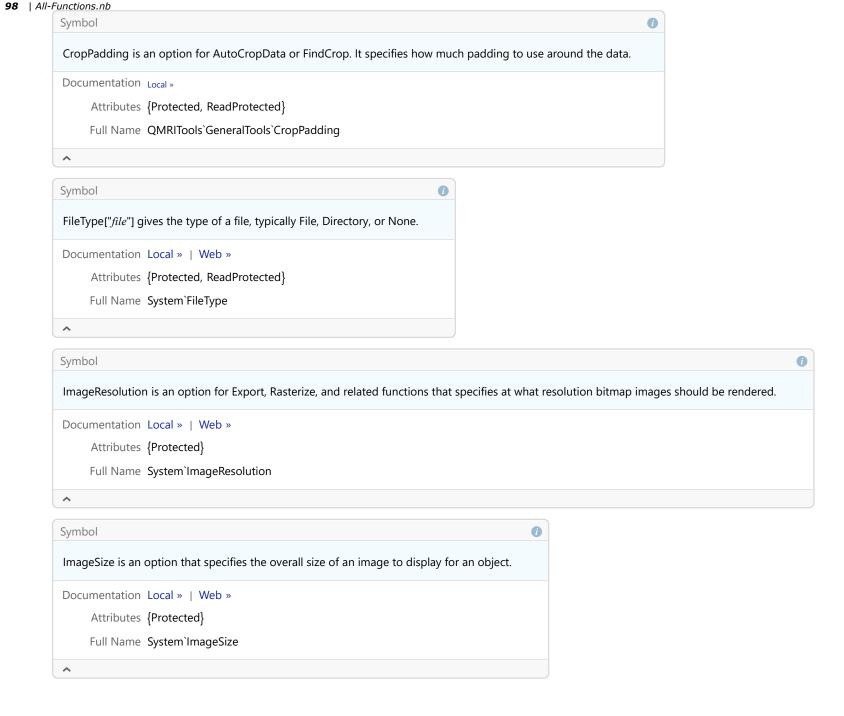


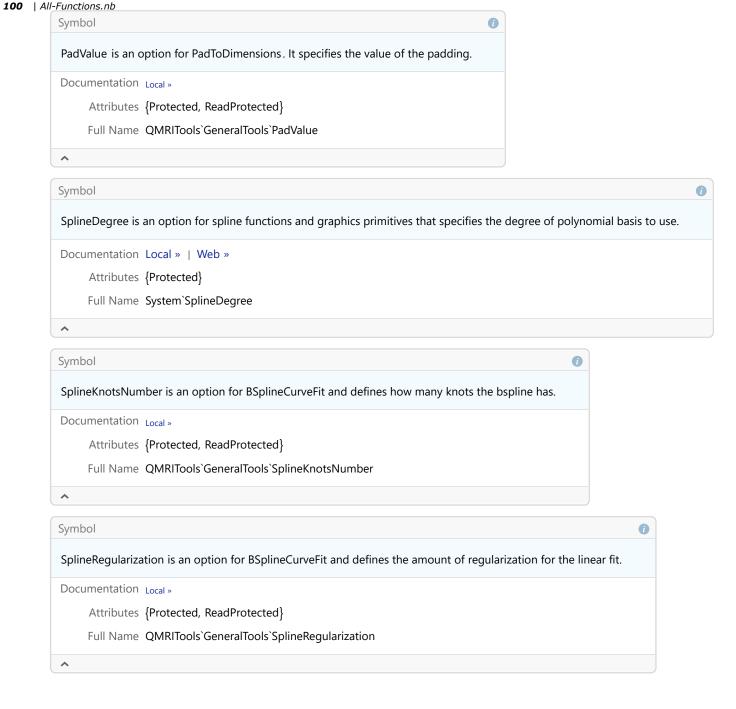


Options









```
WindowTitle is an option that specifies the title to give for a window.

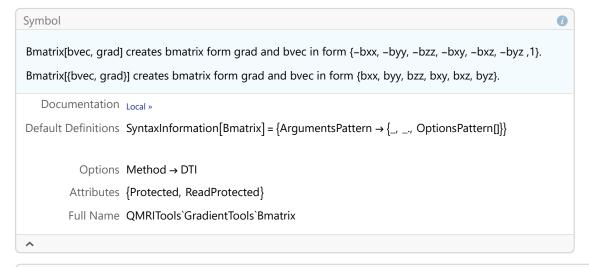
Documentation Local » | Web »

Attributes {Protected}

Full Name System'WindowTitle
```

GradientTools

Functions



```
BmatrixCalc["folder", grads] calculates the true bmatrix from the exported sequence parameters from the philips scanner that are stored in "folder" for each of the gradient directions grads.

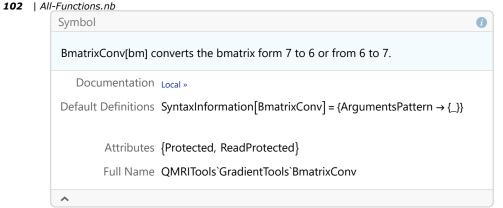
Documentation Local >>

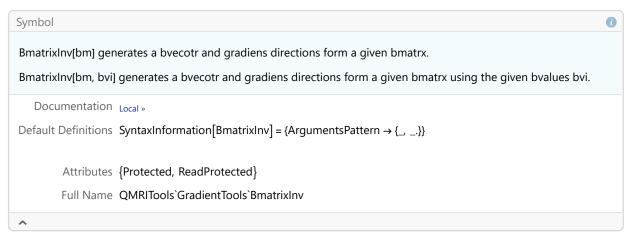
Default Definitions SyntaxInformation[BmatrixCalc] = {ArgumentsPattern → { __ _ _ _ _ _ _ _ OptionsPattern[]}}

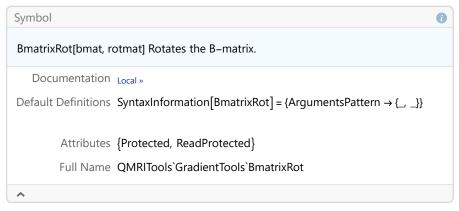
Options > UseGrad → {1, 1, {1, 1}, 1, 1} ... (8 total)

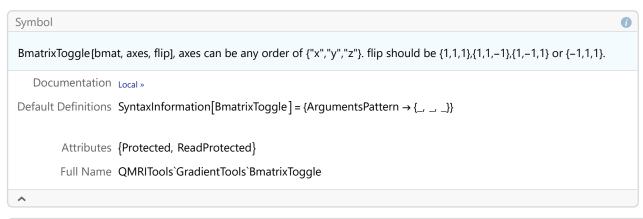
Attributes {Protected, ReadProtected}

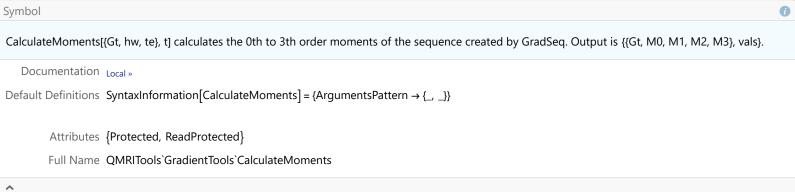
Full Name QMRITools'GradientTools'BmatrixCalc
```

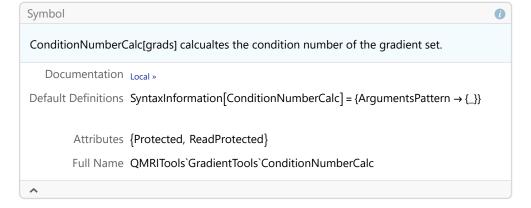


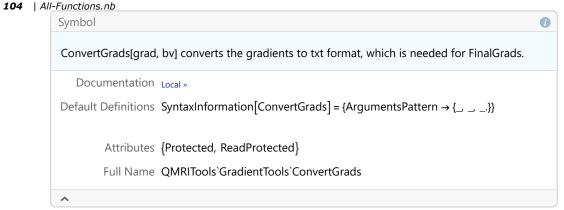


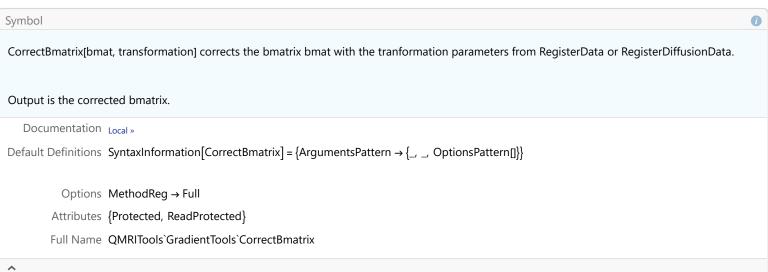


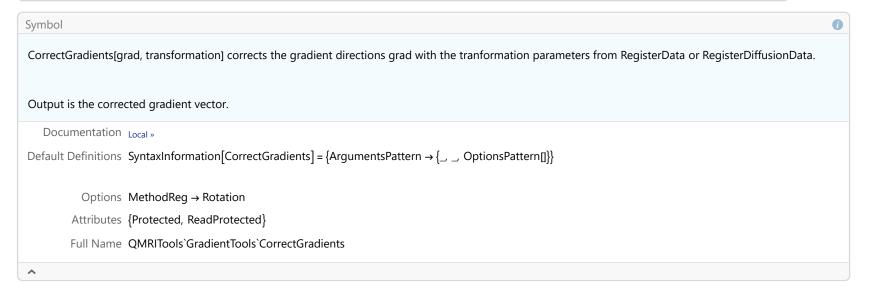


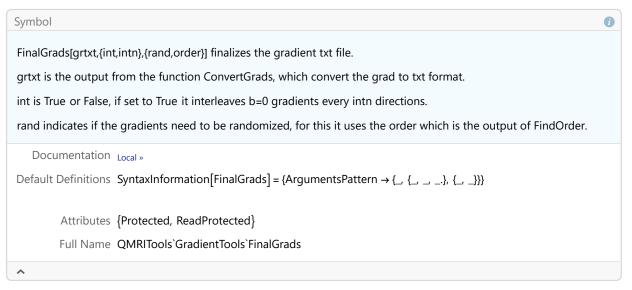


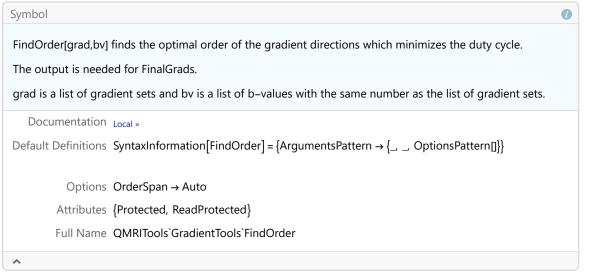


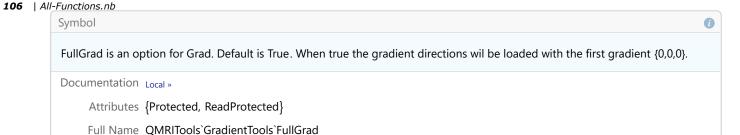


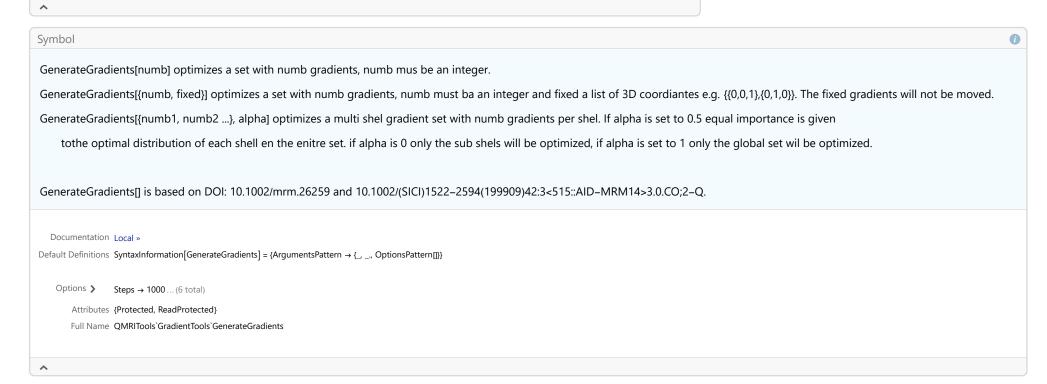


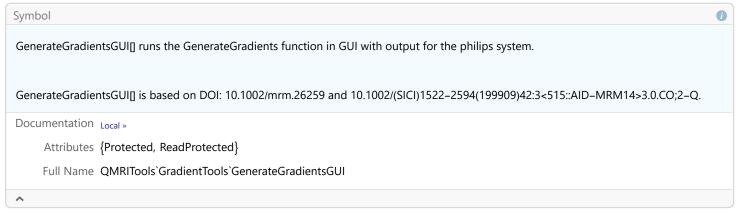


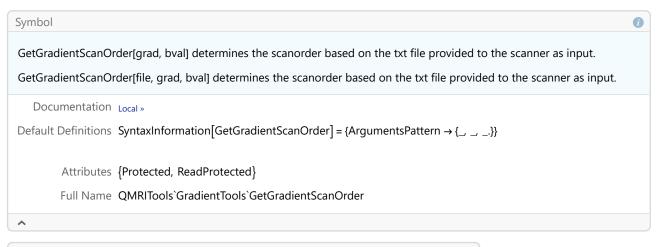


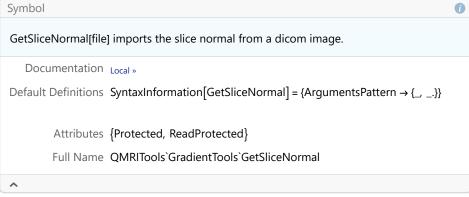


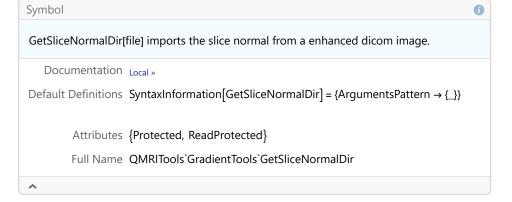


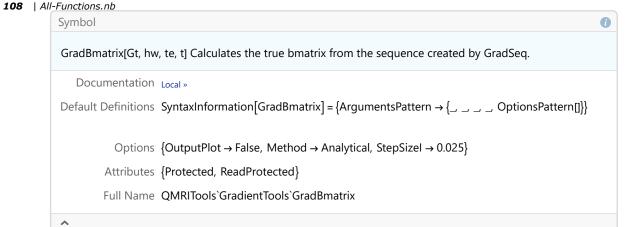


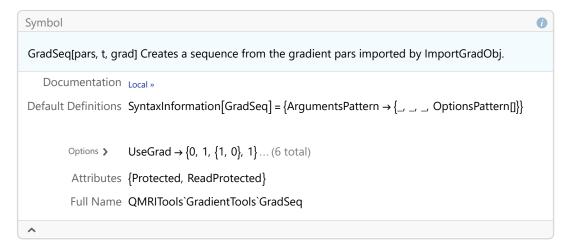


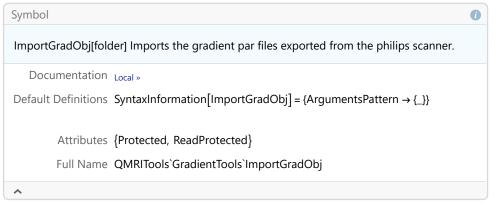


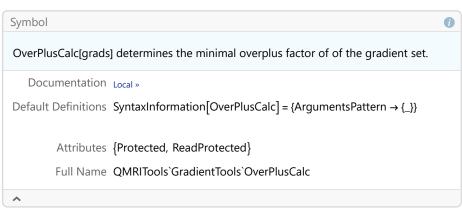


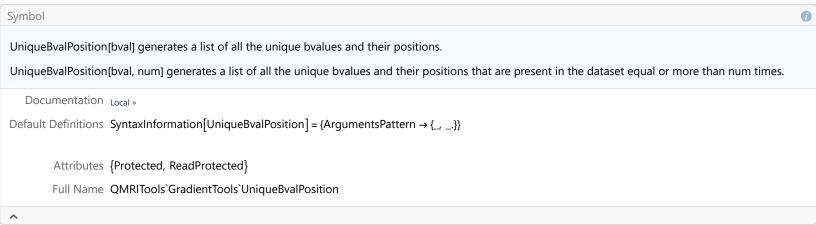




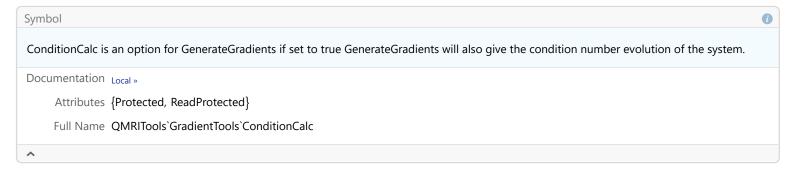


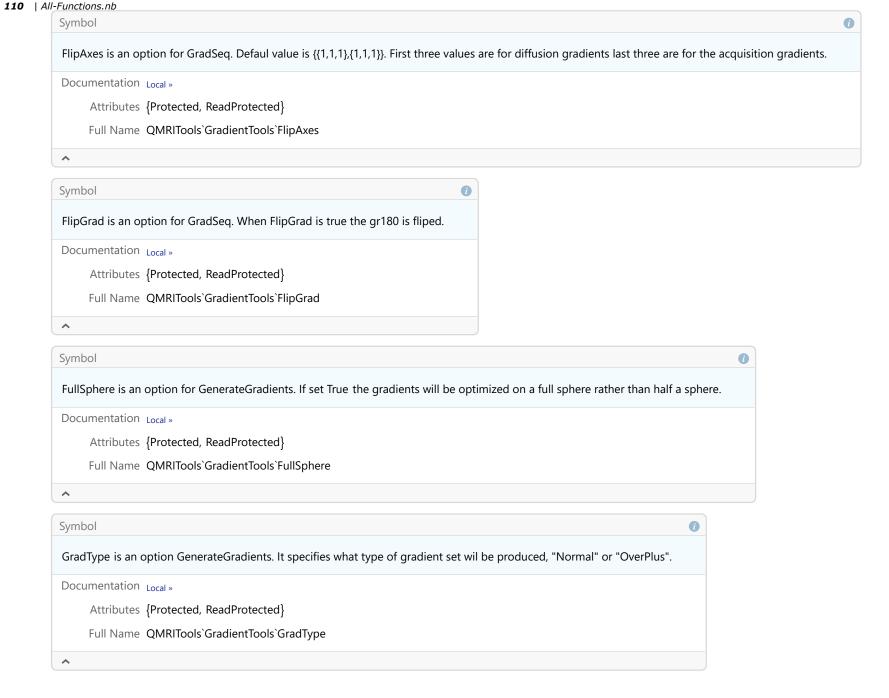


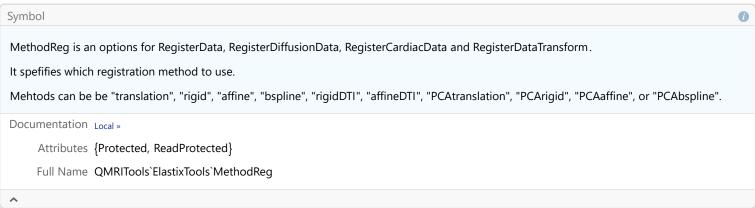


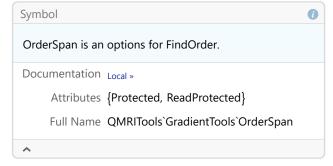


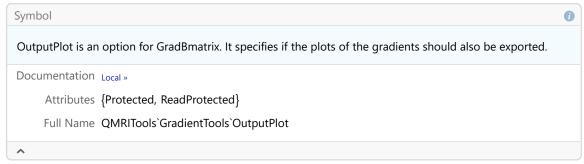
Options

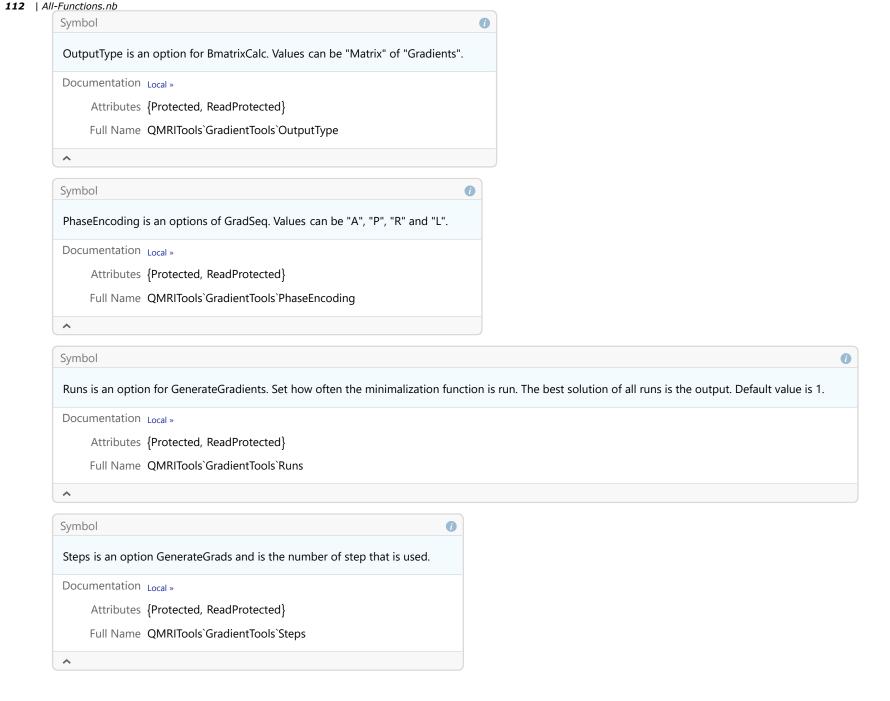


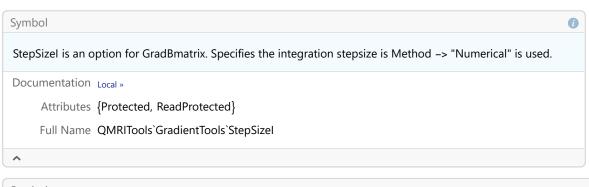


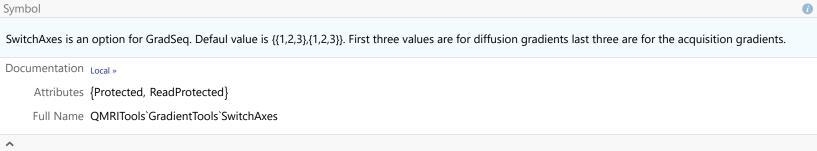


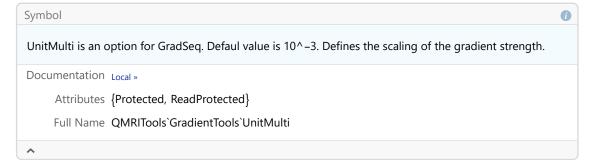


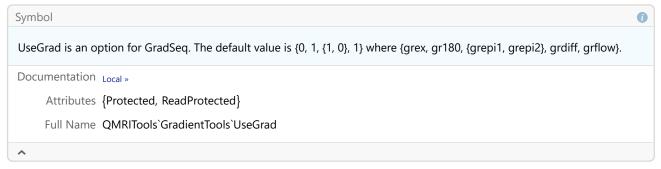


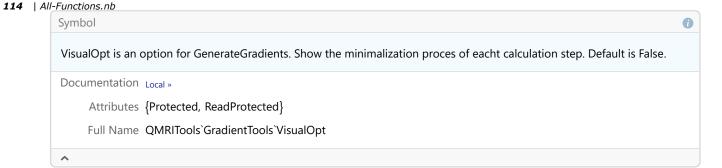






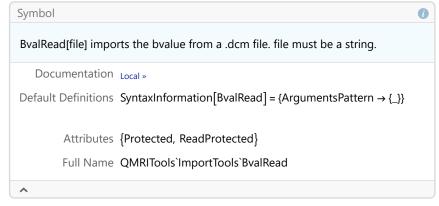


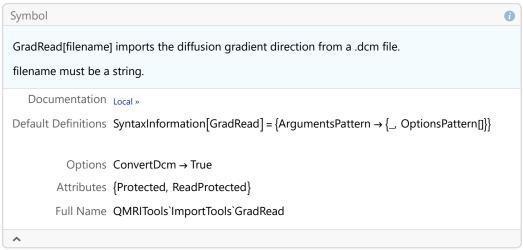


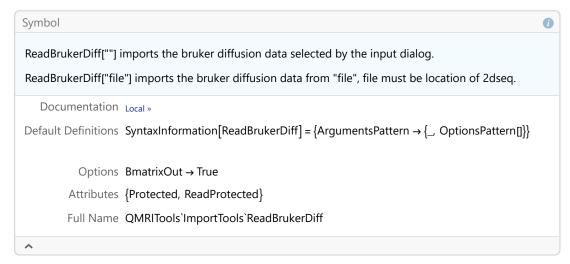


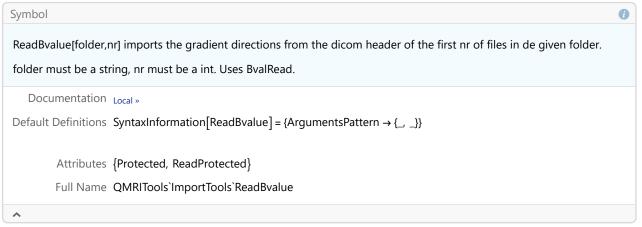
ImportTools

Functions









ReadDicom[folder] imports all dicom files from the given folder.

ReadDicom[{file1, file2,...}] imports all the given filenames.

ReadDicom[folder, {file1, file2,...}] imports all the given filenames from the given folder.

ReadDicom[folder, partsize] imports all dicom files from the given folder and partions them in given partsize.

ReadDicom[{file1, file2, ...}, partsize] imports all the given filenames and partions them in given partsize.

ReadDicom[folder, {file1, file2, ...}, partsize] imports all the given filenames from the given folder and partions them in given partsize.

Documentation Local »

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 $Default\ Definitions\ \ SyntaxInformation[ReadDicom] = \{ArgumentsPattern \rightarrow \{_,_,_,\ OptionsPattern[]\}\}$

Options ScaleCorrect → False

Attributes {Protected, ReadProtected}

Full Name QMRITools`ImportTools`ReadDicom

ReadDicomDiff[folder, part] imports all dicom files from the given folder and the corresponding diffusion parameters.

part is the number of diffusion images per slice including the unweighted images.

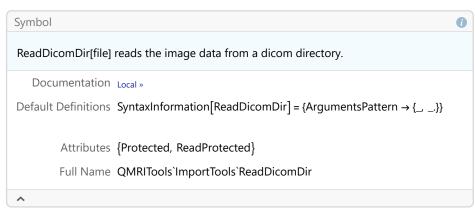
Documentation Local »

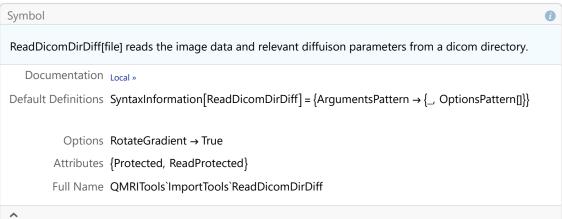
Default Definitions SyntaxInformation[ReadDicomDiff] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}}

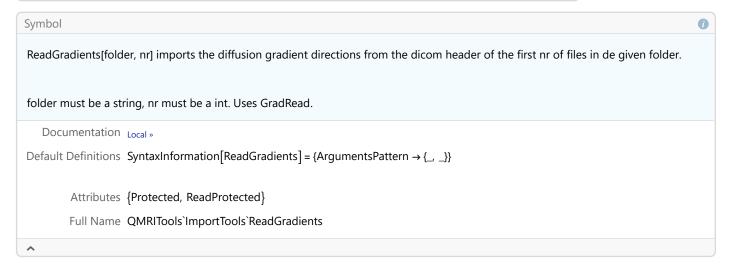
Options ScaleCorrect → False

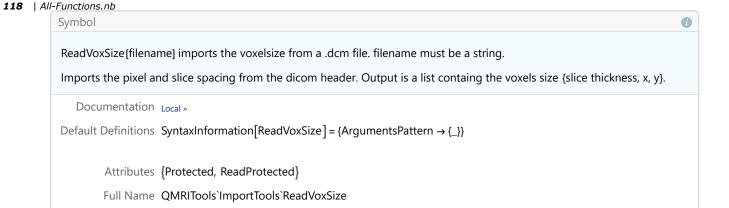
Attributes {Protected, ReadProtected}

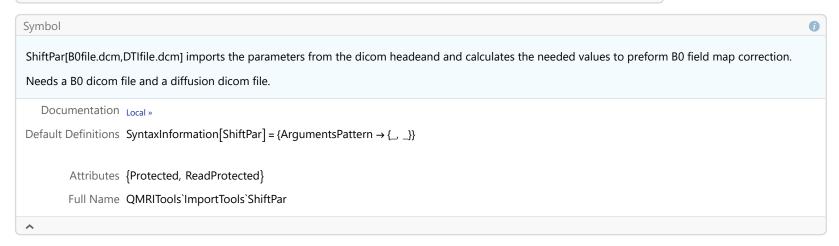
Full Name QMRITools`ImportTools`ReadDicomDiff





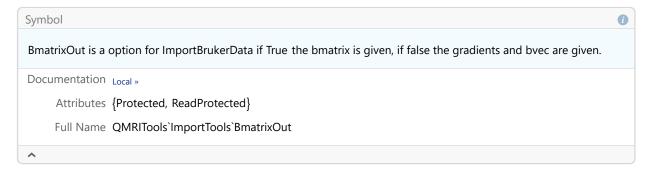




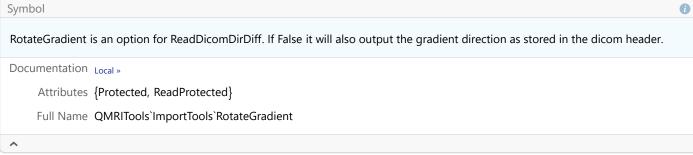


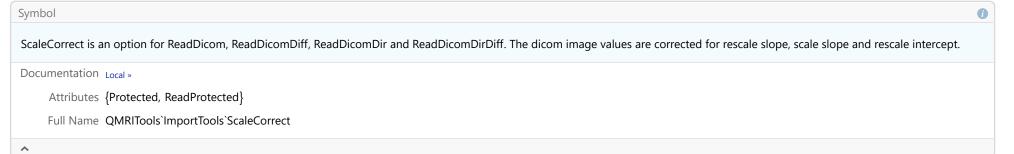
Options

^







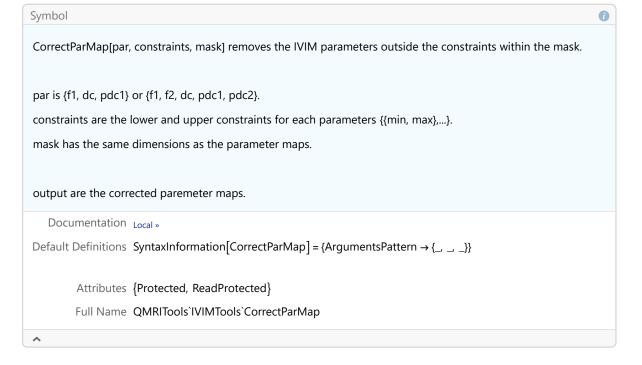


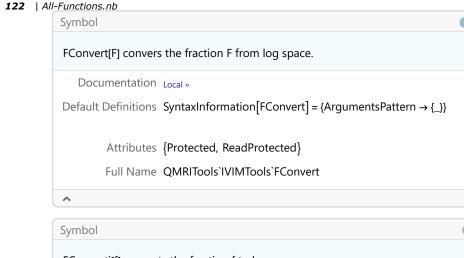
IVIMTools

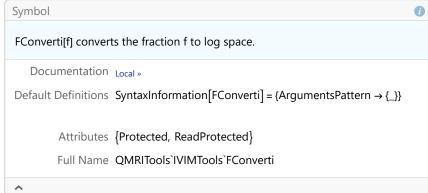
Functions

120 | All-Functions.nb Symbol BayesianIVIMFit2[data, bval, init, mask] performs bayesian IVIM fit of data. data is the data which should be {slice, Ndiff, x, y}. bval is the bvector whould be length Ndiff. init is the initalization of the bayesian fit which comes from IVIMCalc, (without S0 using 2 compartments). mask is the region in which the bayesian fit is performed. output is {f1, dc, pdc1}. The fraction is defined between 0 and 1, the dc, pdc1 is in mm^2/s. Documentation Local » Default Definitions SyntaxInformation[BayesianIVIMFit2] = {ArgumentsPattern → {_, _, _, _, OptionsPattern[]}} ChainSteps \rightarrow {20 000, 1000, 10} ... (7 total) Options > Attributes {Protected, ReadProtected} Full Name QMRITools`IVIMTools`BayesianIVIMFit2 ^

```
Symbol
BayesianIVIMFit3[data, bval, init, mask] performs bayesian IVIM fit of data.
data is the data which should be {slice, Ndiff, x, y}.
bval is the bvector whould be length Ndiff.
init is the initalization of the bayesian fit which comes from IVIMCalC, (without S0 using 3 compartments).
mask is the region in which the bayesian fit is performed.
output is {f1, f2, dc, pdc1, pdc2}. The fractions f1 and f2 are defined between 0 and 1, the dc, pdc1 and pdc1 is in mm^2/s.
   Documentation Local »
Default Definitions SyntaxInformation[BayesianIVIMFit3] = {ArgumentsPattern → {_, _, _, _, OptionsPattern[]}}
                    ChainSteps \rightarrow {20 000, 1000, 10} ... (7 total)
        Options >
         Attributes {Protected, ReadProtected}
         Full Name QMRITools`IVIMTools`BayesianIVIMFit3
\wedge
```







FracCorrect[fraction, time] corrects the signal fraction calculated with the IVIM model for tissue relaxation and acquisition parameters.

After correction the signal fraction can be regarded as volume fraction.

FracCorrect[{fraction1, fraction2}, time] corrects the signal fraction1 and fraction2 from a 3 compartement IVIM model.

time is {{te, tr}, {t2t, t21}, {t1t, t11}} or {{te, tr}, {t2t, t21}, {t1t, t11}}.

where t2t and t1t are "tissue" relaxation times and t11 t12, t21 and t22 the "fluid" relaxation times.

The te and tr as well as the relaxation times T2 and T1 can be defines in any time unit as long as they are consistant for all, e.g. all in ms.

output is the corrected fraction maps.

Documentation Local »

Default Definitions SyntaxInformation[FracCorrect] = {ArgumentsPattern → {_, _, _,}}

Attributes {Protected, ReadProtected}

Full Name QMRITools`IVIMTools`FracCorrect

^

All-Functions.nb | 123

124 | All-Functions.nb Symbol HistogramPar[data, {constraints, Nbins}, style, color, range] plots histograms of IVIM solution. HistogramPar[data, {constraints, Nbins, mu, conv}, components, color, range] plots histograms of IVIM solution. data is {f1, dc, pdc1} or {f1, f2, dc, pdc1, pdc2}. constraints are the ranges of the x-axes for the plots. Nbins are the number of histogram bins. style is the plot type, can be 1, 2, or 3. color is the color of the histogram. range are the ranges of the y-axes. output is a row of histograms. Documentation Local » $Default \ Definitions \ \ SyntaxInformation[HistogramPar] = \{ArgumentsPattern \rightarrow \{_, _, _, _, _\}\}$ Attributes {Protected, ReadProtected} Full Name QMRITools`IVIMTools`HistogramPar

^

All-Functions.nb | 125

IVIMCalc[data, binp, init] calculates the IVIM fit.

data should be 1D, 2D, 3D or 4D.

binp should be full bmatrix which can be calculated from the bvecs en bvals using Bmatrix with the bvalues in s/mm^2.

init should are the initialization parameters for 2 components this is {S0, f, D, Dp} for 3 componentes this is {S0, f1, f2, D, Dp1, Dp2}.

The fraction is defined between 0 and 1, the D, Dp, Dp1 and Dp2 is in mm^2/s.

output is {S0, f1, D, pD1} or {S0, f1, f2, D, pD1, pD2}.

Documentation Local »

Default Definitions SyntaxInformation[IVIMCalc] = {ArgumentsPattern → {_, _, _, _, OptionsPattern[]}}

Options ➤ Method → Automatic ... (8 total)

Attributes {Protected, ReadProtected}

Full Name QMRITools`IVIMTools`IVIMCalc

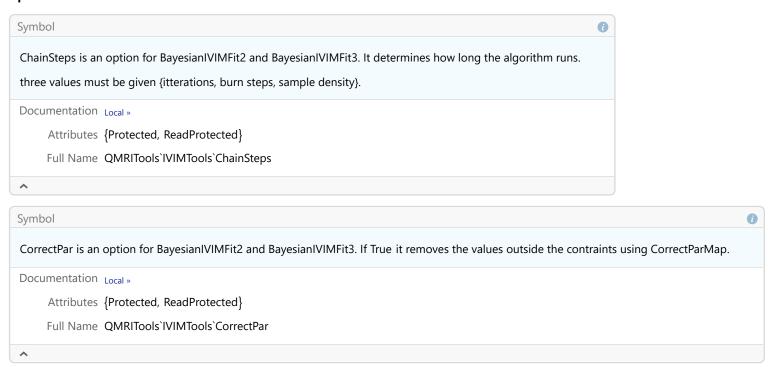
^

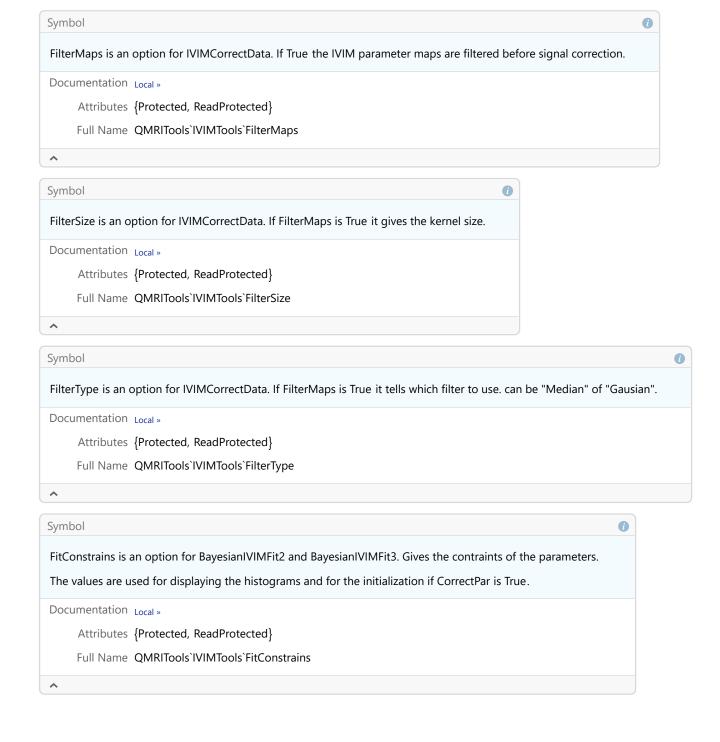
126 | All-Functions.nb Symbol IVIMCorrectData[data, {S0, f, pdc}, bval] removes the ivim signal from the data. data is the original data. {S0, f, pdc} are the solution to a 2 compartment IVIM fit using IVIMCalc or BayesianIVIMFit2. bval are the bvalues. The fraction is defined between 0 and 1, the pdc is in mm²/s. output is the corrected data. Documentation Local » Default Definitions SyntaxInformation[IVIMCorrectData] = {ArgumentsPattern → {_, {_, _, _,}, _, OptionsPattern[]}} Options $\{FilterMaps \rightarrow True, FilterType \rightarrow Median, FilterSize \rightarrow 1\}$ Attributes {Protected, ReadProtected} Full Name QMRITools`IVIMTools`IVIMCorrectData ^

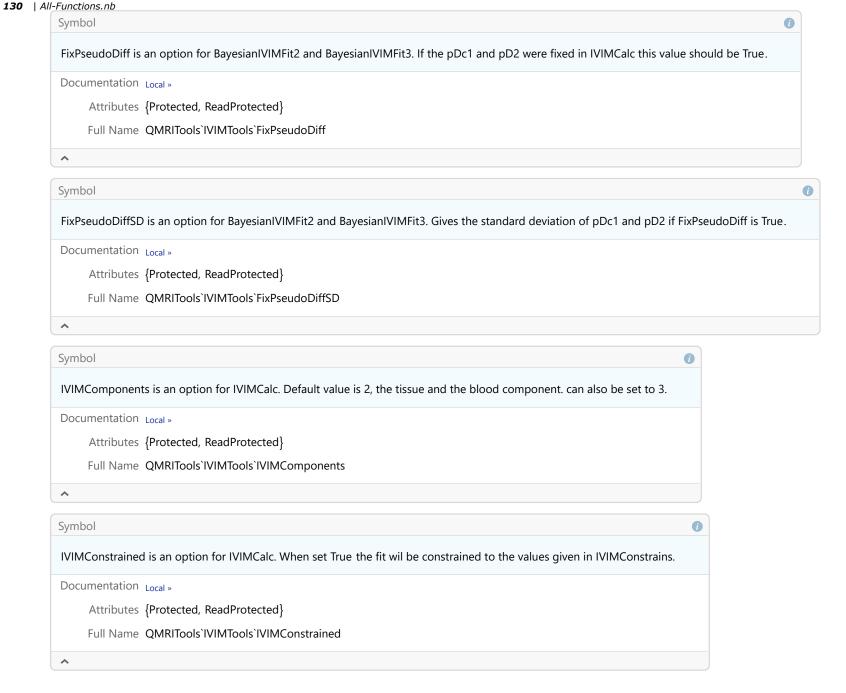
```
Symbol
IVIMFunction[] gives the IVIM function with 2 comps.
IVIMFunction[components] gives the IVIM function.
IVIMFunction[components, type] gives the IVIM function.
type can be "Normal" or "Exp".
componenets can be 2 or 3.
output is the function with b, S0, f1, f2, D, pD1, pD2 as parameters. The fraction is defined between 0 and 1, the D, Dp, Dp1 and Dp2 is in mm^2/s.
   Documentation Local »
Default Definitions SyntaxInformation[IVIMFunction] = {ArgumentsPattern \rightarrow \{\_, \_\}}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`IVIMTools`IVIMFunction
^
Symbol
IVIMResiduals[data, binp, pars] calculates the root mean square residuals of an IVIM fit ussing IVIMCalc, BayesianIVIMFit2 or BayesianIVIMFit3.
Documentation Local »
      Attributes {Protected, ReadProtected}
      Full Name QMRITools`IVIMTools`IVIMResiduals
^
Symbol
ThetaConv[{F1, Fc, pDc}] converts the parameters from Log space to normal space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3.
ThetaConv[{F1, F2, Dc, pDc1}] converts the parameters from Log space to normal space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3.
ThetaConv[{F1, F2, Dc, pDc1, pDc2}] converts the parameters from Log space to normal space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3.
Documentation Local »
     Attributes {Protected, ReadProtected}
      Full Name QMRITools`IVIMTools`ThetaConv
```

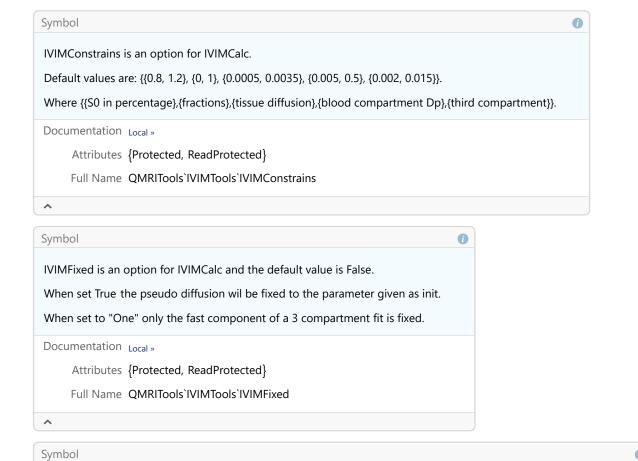
128 | All-Functions.nb Symbol ThetaConvi[{f, dc, pdc}] converts the parameters from Normal space to Log space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3. ThetaConvi[{f1, f2, dc, pdc1}] converts the parameters from Normal space to Log space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3. ThetaConvi[{f1, f2, dc, pdc1, pdc2}] converts the parameters from Normal space to Log space. Is used in BayesianIVIMFit2 and BayesianIVIMFit3. Documentation Local » Default Definitions SyntaxInformation[ThetaConvi] = {ArgumentsPattern \rightarrow {_}} Attributes {Protected, ReadProtected} Full Name QMRITools`IVIMTools`ThetaConvi \wedge

Options









IVIMTensFit is an option for IVIMCalc. When set True the tissue diffusion component wil be calculated as a tensor.

Method is an option for various algorithm-intensive functions that specifies what internal methods they should use.

Documentation Local »

Documentation Local » | Web »

Attributes {Protected}

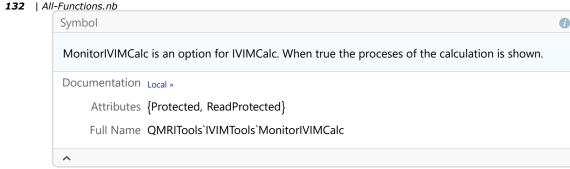
Full Name System`Method

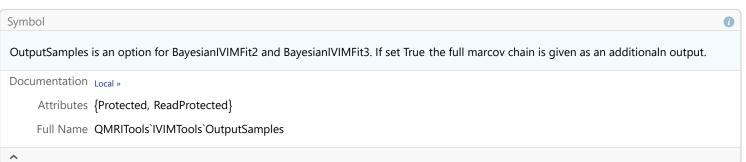
^

Symbol

Attributes {Protected, ReadProtected}

Full Name QMRITools`IVIMTools`IVIMTensFit





```
Symbol
Parallelize[expr] evaluates expr using automatic parallelization.
Definitions
Parallelize[Parallel`Evaluate`Private`expr_, Parallel`Evaluate`Private`opts:OptionsPattern[]]:=
Module[{Parallel`Evaluate`Private`res, Parallel`Evaluate`Private`ehead, Parallel`Evaluate`Private`fopts}, Parallel`Protected`tryRelaunch[];
  If[Parallel`Protected`$seQ, Message[Parallelize::nopar];
   Return[Parallel`Evaluate`Private`expr];
  Parallel`Evaluate`Private`fopts = Sequence @@ {Method → OptionValue [Method],
     DistributedContexts → Parallel`Protected`DistOptCheck[Parallelize, OptionValue[DistributedContexts]], ProgressReporting → OptionValue[ProgressReporting]};
  Parallel`Evaluate`Private`ehead = Replace [Head [Unevaluated [Parallel`Evaluate`Private`expr], Hold],
    {Hold[Parallel`Evaluate`Private`s_Symbol] → Parallel`Evaluate`Private`s, _ → $Failed}];
  With[{Parallel`Evaluate`Private`handler = Lookup[Parallel`Evaluate`$ParallelExtensions, Parallel`Evaluate`Private`ehead, $Failed]},
   If [Parallel`Evaluate`Private`handler = ! = $Failed, Return [Parallel`Evaluate`Private`handler [Parallel`Evaluate`Private`expr, Parallel`Evaluate`Private`fopts]]];
  Parallel`Evaluate`Private`res = Parallel`Evaluate`Private`tryCombine[Parallel`Evaluate`Private`expr, Parallel`Evaluate`Private`fopts];
  If[Head[Parallel`Evaluate`Private`res] =! = Parallel`Evaluate`Private`tryCombine, Return[Parallel`Evaluate`Private`res]];
  Block | {Parallel`Evaluate`Private`$seqWarning = False},
   Parallel`Evaluate`Private`res = Parallel`Evaluate`Private`wrapAround[Parallel`Evaluate`Private`expr, Parallel`Evaluate`Private`fopts];
   If [Head [Parallel`Evaluate`Private`res] =! = Parallel`Evaluate`Private`wrapAround, Return [Parallel`Evaluate`Private`res]];];
  Parallel`Evaluate`Private`res = Parallel`Evaluate`Private`silentFail[Parallel`Evaluate`Private`expr];
  If[Head[Parallel`Evaluate`Private`res] =! = Parallel`Evaluate`Private`silentFail, Return[Parallel`Evaluate`Private`res]];
  If[Parallel`Evaluate`Private`$seqWarning, Message[Parallelize::nopar1, Parallel`Evaluate`Private`expr]];
  Parallel`Evaluate`Private`expr
Documentation Local » | Web »
    Options {DistributedContexts → $Context, Method → Automatic, ProgressReporting} → $ProgressReporting}
   Attributes {HoldFirst, Protected}
   Full Name System'Parallelize
^
Symbol
                                                                                                                                                 0
UpdateStep is an option for BayesianIVIMFit2 and BayesianIVIMFit3. It determines how often the parameters are updated. Is optimized during the first 500 burn steps.
```

JcouplingTools

Attributes {Protected, ReadProtected}

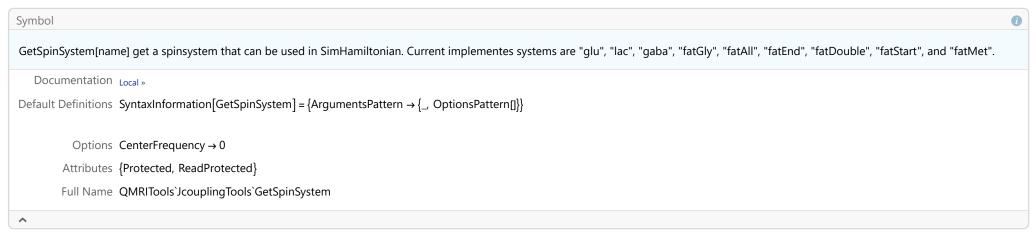
Full Name QMRITools`IVIMTools`UpdateStep

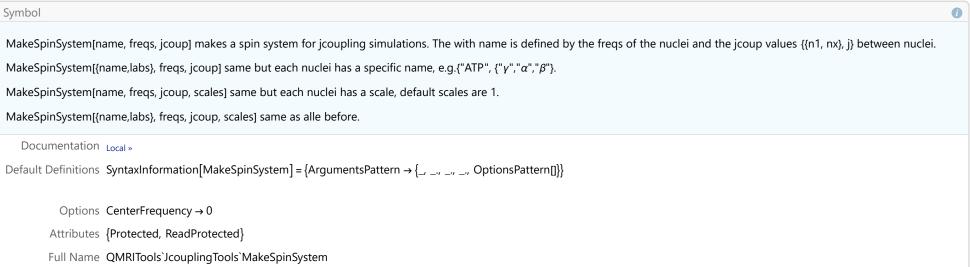
Documentation Local »

134 | All-Functions.nb

Functions

^





```
SequencePulseAcquire[din, H] performs a pulsaquire experiment of the spin system din given the hamiltonian H with a 90 Degree pulse.

SequencePulseAcquire[din, H, b1] performs a pulsaquire experiment of the spin system din given the hamiltonian H with a 90 Degree pulse and b1.

The output is a new spinsystem dout.

Documentation Local >>

Default Definitions SyntaxInformation[SequencePulseAcquire] = {ArgumentsPattern → {_, _, _, _}}}

Attributes {Protected, ReadProtected}

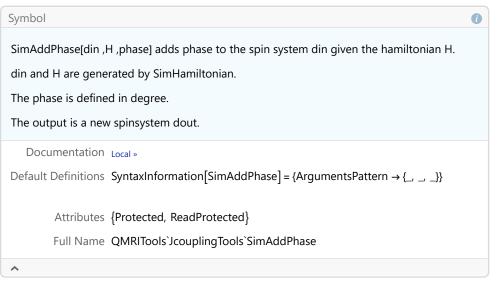
Full Name QMRITools'JcouplingTools'SequencePulseAcquire
```

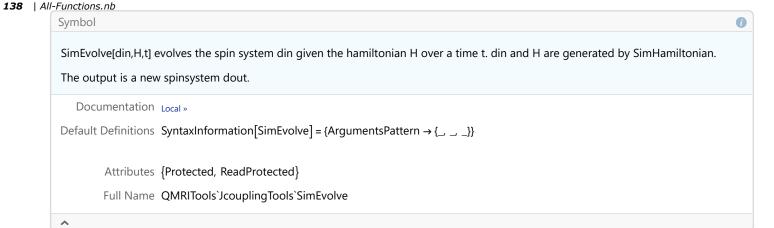
^

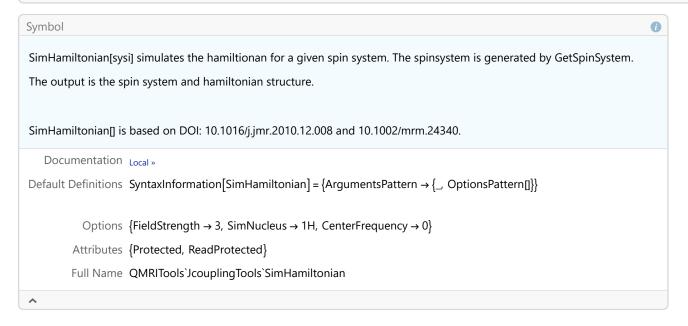
SequenceSpaceEcho[din, H, t1, t2, necho, b1] performs a multi echo spin echo experiment with a 90 degree spin echo, with t1 the time between the 90 degree RF pulse and the first 180 degree RF pulse, t2 the time between a 180 degree RF pulse and the following readout (and 2xt1 the time between two consecutive 180 degree RF pulses. Further defines necho the number of 180 degree RF pulses, din the spin system given the hamiltonian H using b1. The t1 and t2 are defined in ms, and b1 of 100% is defines as 1. The output is a new spinsystem dout. Documentation Local > Default Definitions Syntaxinformation[SequenceSpaceEcho] = (ArgumentPattern → (Lucus - Lucus - Lucus

SequenceSteam[din, H, {te, tm}] performs a stimulated echo experiment with echo time te and mixing time tm of the spin system din given the hamiltonian H with 3 90 Degree pulses. The te and tm are defined in ms. The output is a new spinsystem dout. Documentation Local >> Default Definitions SyntaxInformation[SequenceSteam] = {ArgumentsPattern → {, _ _ , _ }}}} Attributes {Protected, ReadProtected} Full Name QMRITools'JcouplingTools'SequenceSteam

 \wedge







SimReadout[din, H] performs a readout of a spinsystem din with hamiltonian H.

Output is {time,fids,ppm,spec,dout}, which are the free induction decay fids with its time, the spectrum spec with its ppm and the evolved spin system dout.

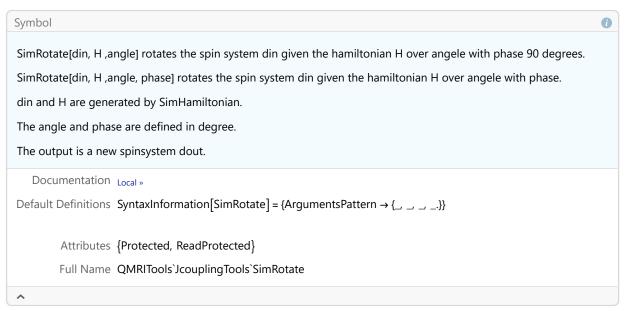
Documentation Local →

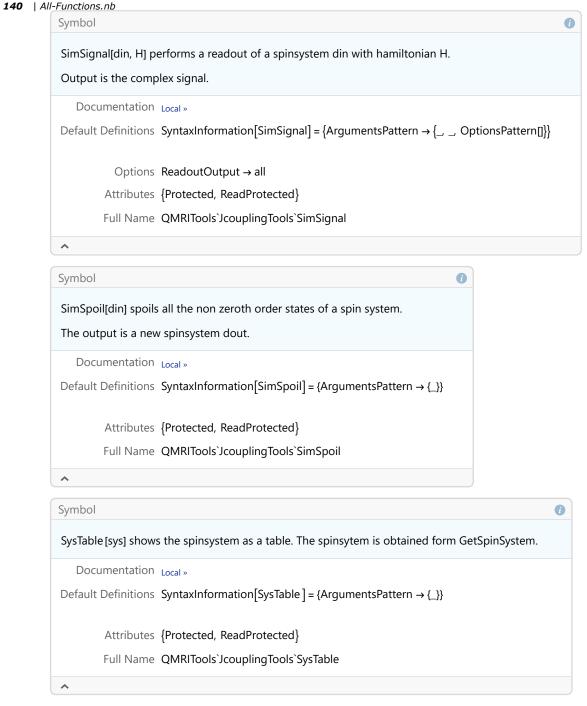
Default Definitions SyntaxInformation[SimReadout] = {ArgumentsPattern → {__ , __ , OptionsPattern[]}}

Options ➤ ReadoutOutput → all ... (8 total)

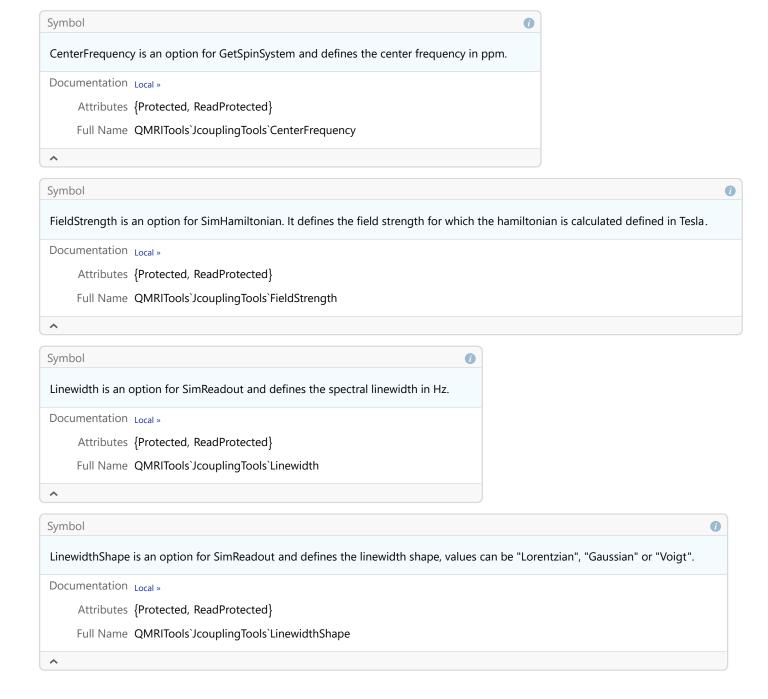
Attributes {Protected, ReadProtected}

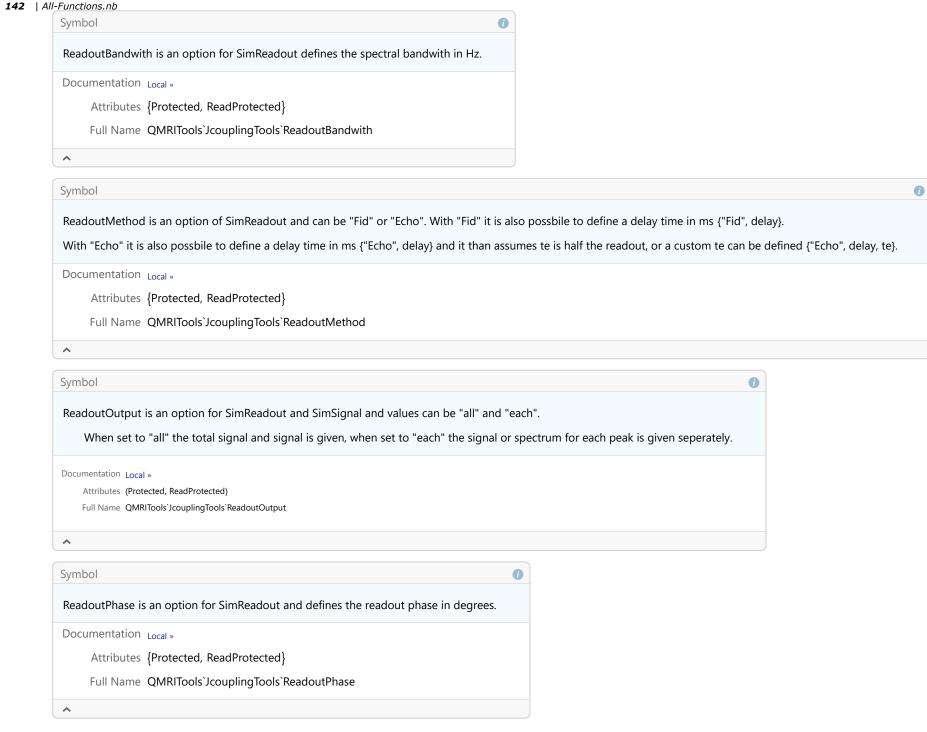
Full Name QMRITools'JcouplingTools'SimReadout





Options





```
Symbol

ReadoutSamples is an option for SimReadout and defines the number of readout samples for the spectrum.

Documentation Local »

Attributes {Protected, ReadProtected}

Full Name QMRITools'JcouplingTools'ReadoutSamples

Symbol

SimNucleus is an option for SimHamiltonian. It defines the nucleus for which to simulate the spectra.

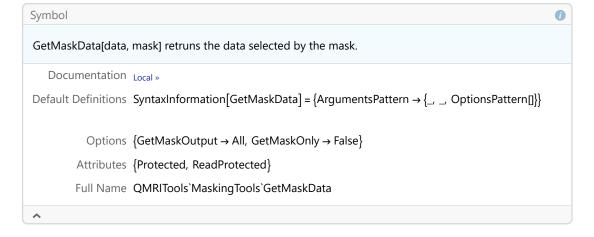
Documentation Local »

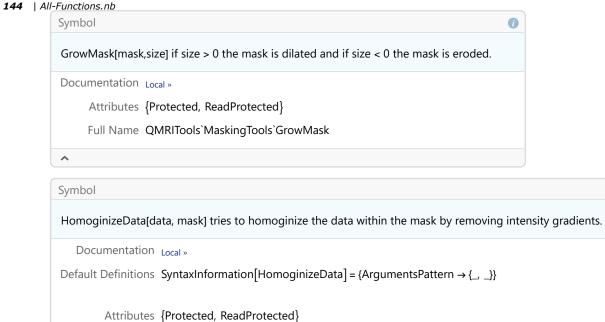
Attributes {Protected, ReadProtected}

Full Name QMRITools'JcouplingTools'SimNucleus
```

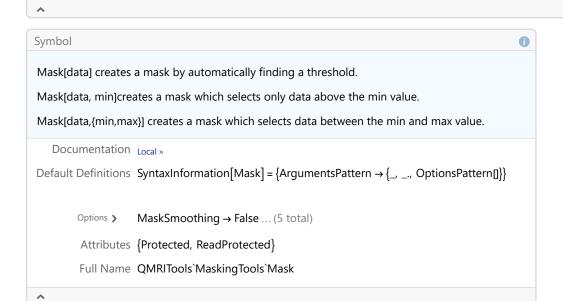
MaskingTools

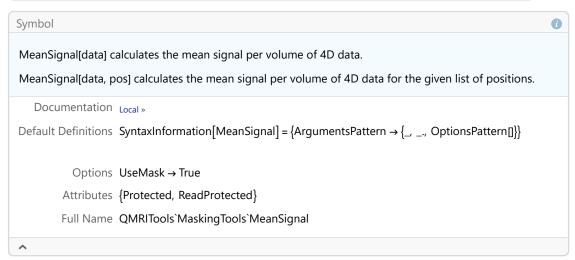
Functions

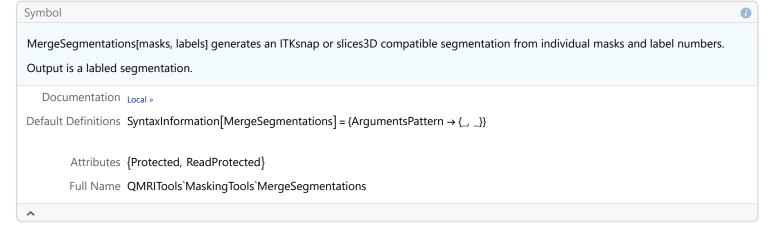


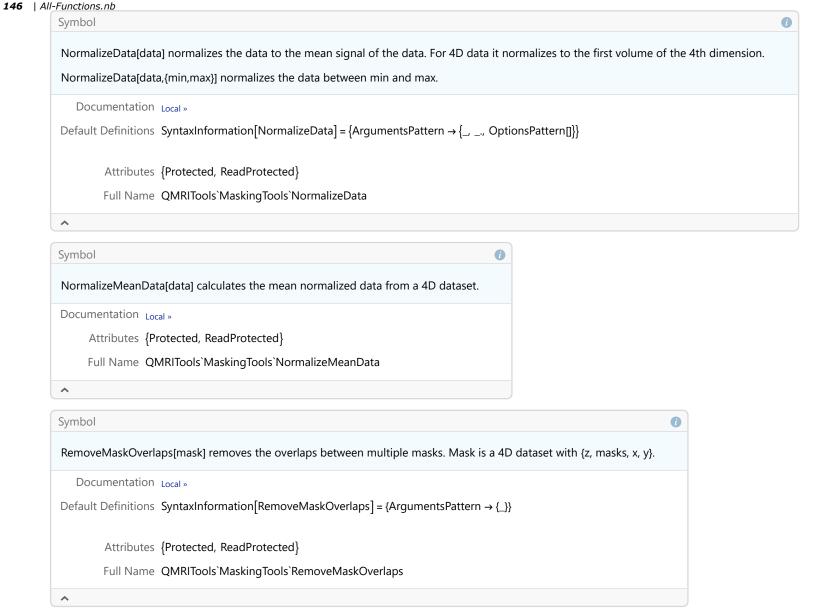


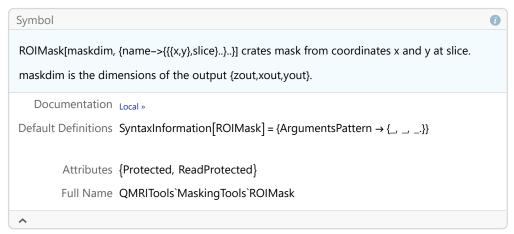
Full Name QMRITools`MaskingTools`HomoginizeData











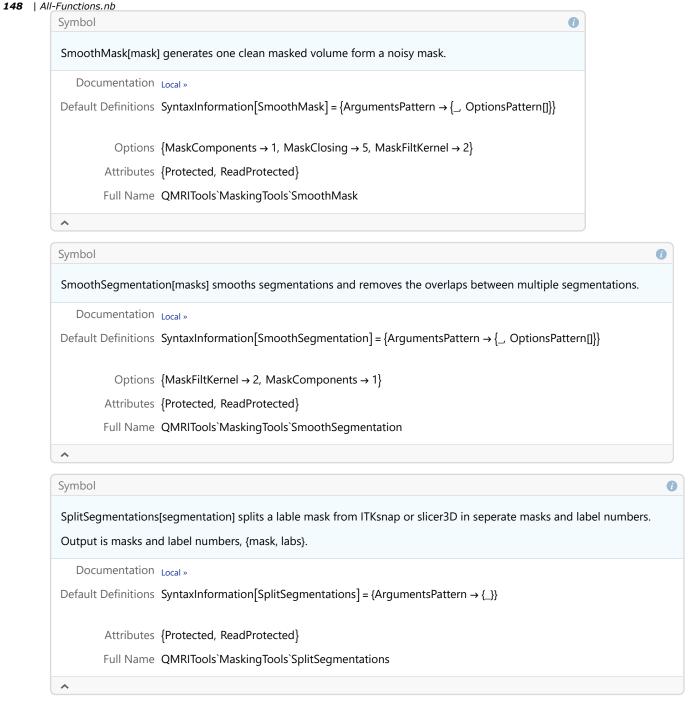
SegmentMask[mask, n] divides a mask in n segments along the slice direction, n must be an integer. The mask is divided in n equal parts where each parts has the same number of slices.

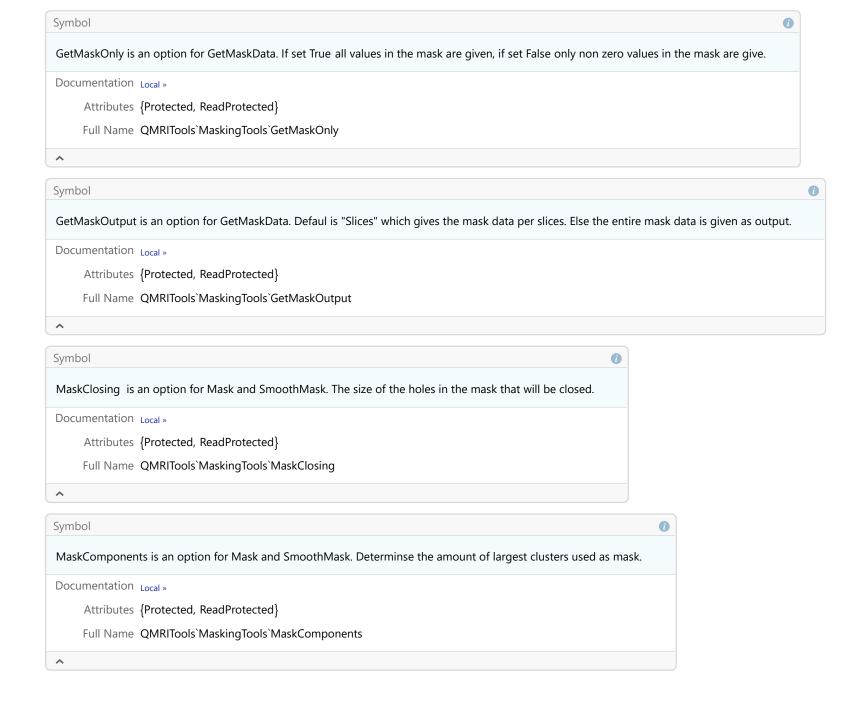
Documentation Local »

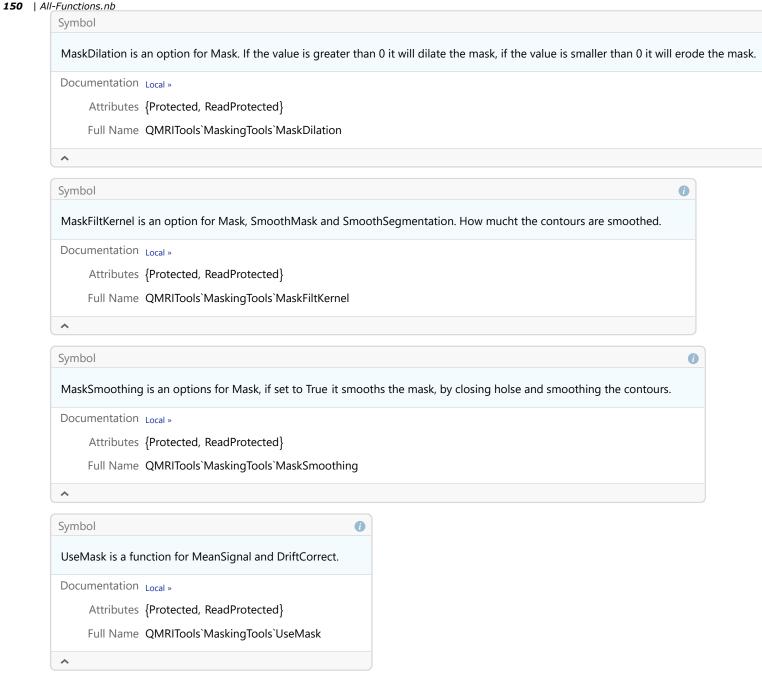
Default Definitions SyntaxInformation[SegmentMask] = {ArgumentsPattern → {_, _, _, _}}}

Attributes {Protected, ReadProtected}

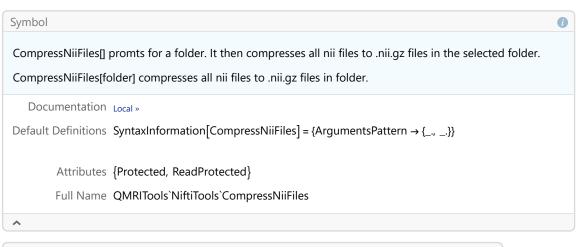
Full Name QMRITools`MaskingTools`SegmentMask

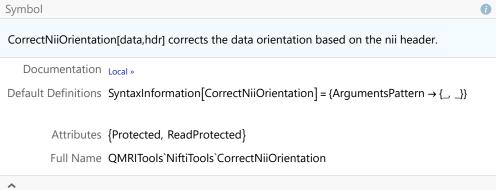


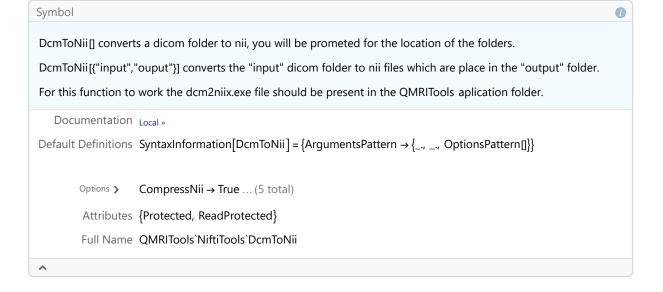


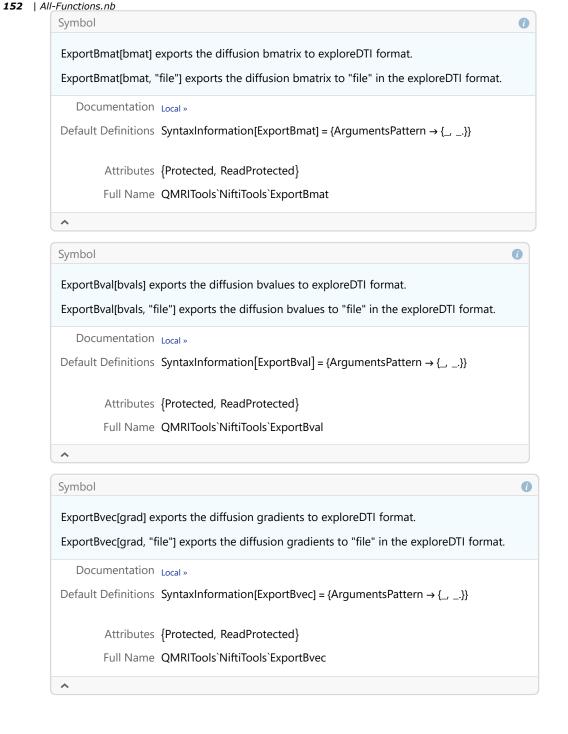


NiftiTools

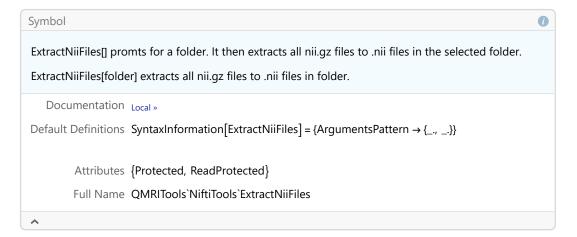


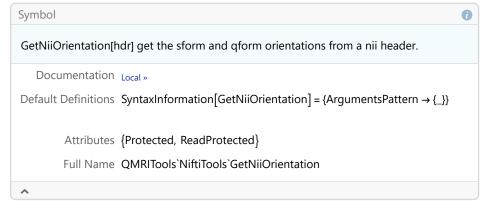


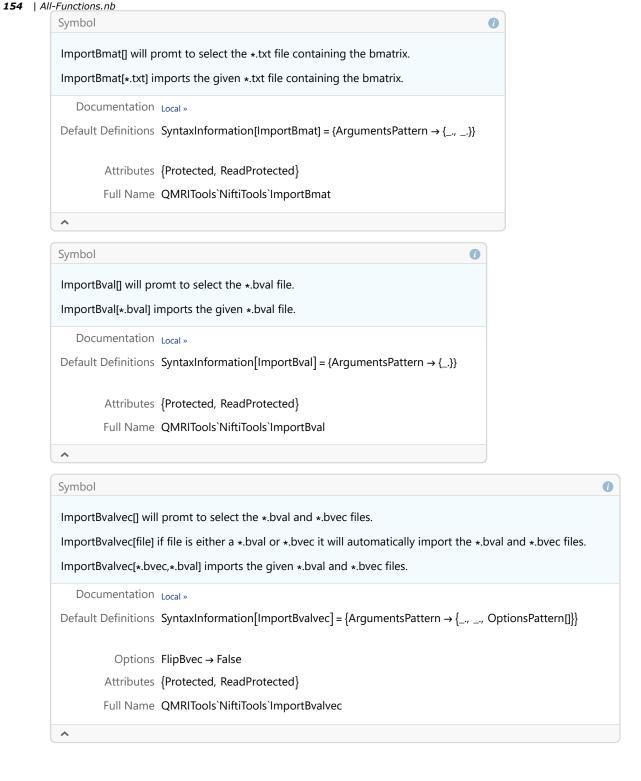




All-Functions.nb | 153







Full Name QMRITools`NiftiTools`ImportBvec

Full Name QMRITools`NiftiTools`ImportExploreDTItens

Attributes {Protected, ReadProtected}

ImportNii[] promts to select the nii file to import.

ImportNii["file"] imports the nii file.

Documentation Local »

ImportExploreDTItens["file"] imports the *.nii export for the tensor from explore DTI.

The default output is {data, vox}, however using NiiMethod various outputs can be given.

Default Definitions SyntaxInformation[ImportNii] = {ArgumentsPattern \rightarrow {__, OptionsPattern[]}}

The Nii import is also suported using the native Import function from Mathematica.

Options {NiiMethod → default, NiiScaling → False}

Attributes {Protected, ReadProtected}
Full Name QMRITools`NiftiTools`ImportNii

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 \wedge

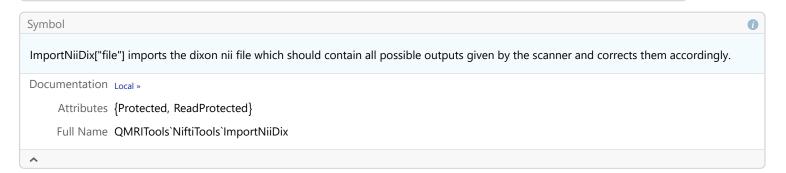
Symbol

Symbol

Documentation Local »

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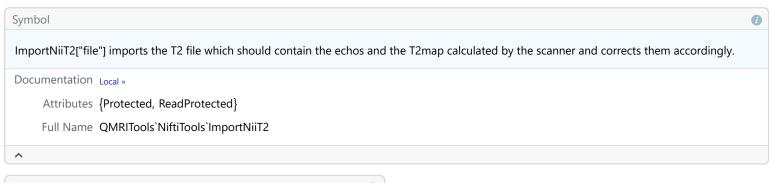


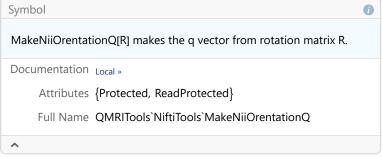
ImportNiiT1["file"] imports the T1 file which should contain the echos and the T1map calculated by the scanner and corrects them accordingly.

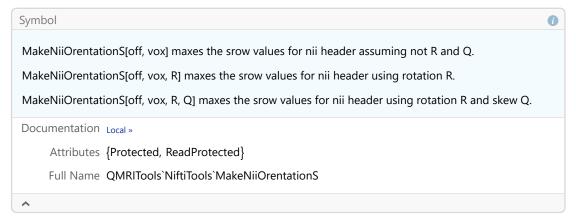
Documentation Local »

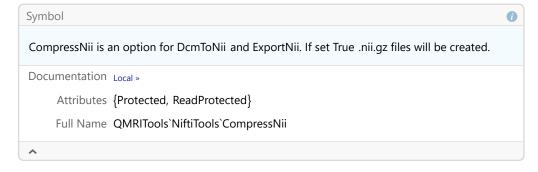
Attributes {Protected, ReadProtected}

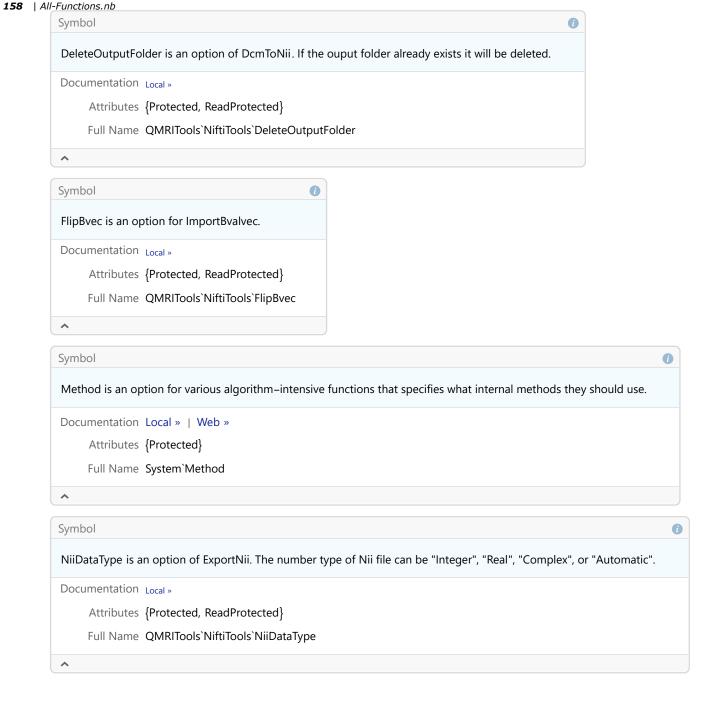
Full Name QMRITools`NiftiTools`ImportNiiT1

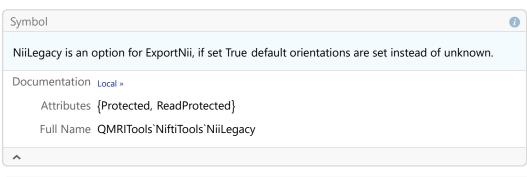


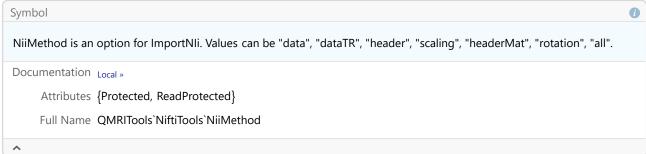




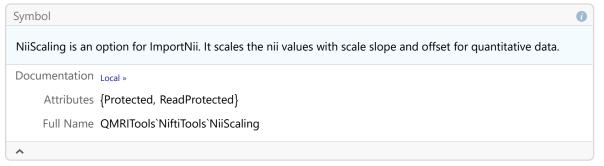


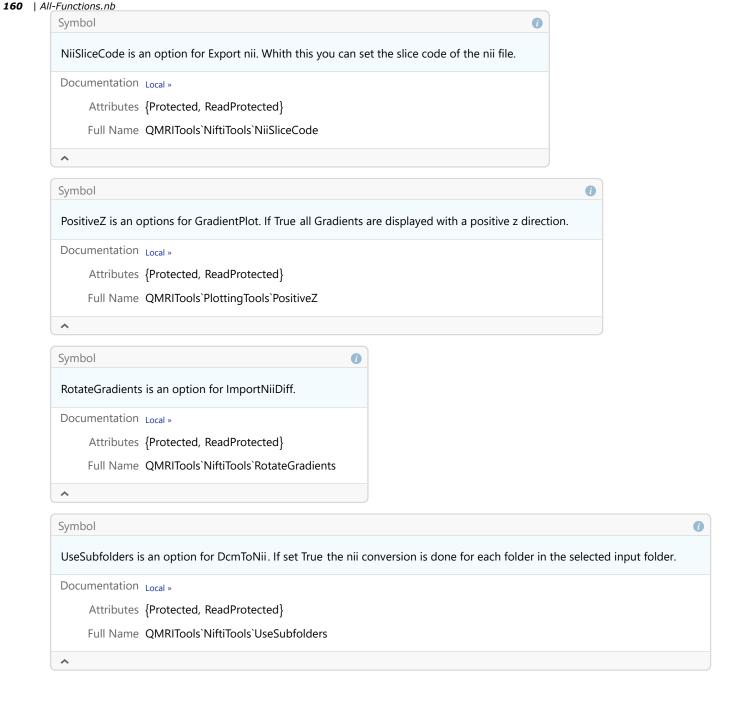












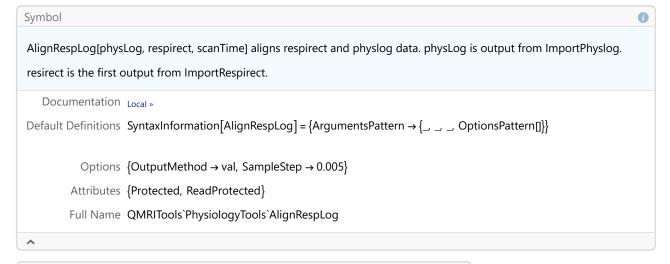
```
UseVersion is an option for DcmToNii. For windows it allows to switch between different versions of dcm2niix.exe.

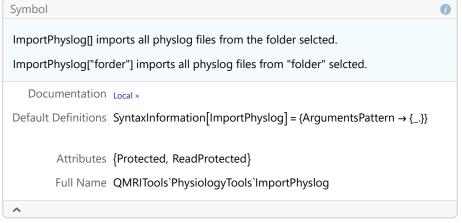
Documentation Local »

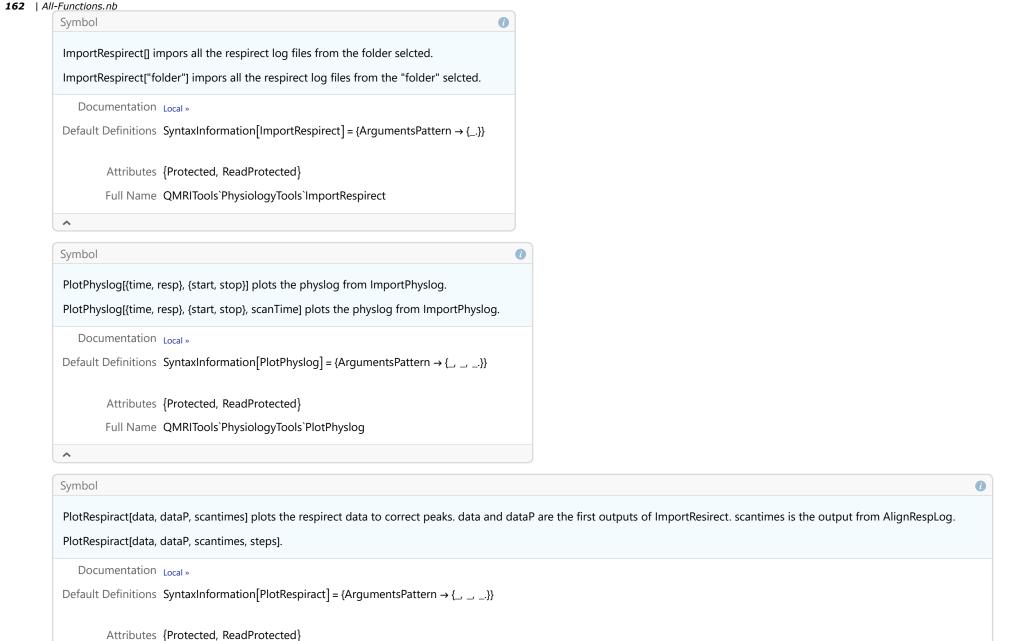
Attributes {Protected, ReadProtected}

Full Name QMRITools`NiftiTools`UseVersion
```

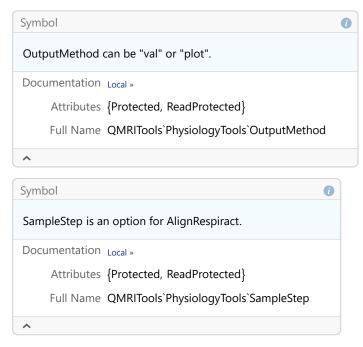
PhysiologyTools



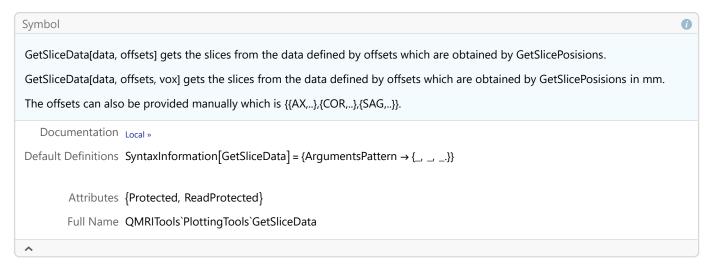


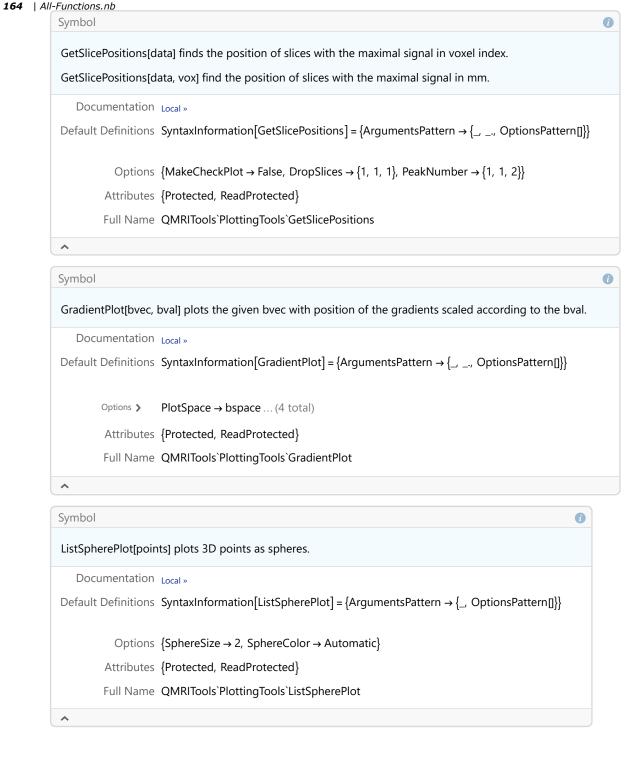


Full Name QMRITools`PhysiologyTools`PlotRespiract



PlottingTools





MakeSliceImages[imgData] generates images from the imgData which is obtained form GetSliceData.

MakeSliceImages[imgData, vox] generates images from the imgData which is obtained form GetSliceData, vox is used for the correct aspect ratio of the images.

MakeSliceImages[imgData, {labData, labels}] generates images from the imgData which is obtained

form GetSliceData with an overlay of the segmentations in labData, which can also be obtained using GetSliceData on the segmentations.

labels should be the label numbers used in the original segmentation (to allow correct scaling between slices).

MakeSliceImages[imgData, {labData, labels},vox] generates images from the imgData which is obtained form GetSliceData with an overlay

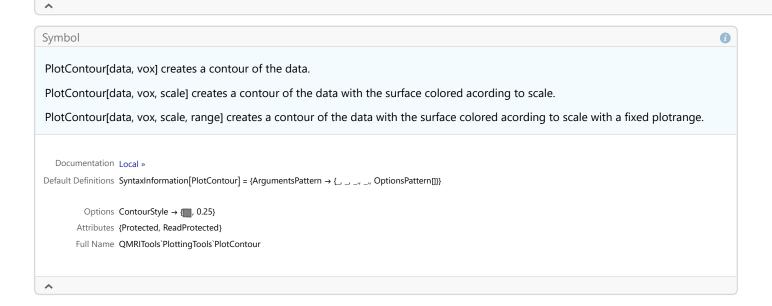
of the segmentations in labData, which can also be obtained using GetSliceData on the segmentations, vox is used for the correct aspect ratio of the images.

Documentation Local *

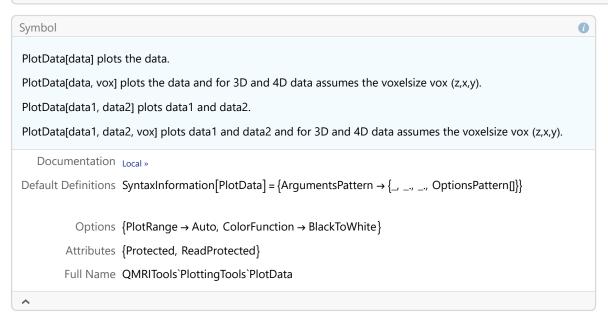
Default Definitions Syntaxinformation[MakeSliceImages] = (ArgumentsPattern → L. OptionsPattern[]))

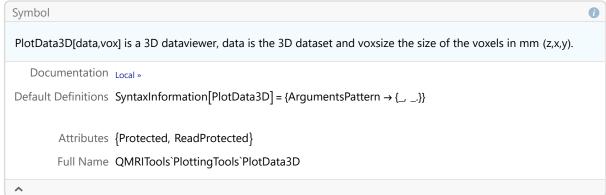
Attributes (Protected, ReadProtected)

Full Name QMRITools' PlottingTools 'MakeSliceImages



Symbol PlotCorrection[w] plots deformation vectors w {w1,w2..} generated by Registration2D and Registration3D for multiple datasets or registration steps. Documentation Local » Default Definitions SyntaxInformation[PlotCorrection] = $\{ArgumentsPattern \rightarrow \{_\}\}\$ Attributes {Protected, ReadProtected} Full Name QMRITools`PlottingTools`PlotCorrection ^



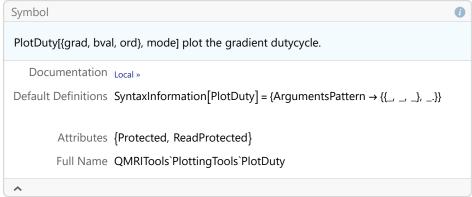


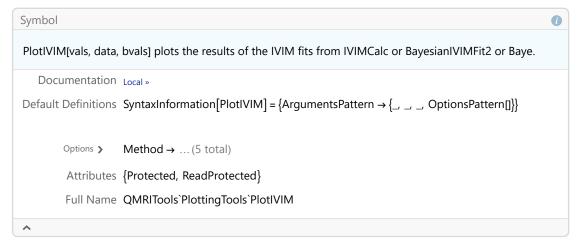
```
PlotDefGrid[data, phasemap, shiftpar] plots the dataset on the background with on top the non deformed and the deformed grid, or arrows or lines.

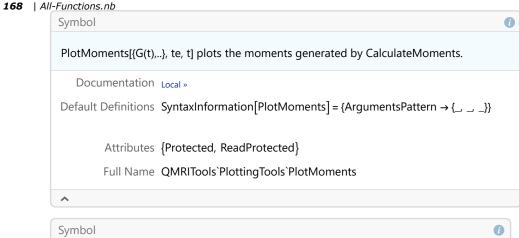
Documentation Local »

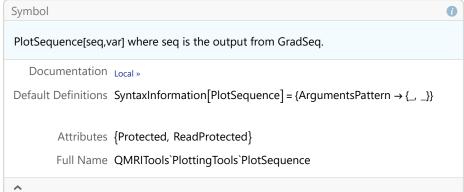
Attributes {Protected, ReadProtected}

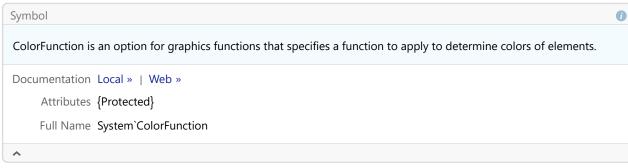
Full Name QMRITools`PlottingTools`PlotDefGrid
```

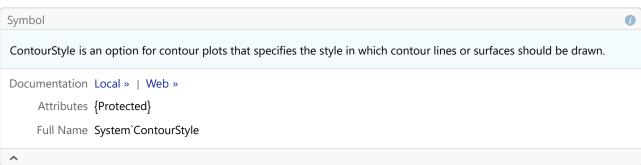


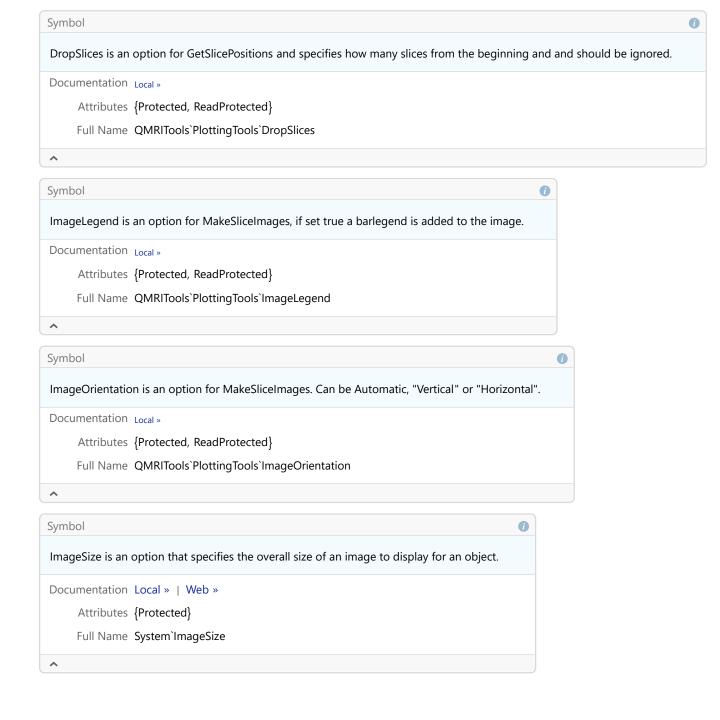


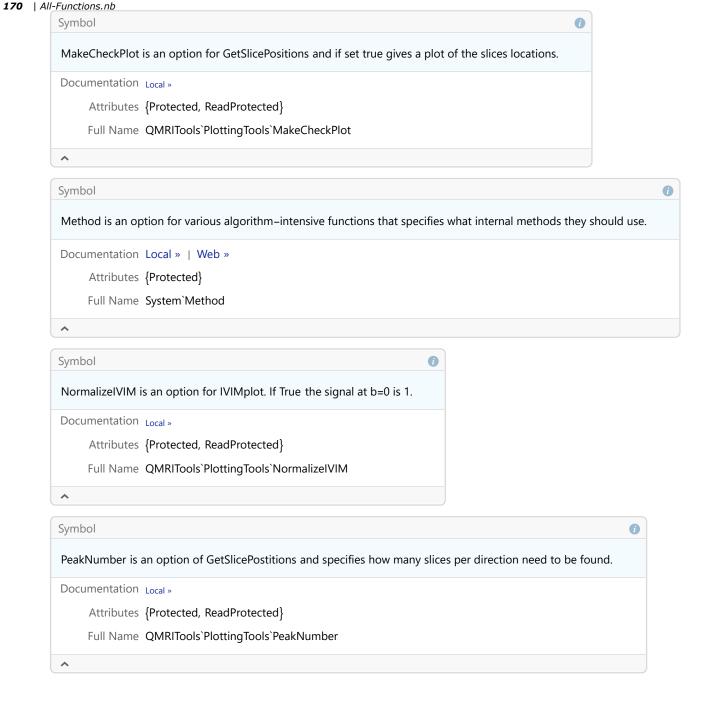


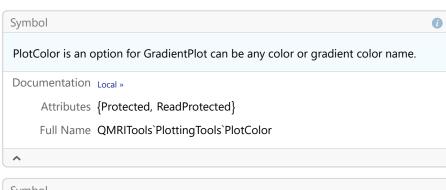


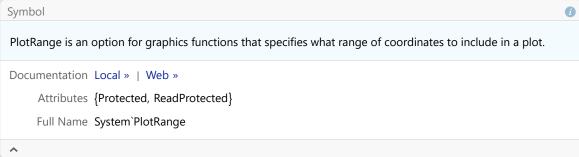




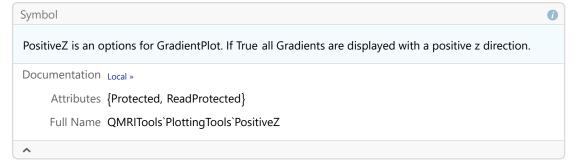


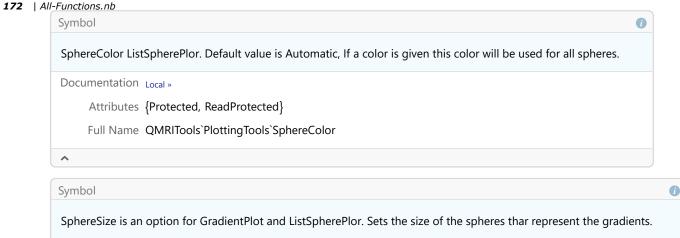










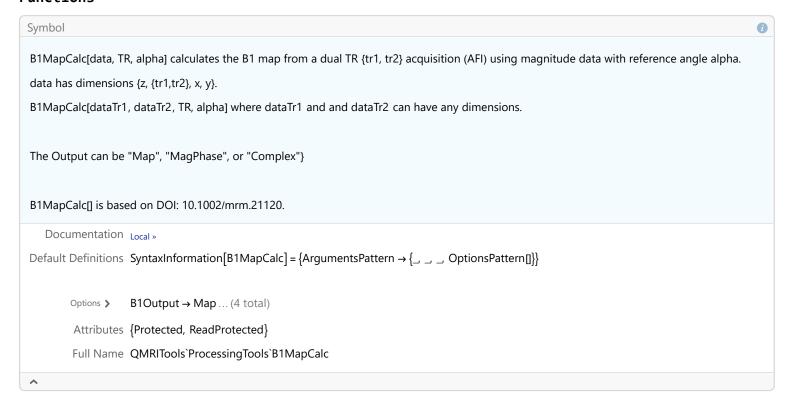


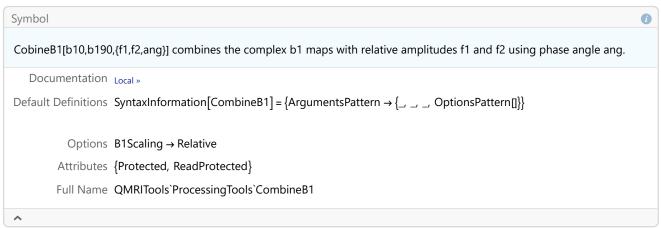
ProcessingTools

Attributes {Protected, ReadProtected}

Full Name QMRITools`PlottingTools`SphereSize

Documentation Local »





```
CorrectJoinSetMotion[[{dat1, dat2, ...}, vox, over] motion correts multiple sets with overlap. Over is the number of slices overlap between stes. A Translation registration is performed.

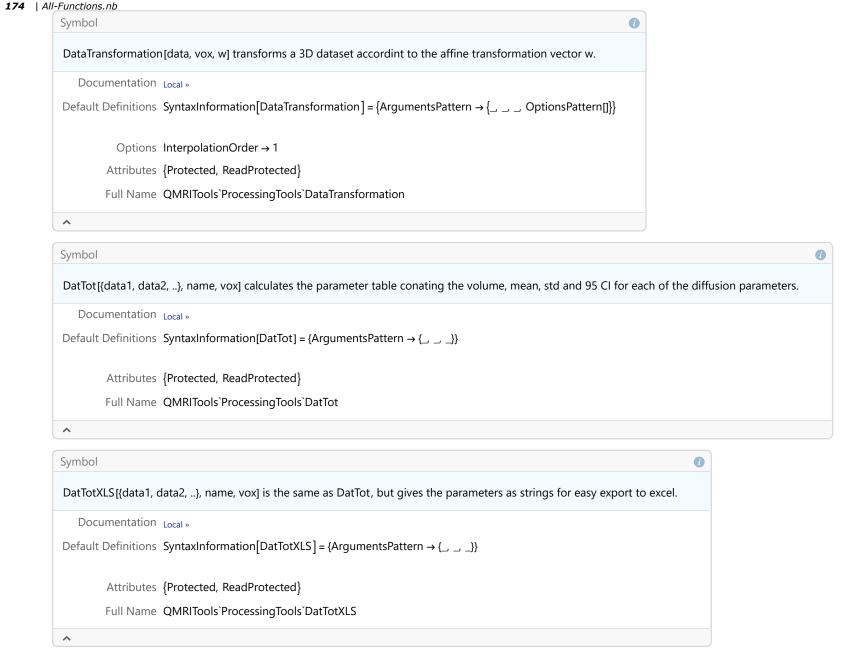
Documentation Local >

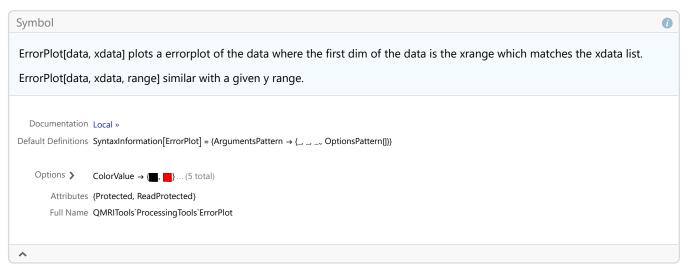
Default Definitions SyntaxInformation[CorrectJoinSetMotion] = {ArgumentsPattern → { _ _ _ _ _ OptionsPattern[]}}

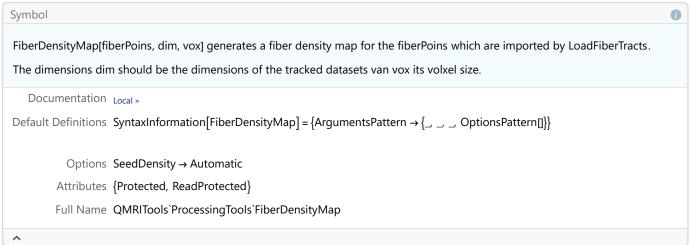
Options {JoinSetSplit → True, PaddOverlap → 2}

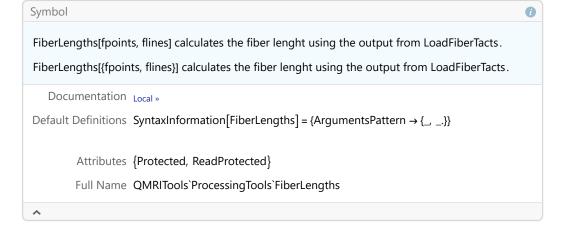
Attributes {Protected, ReadProtected}

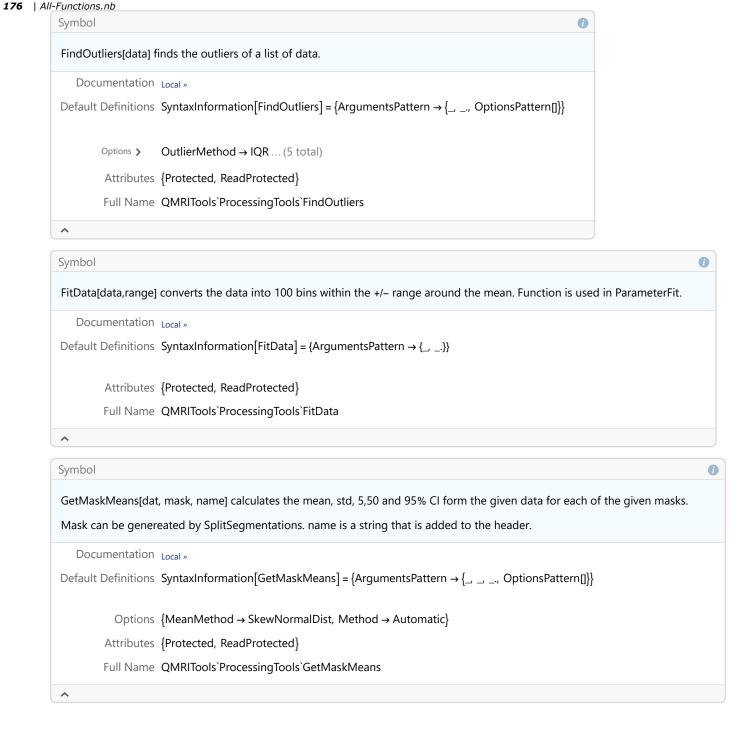
Full Name QMRITools'ProcessingTools'CorrectJoinSetMotion
```



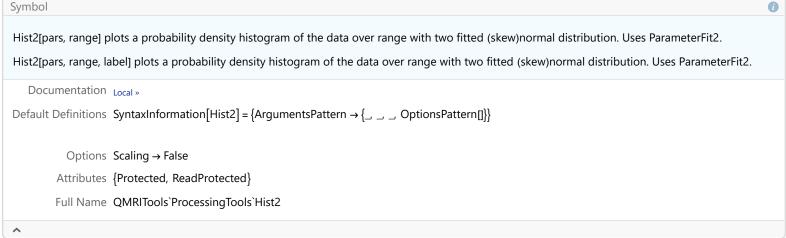




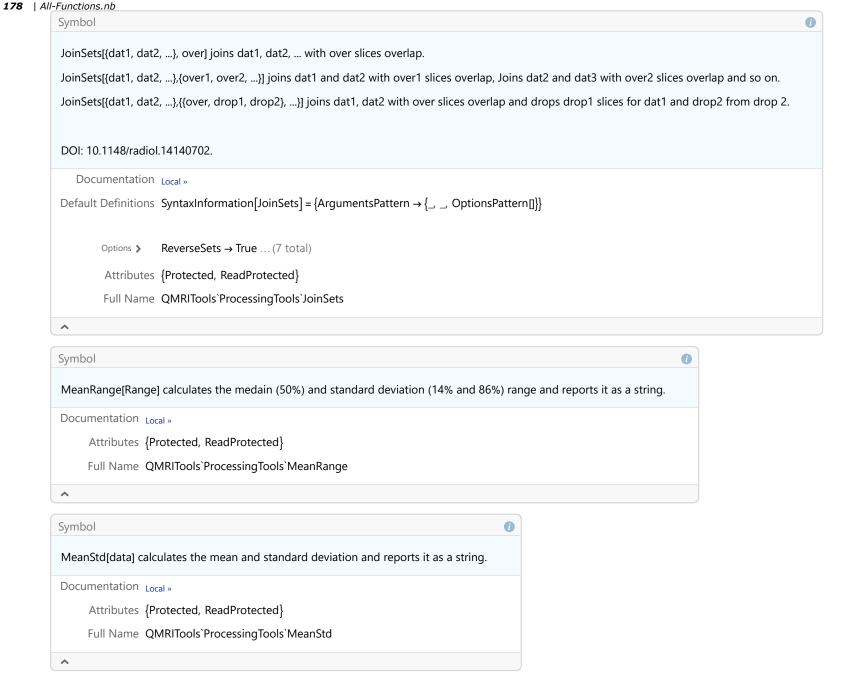


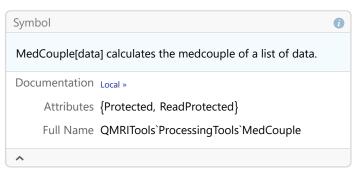


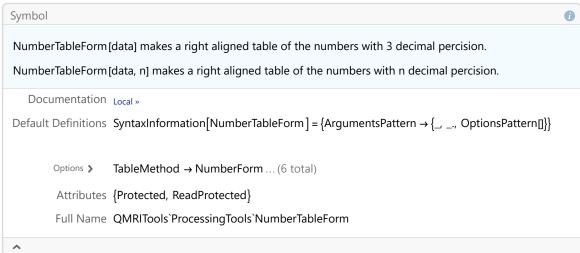
```
Symbol
Hist[data, range] plots a probability density histogram of the data from xmin to xmax with a fitted (skew)normal distribution. Uses ParameterFit.
Hist[data, range, label] plots a probability density histogram of the data from xmin to xmax with a fitted (skew)normal distribution and label as x-axis label.
Hist[{data1..., data2,...}, {range1, range2,...}] plots a probability density histogram of the data from xmin to xmax with a fitted (skew)normal distribution. Uses ParameterFit.
Hist[{data1, data2,...}, {range1, range2,...}, {label1, label2,...}] plots a probability density histogram of the data from xmin to xmax with a fitted (skew)normal distribution and label as x-axis label.
  Documentation Local »
Default Definitions SyntaxInformation[Hist] = {ArgumentsPattern → {_, _,, OptionsPattern[]}}
   Options >
                 ColorValue \rightarrow \{\{ \blacksquare, \, \bigcap \}, \, \blacksquare, \, \bigcap, \, \bigcap \} \dots (5 \text{ total})
       Attributes (Protected, ReadProtected)
       Full Name QMRITools`ProcessingTools`Hist
^
```

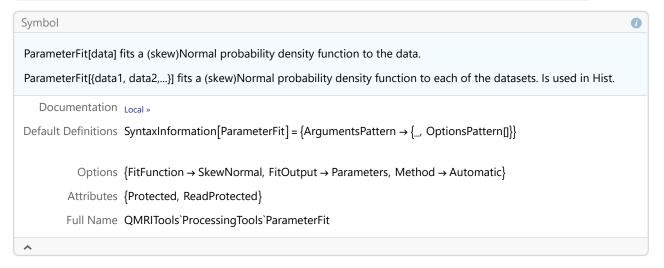


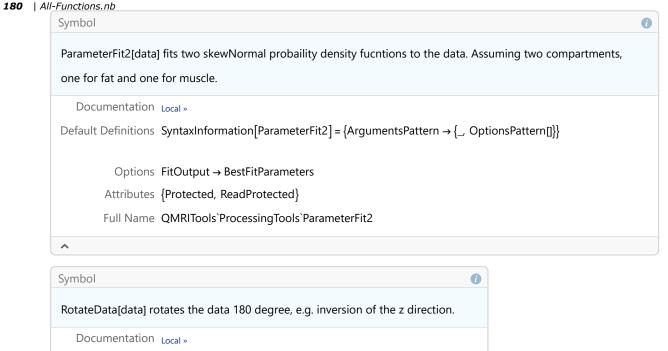
```
Symbol
InvertDataset[data] inverts the data along the x y and z axes. In other words it is rotated aroud the origin such that (x,y,z)=(-x,-y,-z) and (0,0,0)=(0,0,0).
Documentation Local »
      Attributes {Protected, ReadProtected}
     Full Name QMRITools`ProcessingTools`InvertDataset
\wedge
```

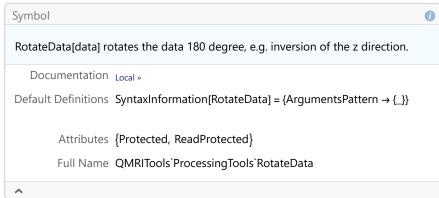


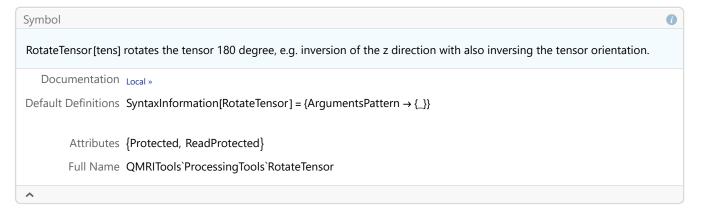












SetupDataStructure[dcmFolder] makes nii folders and generates nii files for a directory of dmc data where the data is structured per subject.

Documentation Local »

Attributes {Protected, ReadProtected}

Full Name QMRITools`ProcessingTools`SetupDataStructure

SmartMask[input] crates a smart mask of input, which is either the tensor or the tensor parameters calculated using ParameterCalc.

SmartMask[input, mask] crates a smart mask of input and used the mask as a prior selection of the input.

Documentation Local »

Default Definitions SyntaxInformation[SmartMask] = {ArgumentsPattern → {____, ___, OptionsPattern[]}}

Options ➤ Strictness → 0.5 ... (4 total)

Attributes {Protected, ReadProtected}

Full Name QMRITools`ProcessingTools`SmartMask

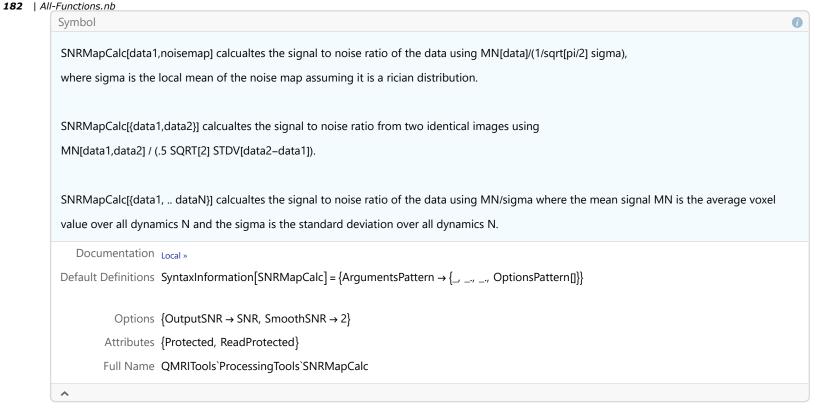
SNRCalc[data,masksig,masknoise] calculates the Signal to noise ratio of the signal selected by masksig and the noise selected by masknoise.

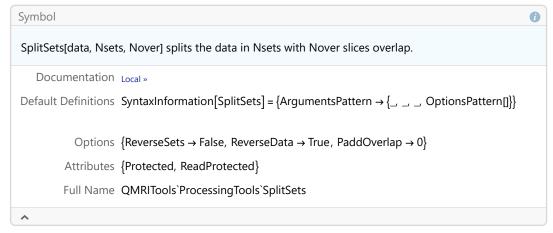
Documentation Local »

Default Definitions SyntaxInformation[SNRCalc] = {ArgumentsPattern → {_, _, _}}}

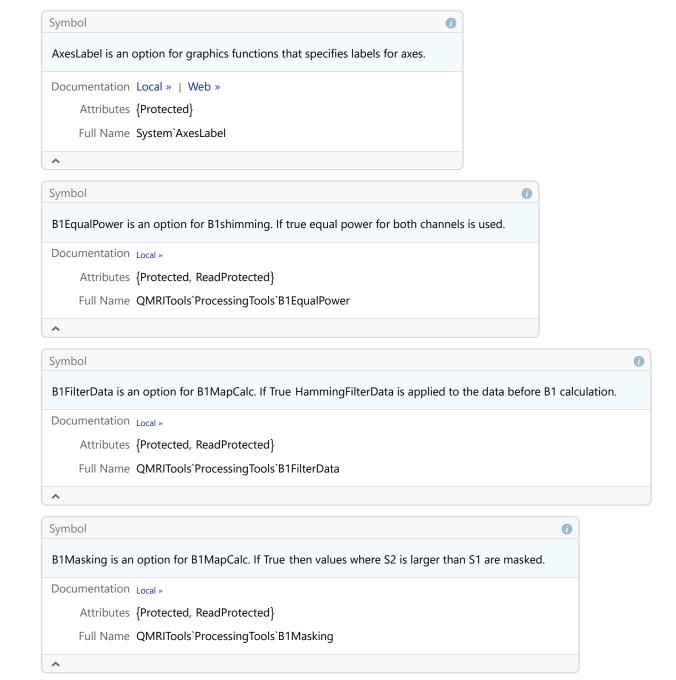
Attributes {Protected, ReadProtected}

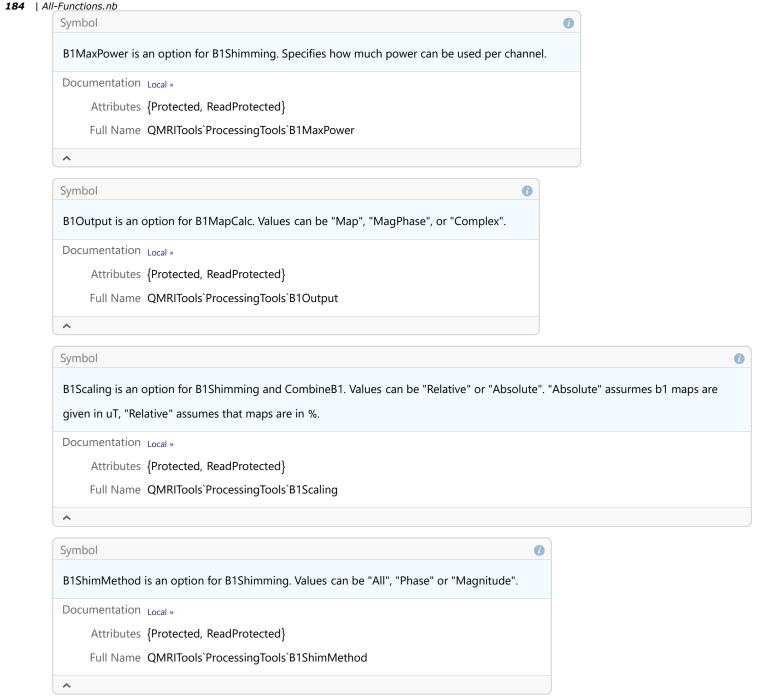
Full Name QMRITools`ProcessingTools`SNRCalc

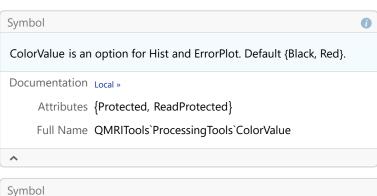


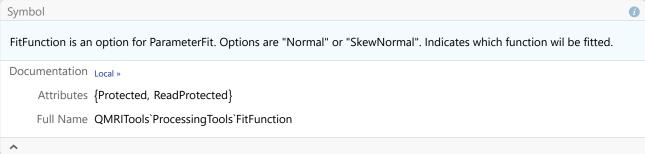


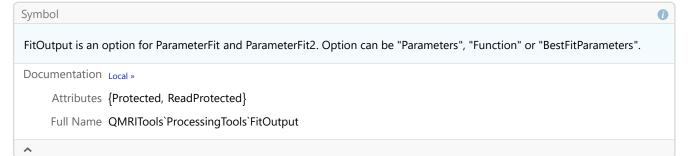
Options





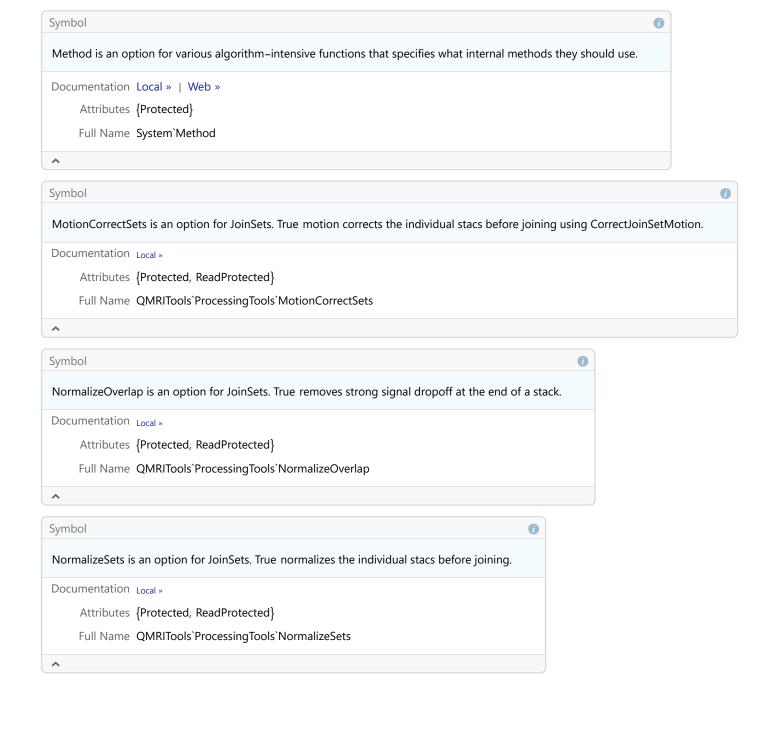


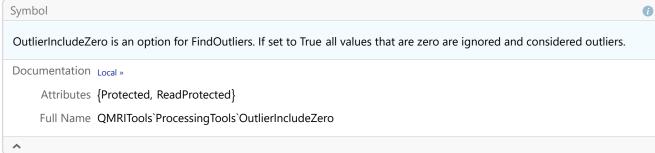


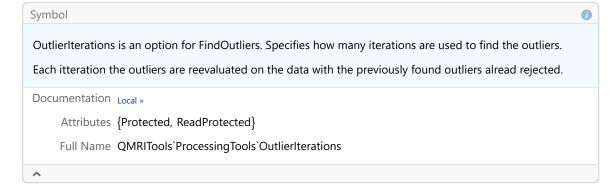


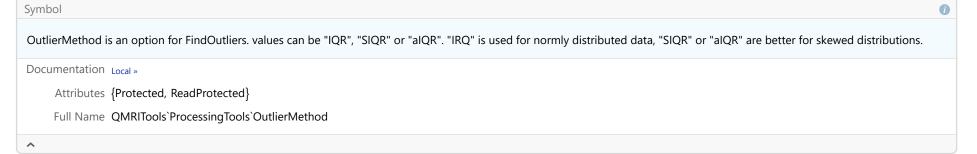


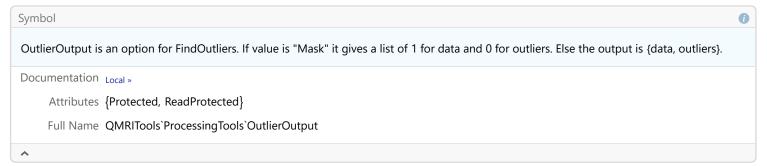
^

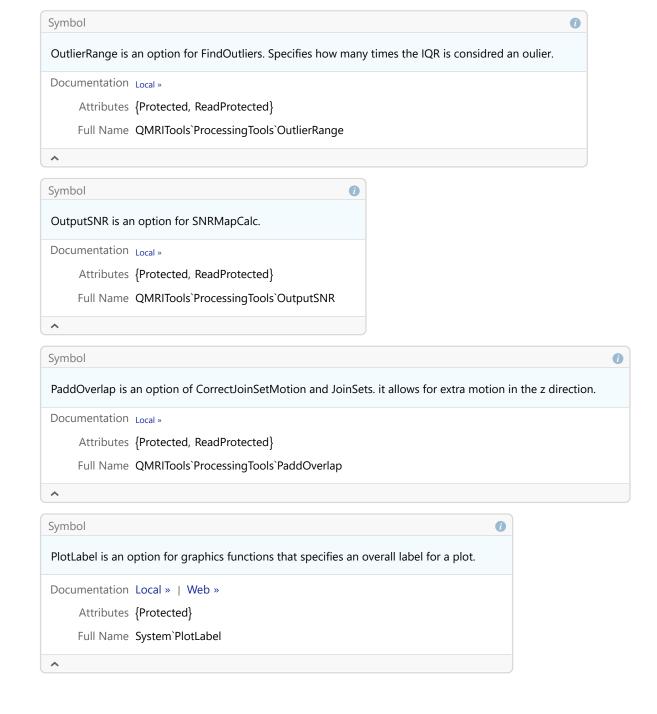


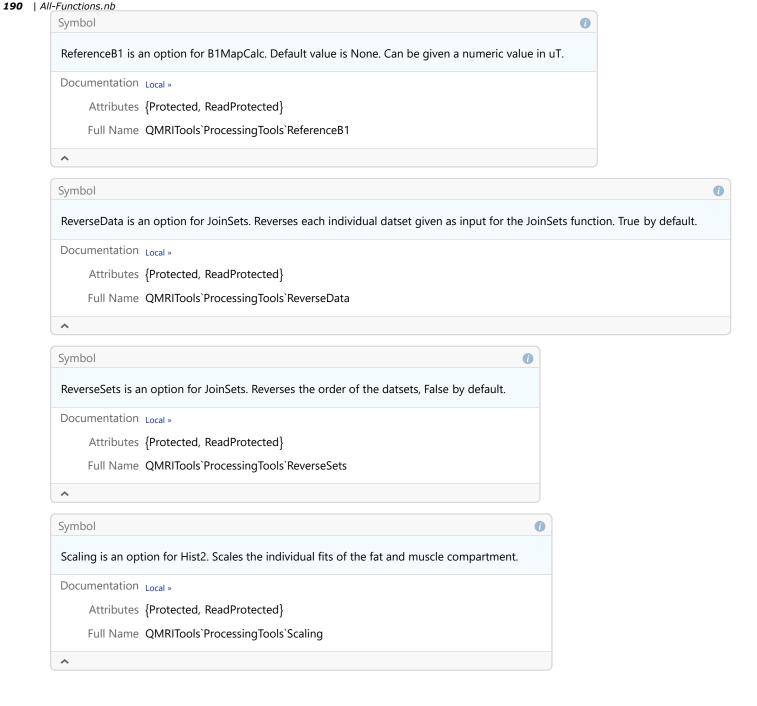


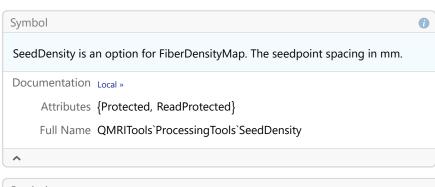


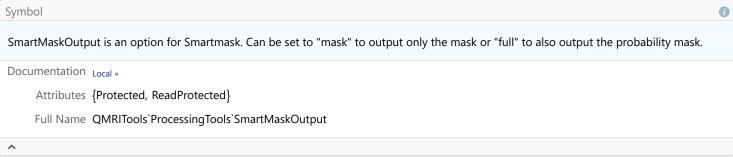


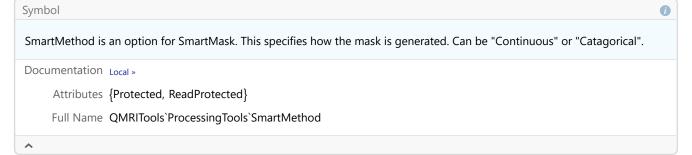




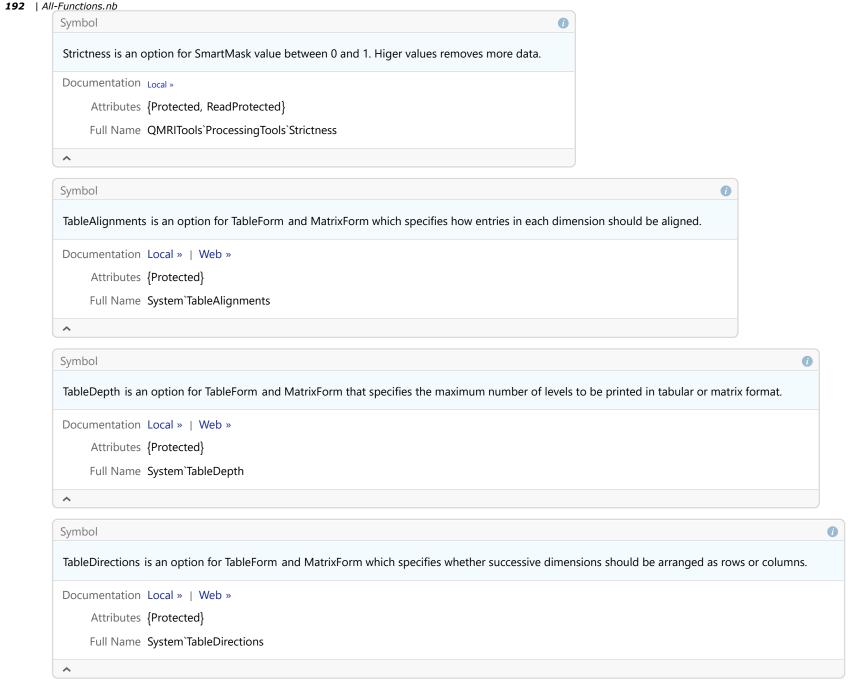


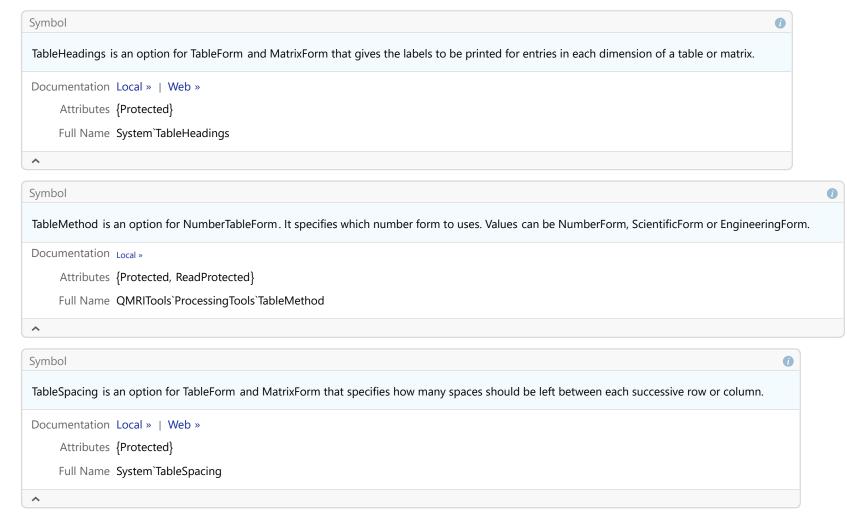












ReconstructionTools

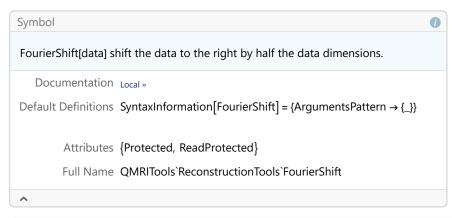
Functions

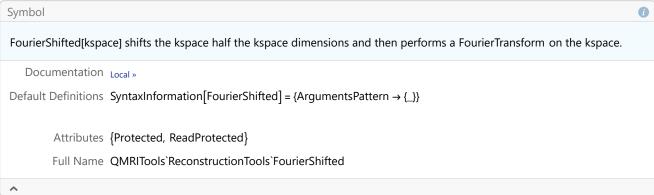
Full Name QMRITools'ReconstructionTools'CoilCombine ^

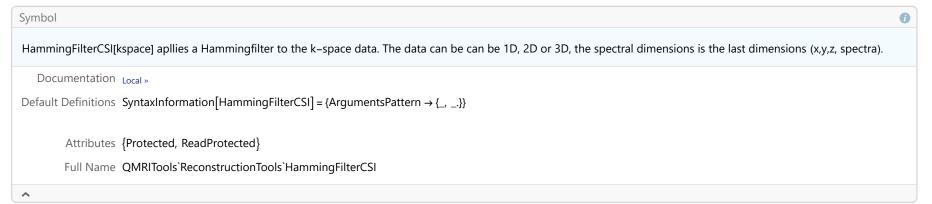
Symbol 0 CoilWeightedRecon[kspace, noise, head] performs reconstuction of raw MS2D MRI data. The input kspace, noise and head are obtained using ReadListData. The coil combination Methods can be "Roemer" or "RSS". Documentation Local » EchoShiftData $\rightarrow 0 \dots (6 \text{ total})$ Options > Attributes {Protected, ReadProtected} Full Name QMRITools`ReconstructionTools`CoilWeightedRecon \wedge

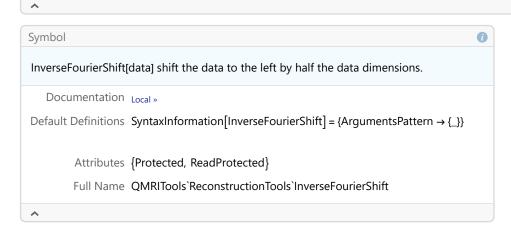
```
Symbol
CoilWeightedReconCSI[kspace, noise, head] performs reconstuction of raw 3DCSI data. The input kspace, noise and head are obtained using ReadListData.
The coil combination Methods can be "Roemer" or "WSVD".
Documentation Local »
                 HammingFilter → False ... (5 total)
     Options >
     Attributes {Protected, ReadProtected}
     Full Name QMRITools`ReconstructionTools`CoilWeightedReconCSI
Symbol
                                                                                                                                               0
DeconvolveCSIdata[spectra] deconvolves the CSI spectra after HammingFilterCSI to revert the blurring of the hammingfiltering.
DeconvolveCSIdata[spectra, ham] deconvolves the CSI spectra with the acquired weighting ham to revert the blurring of the kspace weighting.
   Documentation Local »
Default Definitions SyntaxInformation[DeconvolveCSIdata] = \{ArgumentsPattern \rightarrow \{\_, \_, OptionsPattern[]\}\}
          Options {WienerRegularization → 0.007, DeconvolutionMethod → Wiener}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'ReconstructionTools'DeconvolveCSIdata
\wedge
                                                                                                                                         0
Symbol
FourierKspace2D[kspace,head] performs a 2D reconstruction of 2D kspace data. Where kspace and head are generated by ReadListData.
   Documentation Local »
Default Definitions SyntaxInformation[FourierKspace2D] = {ArgumentsPattern \rightarrow {__ ___.}}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`ReconstructionTools`FourierKspace2D
^
```

Full Name QMRITools'ReconstructionTools'FourierRescaleData









Full Name QMRITools`ReconstructionTools`HammingFilterData

InverseFourierShifted[data] performs a InverseFourierTransform on the data and then shifts the kspace half the kspace dimensions.

Documentation Local »

Default Definitions SyntaxInformation[InverseFourierShifted] = {ArgumentsPattern → {_}}}

Attributes {Protected, ReadProtected}

Full Name QMRITools`ReconstructionTools`InverseFourierShifted

```
MakeHammingFilter[xdim] makes a 1D HammingKernel for filtering k-space.

MakeHammingFilter[xdim] makes a 1D HammingKernel for filtering k-space.

MakeHammingFilter[xdim, ydim] makes a 2D HammingKernel for filtering k-space in 2D CSI data of size {xdim, ydim}.

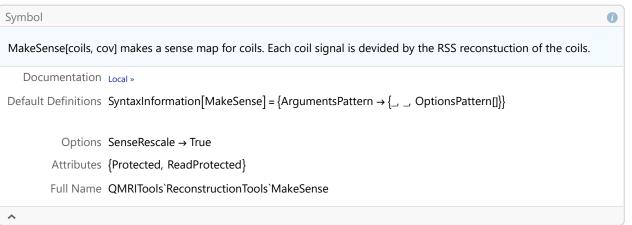
MakeHammingFilter[xdim, ydim, zdim}] makes a 3D HammingKernel for filtering k-space in 3D CSI data of size {xdim, ydim, zdim}.

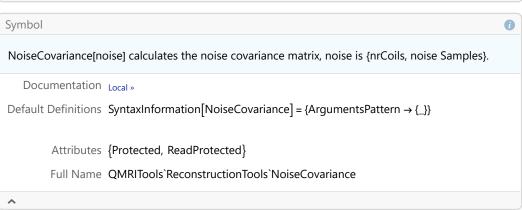
Documentation Local >

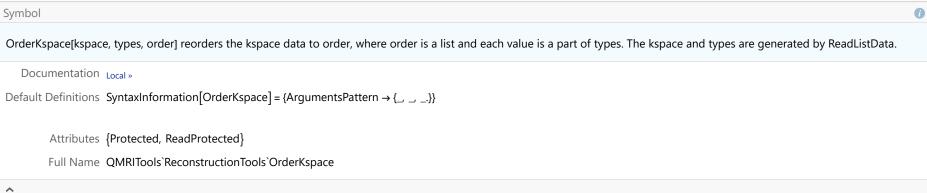
Default Definitions SyntaxInformation[MakeHammingFilter] = {ArgumentsPattern → {_}}}

Attributes {Protected, ReadProtected}

Full Name QMRITools'ReconstructionTools'MakeHammingFilter
```







ReadListData[file] reads a list/data raw data file from the philips MR platform. The input file can either be .list or .data file.

Ouput is {{rawData, noise}, {head, types}}.

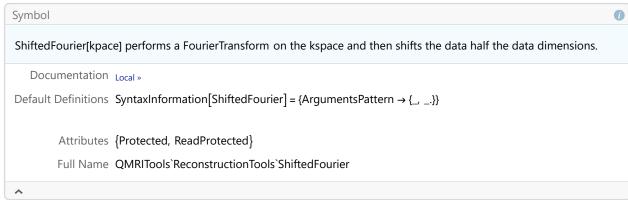
ReadListData[file, print] does the same but if print is set False no reporting is done.

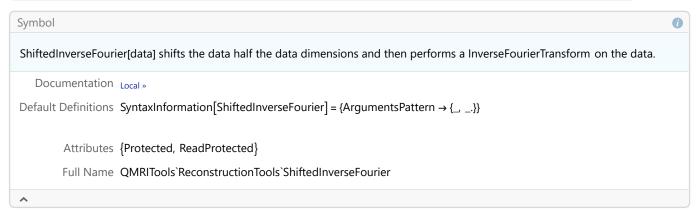
Documentation Local »

Default Definitions SyntaxInformation[ReadListData] = {ArgumentsPattern → {____}}}

Attributes {Protected, ReadProtected}

Full Name QMRITools'ReconstructionTools'ReadListData





```
TotalType [kspace, types, type] calcualtes the Total of the kspace data on type, where type is part of types. The kspace and types are generated by ReadListData.

TotalType [kspace, types], type] calcualtes the Total of the kspace data on type, where type is part of types.

TotalType [kspace, types, {type,...}] calcualtes the Total of the kspace data on each of the list type, where type is part of types.

Output is {kspace, types}.

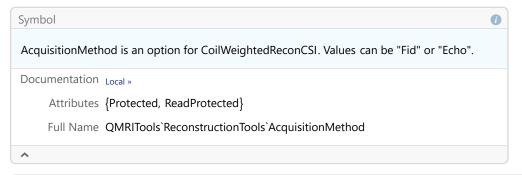
Documentation Local >>

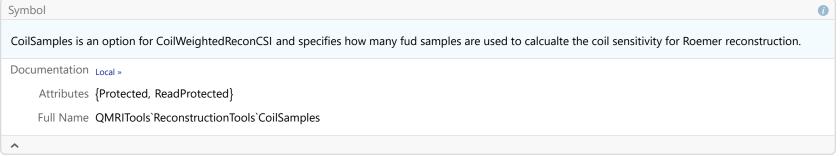
Default Definitions SyntaxInformation[TotalType] = {ArgumentsPattern → {_, _, __...}}}

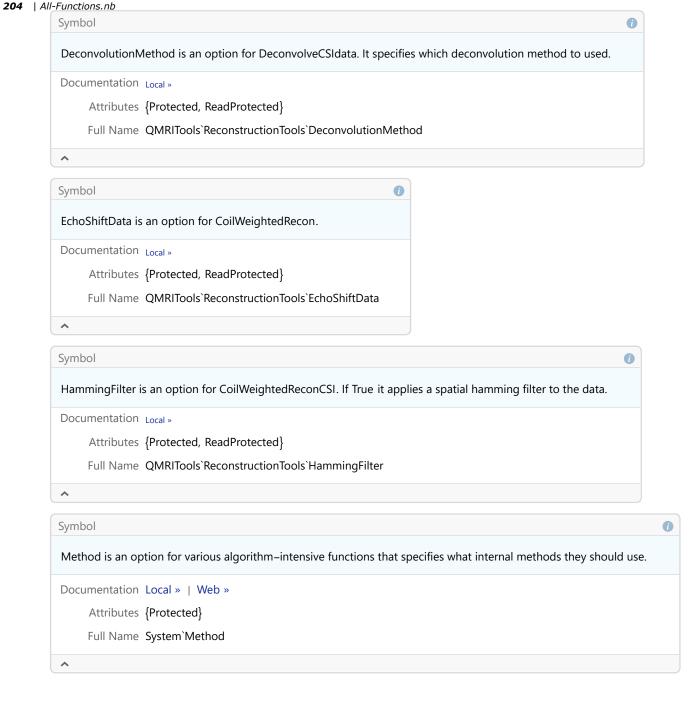
Attributes {Protected, ReadProtected}

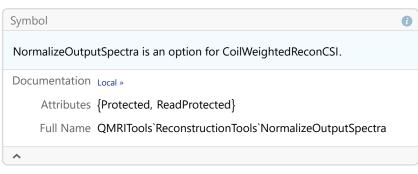
Full Name QMRITools'ReconstructionTools'TotalType
```

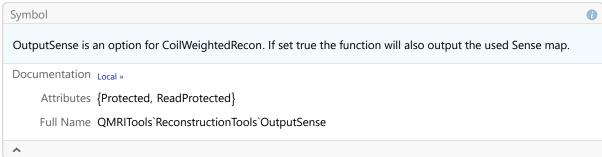
Options







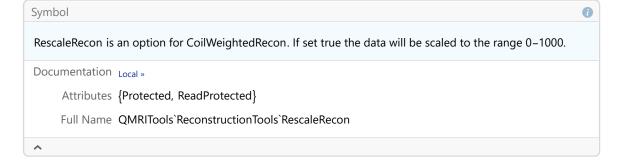




Symbol

QMRITools`ReconstructionTools`Private`ReconFilter

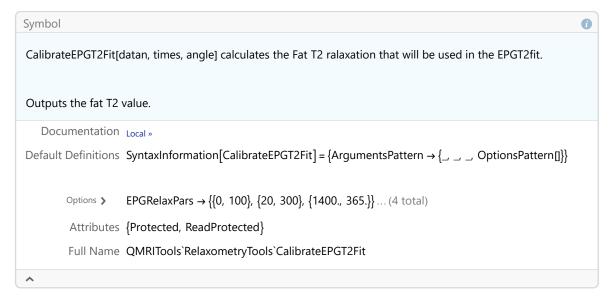
Full Name QMRITools`ReconstructionTools`Private`ReconFilter





RelaxometryTools

Functions



```
CreateT2Dictionary[{T1m, T1f}, {Necho, detlaTE}, angle] Creates a EPG signal dictionary used for EPGT2fit.

Every dictionary that is defined is cached.

The output is in units as defined by the detlaTE, e.g. if detlaTE is in ms the output is in ms.

The TR and TE should be in the same units as Dela.

Output is {dictionary, vals}.

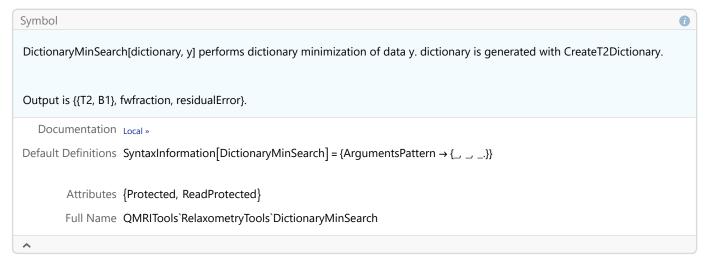
Documentation Local >>

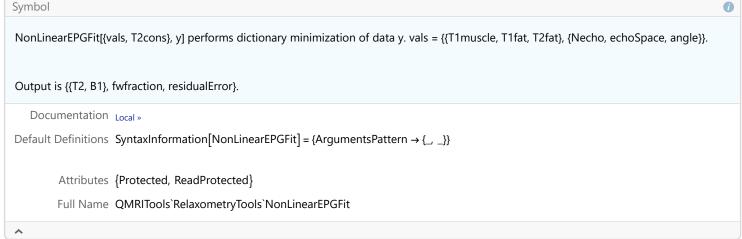
Default Definitions SyntaxInformation[CreateT2Dictionary] = {ArgumentsPattern → {___, __, __, OptionsPattern[]}}

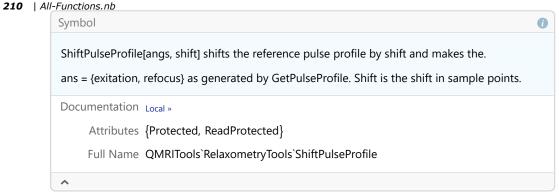
Options > DictB1Range → {0.5, 1.4, 0.01}... (5 total)

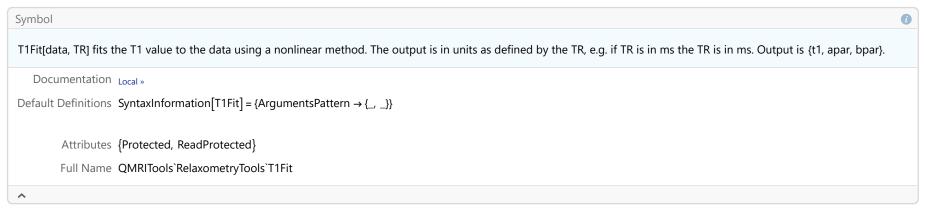
Attributes {Protected, ReadProtected}

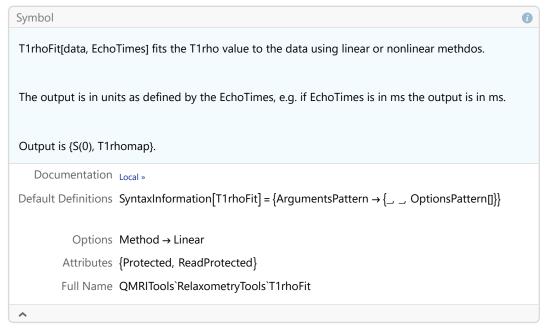
Full Name QMRITools`RelaxometryTools`CreateT2Dictionary
```

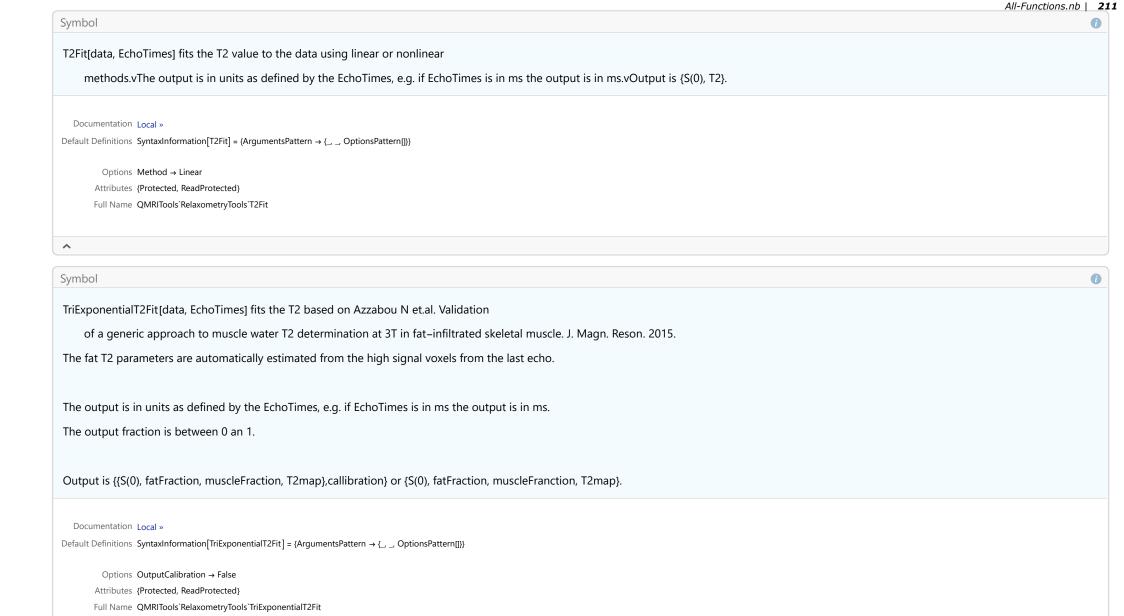




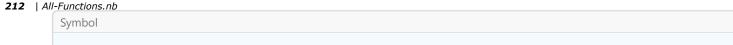




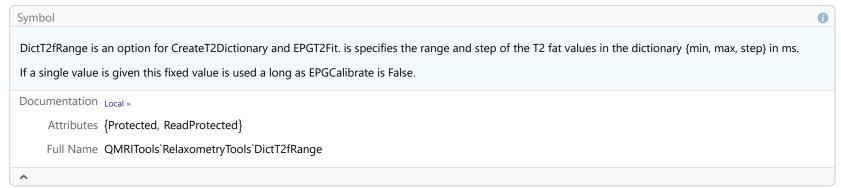




Options

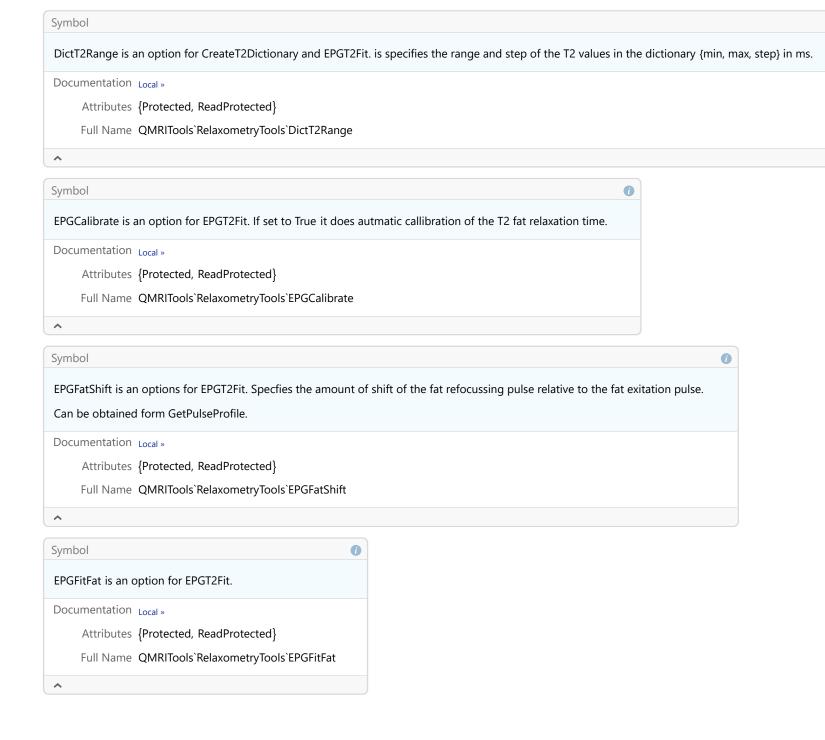


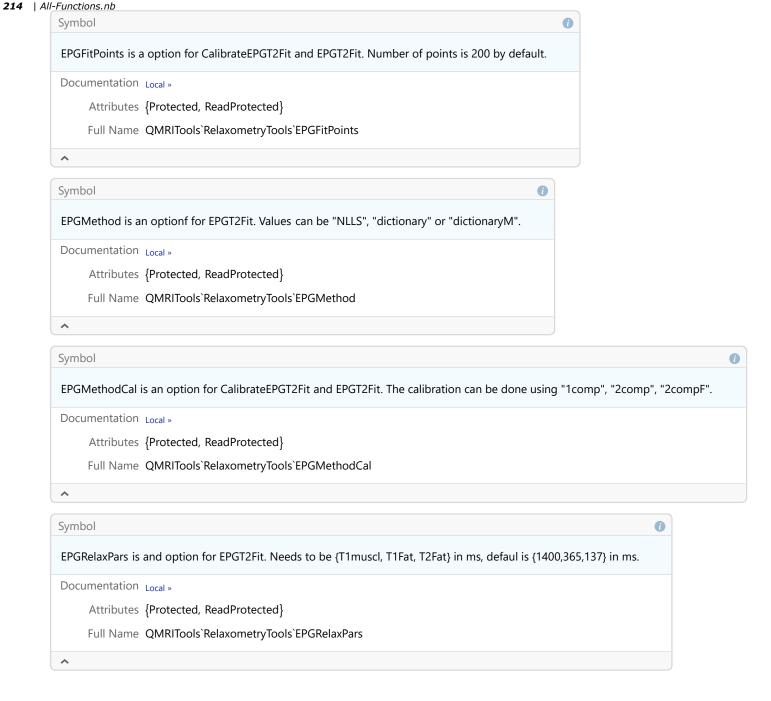
DictB1Range is an option for CreateT2Dictionary and EPGT2Fit. It specifies the range and step of the B1 values in the dictionary {min, max, step}. Documentation Local » Attributes {Protected, ReadProtected} Full Name QMRITools`RelaxometryTools`DictB1Range ^

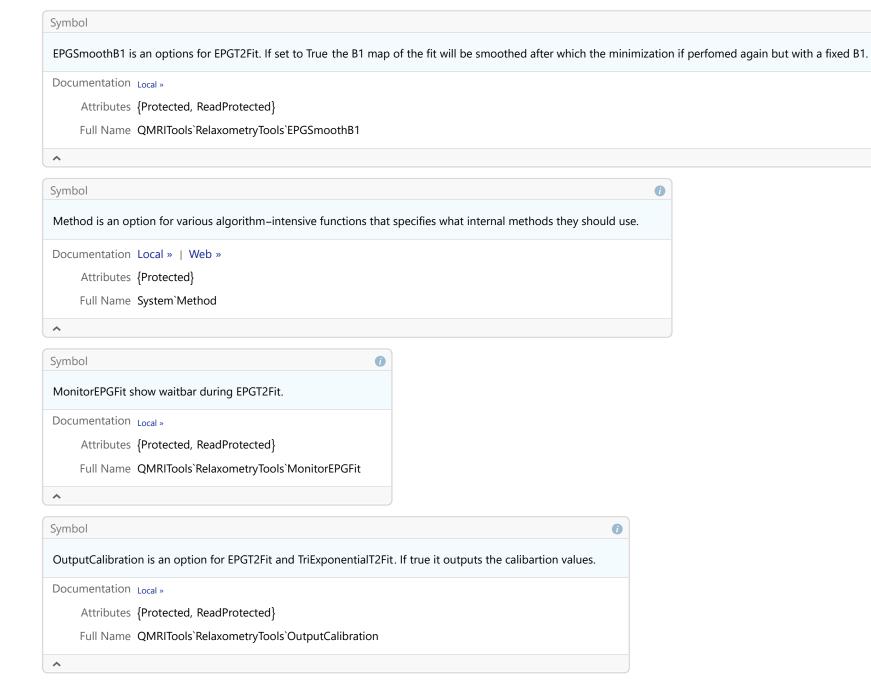












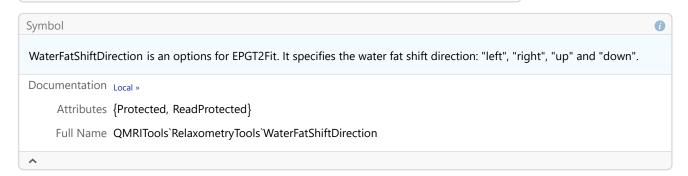


WaterFatShift is an options for EPGT2Fit. It specifies the amount of water fat shift in voxels.

Documentation Local »

Attributes {Protected, ReadProtected}

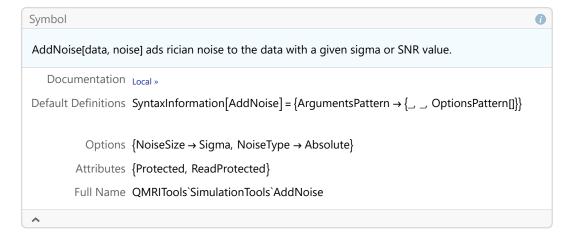
Full Name QMRITools`RelaxometryTools`WaterFatShift

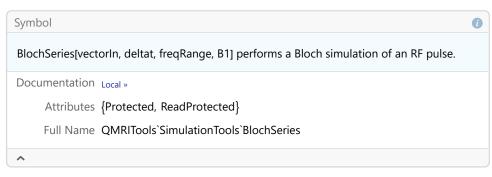


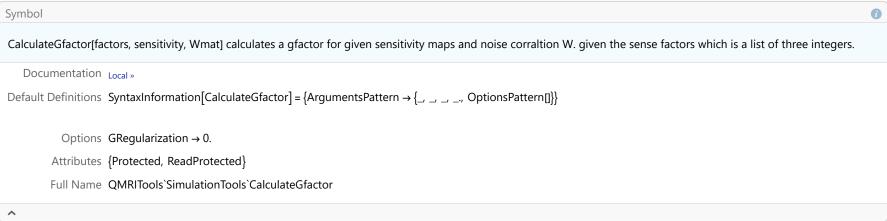
SimulationTools

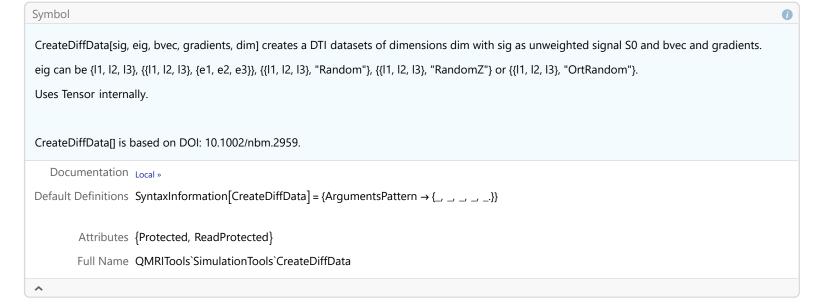
Functions

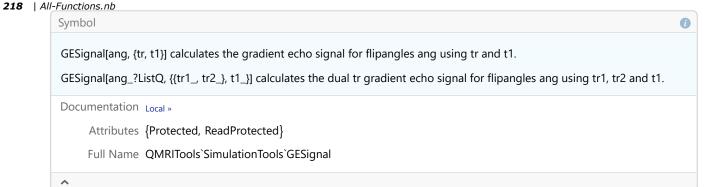
^

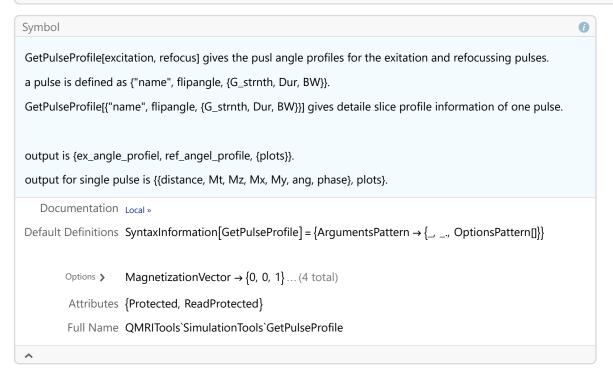


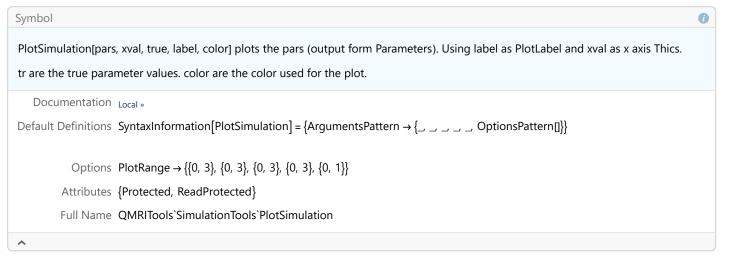












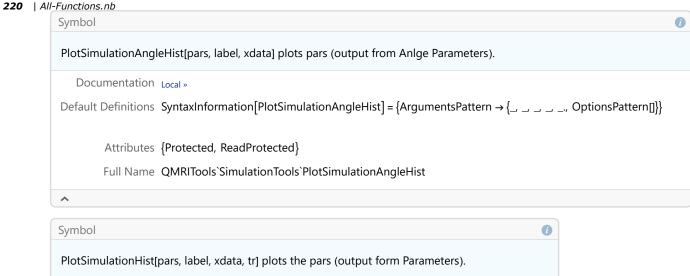
```
PlotSimulationAngle[par, xdata, label, col] plots pars (output from Anlge Parameters).

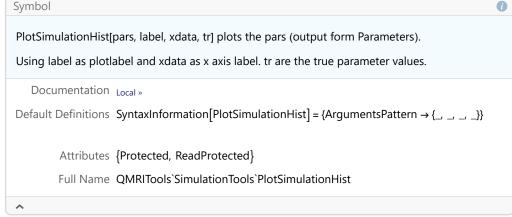
Documentation Local »

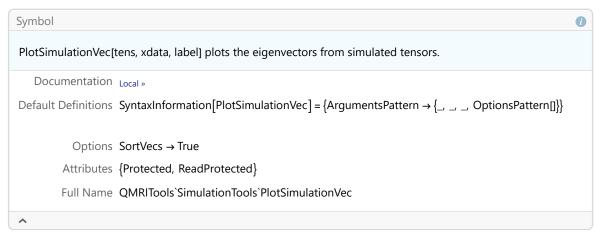
Options PlotRange → {0, 90}

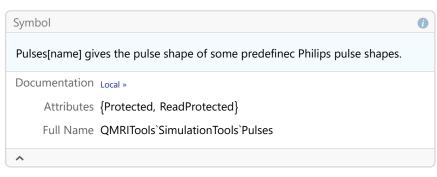
Attributes {Protected, ReadProtected}

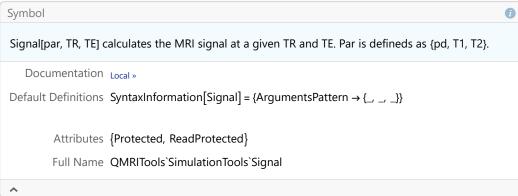
Full Name QMRITools`SimulationTools`PlotSimulationAngle
```

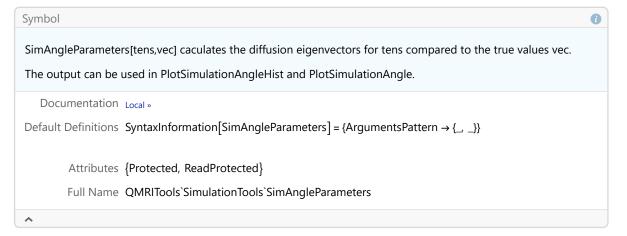


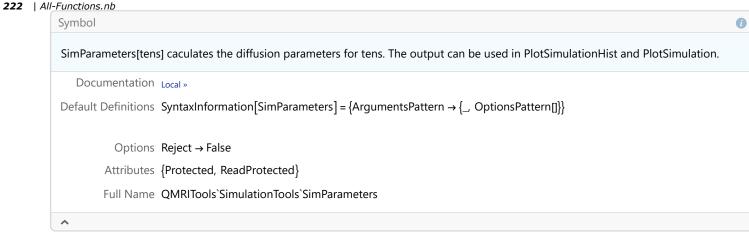




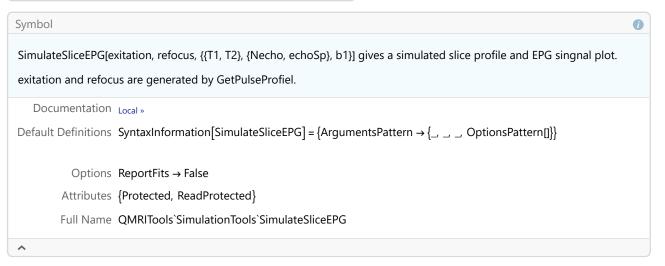












```
Tensor{{11, 12, 13}} creates a diffuison tensor with vectors {{0,0,1},{0,1,0,}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, {e1, e2, e3}} creates a diffuison tensor with vectors {e1, e2, e3} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "Random"} creates a diffuison tensor with random orthogonal eigenvectors {e1, e2, e2} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "RandomZ"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0}, e2, e3} with random eigenvectors and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {11, 12, 13}.

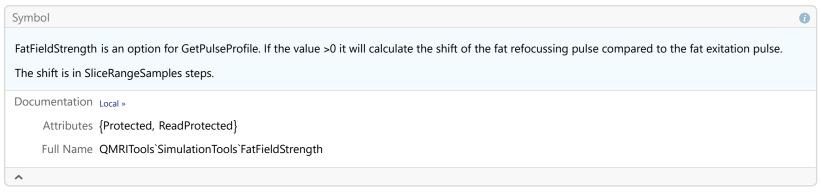
Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {{11, 12, 13}}.

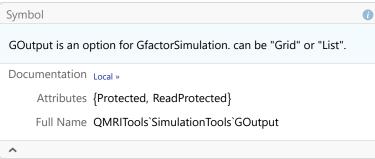
Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {{11, 12, 13}}.

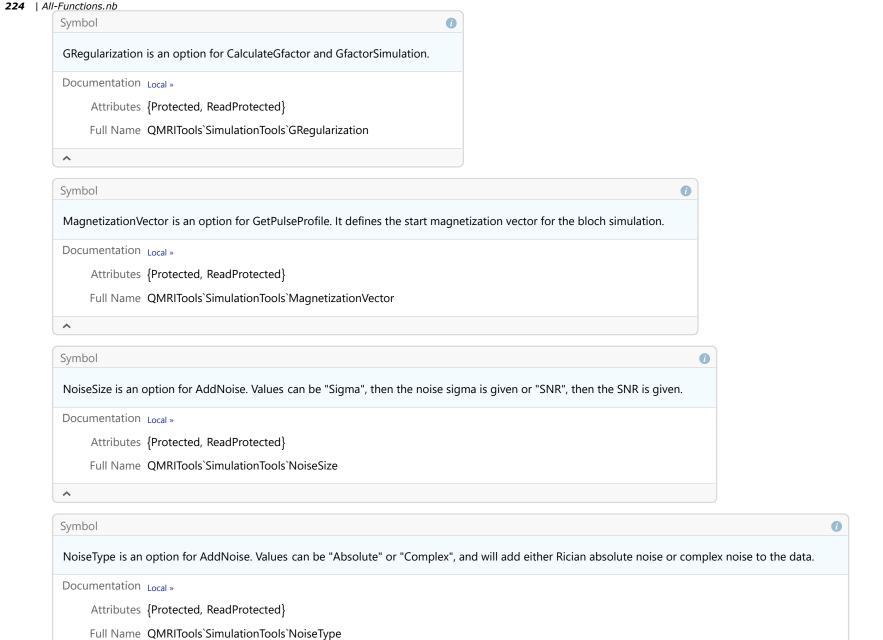
Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0,0,1}} and eigenvalues {{11, 12, 13}}.

Tensor{{11, 12, 13}, "OrtRandom"} creates a diffuison tensor with random orthogonal eigenvectors {{1,0,0},{0,1,0},{0
```

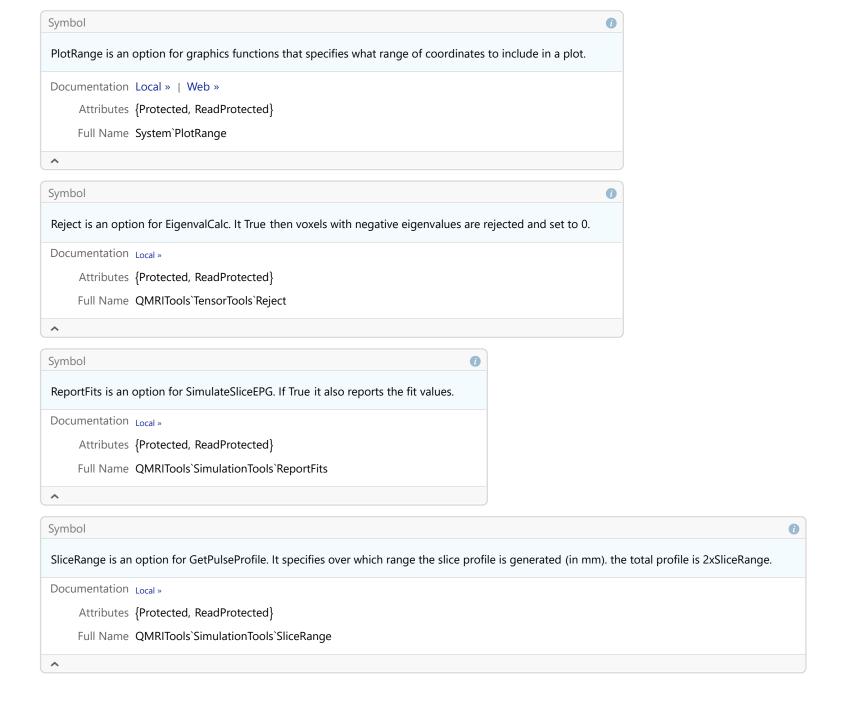
Options

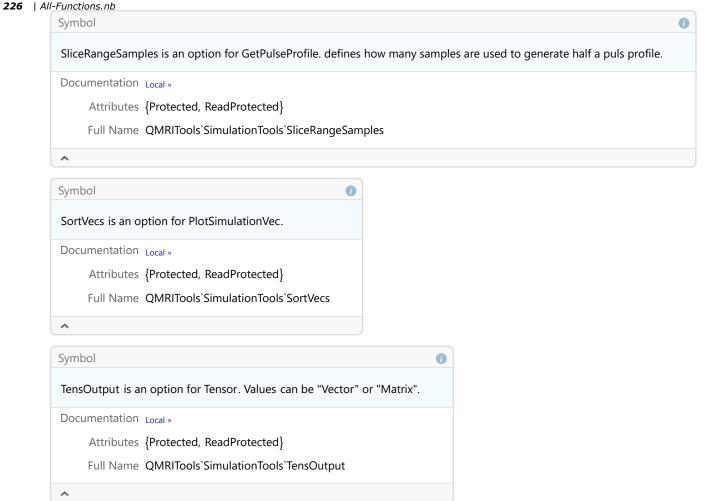






 \wedge

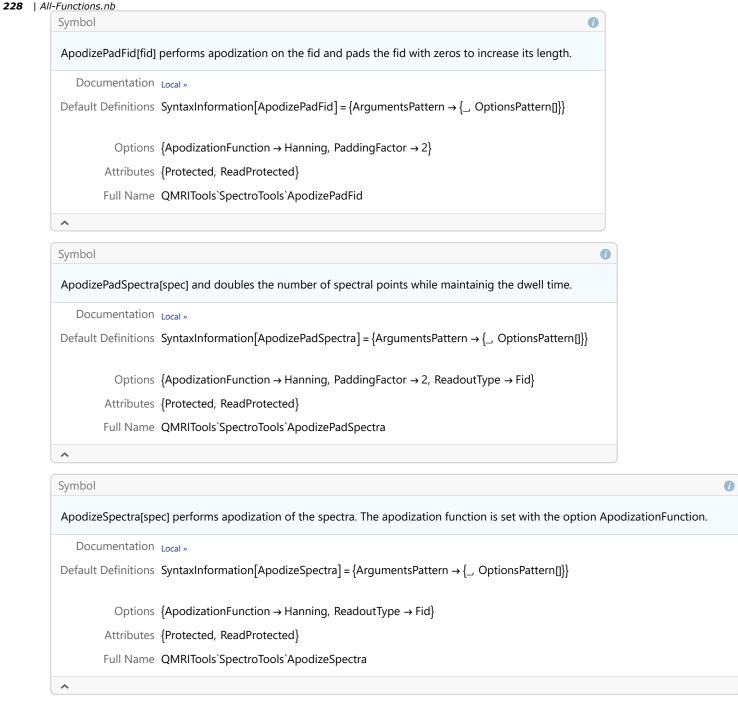


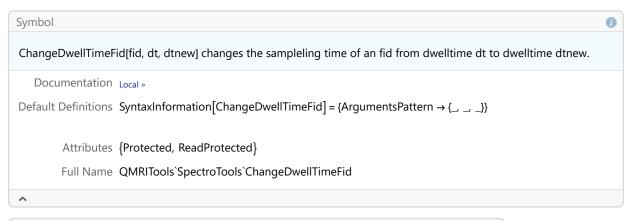


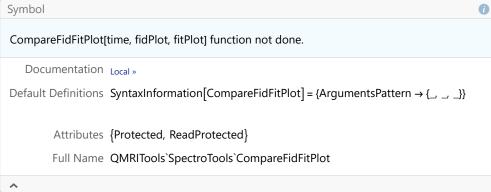
SpectroTools

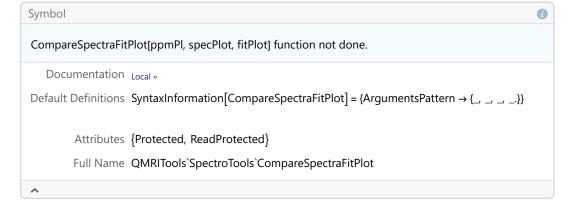
Functions

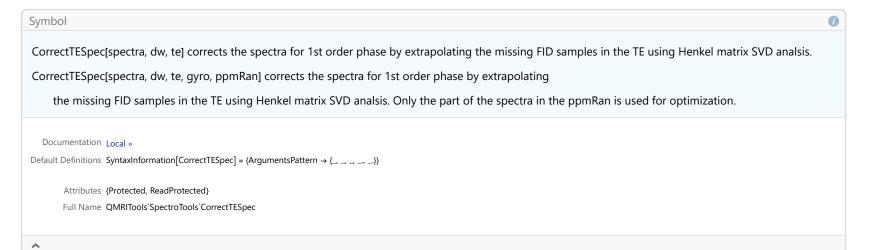
```
Symbol
ApodizeEcho[echo] performs apodization on the echo. The apodization function is set with the option ApodizationFunction.
   Documentation Local »
Default Definitions SyntaxInformation[ApodizeEcho] = {ArgumentsPattern → {_, OptionsPattern[]}}
          Options ApodizationFunction → Hanning
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`SpectroTools`ApodizeEcho
^
Symbol
ApodizeFid[fid] performs apodization on the fid. The apodization function is set with the option ApodizationFunction.
   Documentation Local »
Default Definitions SyntaxInformation[ApodizeFid] = {ArgumentsPattern → {_, OptionsPattern[]}}
          Options ApodizationFunction → Hanning
        Attributes {Protected, ReadProtected}
        Full Name QMRITools'SpectroTools'ApodizeFid
\wedge
Symbol
ApodizePadEcho[echo] performs apodization on the echo and pads the echo with zeros to increase its length.
   Documentation Local »
Default Definitions SyntaxInformation[ApodizePadEcho] = {ArgumentsPattern → {_, OptionsPattern[]}}
          Options {ApodizationFunction \rightarrow Hanning, PaddingFactor \rightarrow 2}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`SpectroTools`ApodizePadEcho
\wedge
```











```
CSIInterface[] opens the CSI interface. Function not done.

CSIInterface[te, bw] opens the CSI interface with known te and bw.

CSIInterface[file] opens the CSI interface with the data from file loaded.

CSIInterface[file, {tei, bwi}] opens the CSI interface with the data from file loaded with known te and bw.

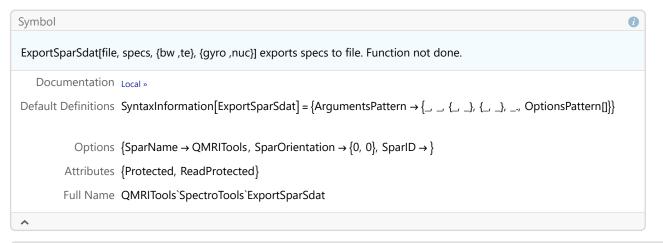
Documentation Local.

Default Definitions SyntaxInformation[CSIInterface] = {ArgumentsPattern → {__,,__,,_, OptionsPattern[]}}

Options {SpectraFieldStrength → 7, SpectraNucleus → 31P}

Attributes {Protected, ReadProtected}

Full Name QMRITools'SpectroTools'CSIInterface
```



```
FindSpectraPpmShift[spectra, {dw, gyro}, peaks] finds the ppm value that aligns the spectra with the given peak positions peaks wich is a list of ppm values.

FindSpectraPpmShift[spectra, {dw, gyro}, {peaks, amps}] finds the ppm value

that aligns the spectra with the given peak positions peaks wich is a list of ppm values and amps are ther relative amplitudes.

FindSpectraPpmShift[spectra, {dw, gyro}, specTar] finds the ppm value that aligns the spectra with the given target spectra specTar.

Documentation Local >>

Attributes (Protected, ReadProtected)

Full Name QMRITools SpectroTools FindSpectraPpmShift
```

```
Symbol
FitSpectra[specBasis, spec, {st,end}, dt, {lwvals,lwamsp}] Fits the basis spectra from GetSpectraBasisFunctions to the spec overt the ppm range {st, end} and dt the dweltime.
   Documentation Local »
Default Definitions SyntaxInformation[FitSpectra] = {ArgumentsPattern → {_, _, _, _, _, OptionsPattern[]}}
                    SpectraNucleus → 1H ... (10 total)
        Options >
         Attributes {Protected, ReadProtected}
         Full Name QMRITools`SpectroTools`FitSpectra
^
Symbol
                                                                                                      0
FitSpectraResultTable [parFit, parsF, names, ref, out] function not done.
   Documentation Local »
Default Definitions SyntaxInformation[FitSpectraResultTable] = {ArgumentsPattern \rightarrow {__ _, _, _, __.}}
         Attributes {Protected, ReadProtected}
         Full Name QMRITools`SpectroTools`FitSpectraResultTable
^
Symbol
                                                                                                                                            0
GetGyro[nuc, field] geth the gyromagnetic ratio with field the field strength in Tesla and nuc the nucleus availible in GyromagneticRatio.
   Documentation Local »
Default Definitions SyntaxInformation[GetGyro] = {ArgumentsPattern \rightarrow {_, __}}
         Attributes {Protected, ReadProtected}
         Full Name QMRITools`SpectroTools`GetGyro
```

0

Symbol

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 $Get Spectra Basis Functions \cite{Met1, ..., metn}\cite{Met1, ..$

GetSpectraBasisFunctions[{{props1}, ..., {propsn}}] generates a list of spectra baisis functions with properties prop1 to propn. The properties are those specified in MakeSpinSystem.

GetSpectraBasisFunctions[inp, split] generates a list of spectra basisfunctions. Each metabolite name present in the list split wil be split in individual spectra per peak.

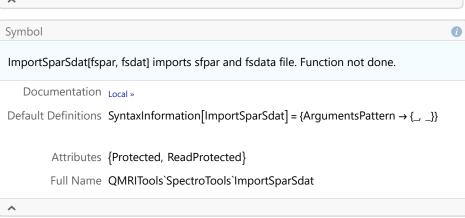
Documentation Local »

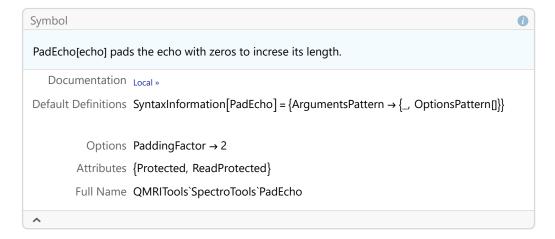
 $\label{eq:definitions} Default\ Definitions\ \ SyntaxInformation[GetSpectraBasisFunctions] = \\ \left\{ ArgumentsPattern \rightarrow \left\{ _, _, \ OptionsPattern[] \right\} \right\}$

Options \Rightarrow BasisSequence \Rightarrow {PulseAcquire, 0}...(6 total)

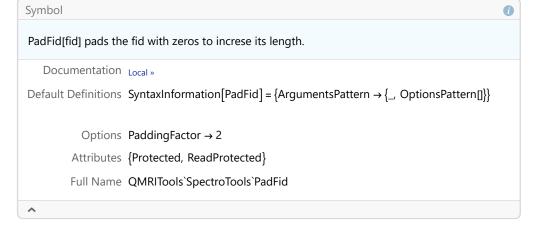
Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`GetSpectraBasisFunctions

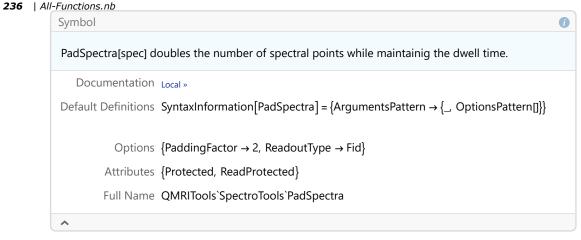


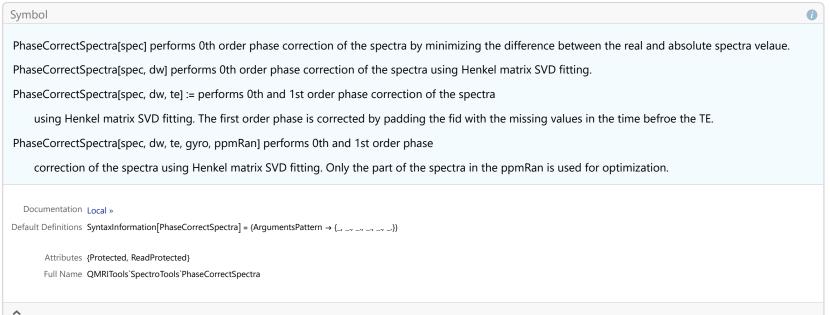


^



All-Functions.nb | 235





PhaseShiftSpectra[spectra, phi0] aplies the 0th order phase phi0 to the spectra.

PhaseShiftSpectra[spectra, ppm, gyro, phi1] aplies the 1st order phase phi1 to the spectra. The ppm can be obtained using GetPpmRange and gyro with GetGyro.

PhaseShiftSpectra[spec, ppm, gyro, {phi0, phi1}] aplies the 0th and 1st order phases {phi0, phi1} to the spectra. The ppm can be obtained using GetPpmRange and gyro with GetGyro.

The 0th order phase phi0 is in radians and the 1st order phase phi1 is in ms.

Documentation Local »

Default Definitions SyntaxInformation[PhaseShiftSpectra] = {ArgumentsPattern \rightarrow {_, _, _, _.}}

Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`PhaseShiftSpectra

^

Symbol

Symbol

with CatComa

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PlotCSIData[spectra, {dwell, gyro}] plots the CSI spectra which has dimensions {z,y,x,nsamp}. The ppm axes is determined by dwell and gyro. Gyro can be obtained with GetGyro.

PlotCSIData[spectra, {dwell, field, nuc}] plots the CSI spectra which has dimensions {z,y,x,nsamp}. The ppm axes is determined by dwell and field and nuc.

Documentation Local »

 $\label{eq:definitions} Default \ Definitions \ \ SyntaxInformation[PlotCSIData] = \{ArgumentsPattern \rightarrow \{_,_,_,_,OptionsPattern[]\}\}$

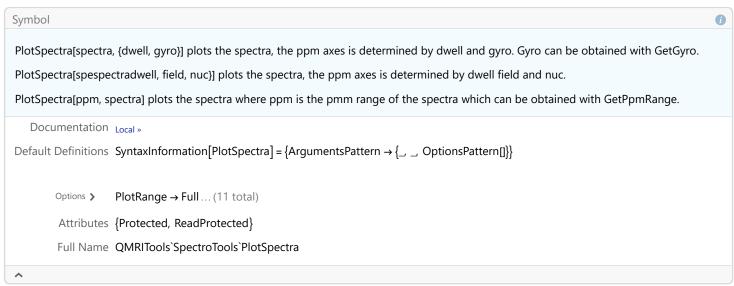
Options PlotRange → Full

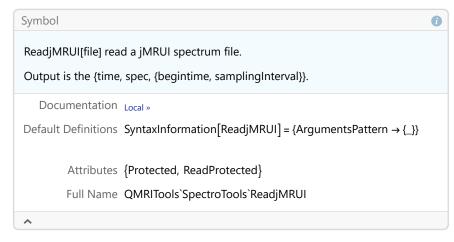
Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`PlotCSIData

^

238 | All-Functions.nb Symbol PlotFid[fid, dwell] plots the fid assuming dwell as the sampeling time. PlotFid[time, fid] plot the fid where time is the timing of the fid which can be obtained with GetTimeRange. Documentation Local » Default Definitions SyntaxInformation[PlotFid] = {ArgumentsPattern → {_, _, OptionsPattern[]}} Options > PlotRange → Full ... (8 total) Attributes {Protected, ReadProtected} Full Name QMRITools`SpectroTools`PlotFid ^





```
ShiftSpectra[speca, {dw, gyro}, shift] shifts the spectra by shift. The shift is in ppm.

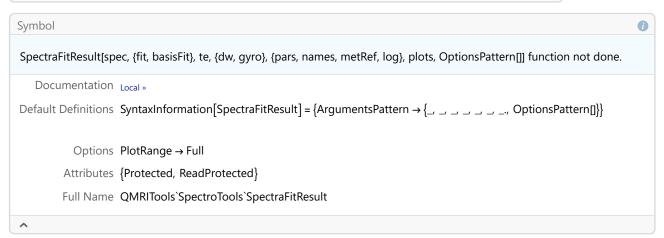
Documentation Local »

Default Definitions SyntaxInformation[ShiftSpectra] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}}

Options ReadoutType → Fid

Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`ShiftSpectra
```



Symbol

TimeShiftEcho[fid, time, gam] aplies a linebroadening with linewidth gam and a Voigt lineshape to the fid. The time can be obtained using GetTimeRange.

TTimeShiftEcho[fid, time, {gam, f}] aplies a linebroadening with linewidth gam and a custom lineshape f to the fid (f=0, "Gaussinan", f=1 "Lorentzian").

TTimeShiftEcho[fid, time, gyro, {gam, eps}] aplies a linebroadening with linewidth gam to the fid and a phase eps that results in eps ppm shift of the spectra. The gyro can be obtained with GetGyro.

TTimeShiftEcho[fid, time, gyro, {gam, eps, f}] aplies a linebroadening with linewidth gam using a custom lineshape f to the fid and a phase eps that results in eps ppm shift of the spectra.

The linewidth gam is given in ms and the spectra shift eps is given in ppm.

Documentation Local »

Default Definitions SyntaxInformation[TimeShiftEcho] = {ArgumentsPattern \rightarrow {_, _, _, _.}}

Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`TimeShiftEcho

^

Symbol



TimeShiftFid[fid, time, gam] aplies a linebroadening with linewidth gam and a Voigt lineshape to the fid. The time can be obtained using GetTimeRange.

TimeShiftFid[fid, time, {gam, f}] aplies a linebroadening with linewidth gam and a custom lineshape f to the fid (f=0, "Gaussian", f=1 "Lorentzian").

TimeShiftFid[fid, time, gyro, {gam, eps}] aplies a linebroadening with linewidth gam to the fid and a phase eps that results in eps ppm shift of the spectra. The gyro can be obtained with GetGyro.

TimeShiftFid[fid, time, gyro, {gam, eps, f}] aplies a linebroadening with linewidth gam using a custom lineshape f to the fid and a phase eps that results in eps ppm shift of the spectra.

The linewidth gam is given in ms and the spectra shift eps is given in ppm.

Documentation Local »

Default Definitions SyntaxInformation[TimeShiftFid] = {ArgumentsPattern → {_, _, _, _.}}

Attributes {Protected, ReadProtected}

Full Name QMRITools`SpectroTools`TimeShiftFid

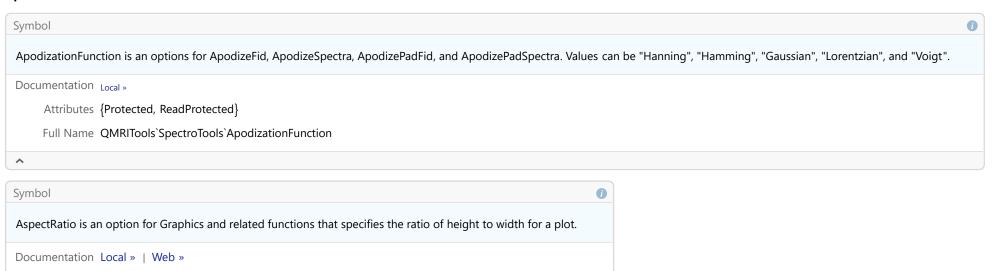
 \wedge

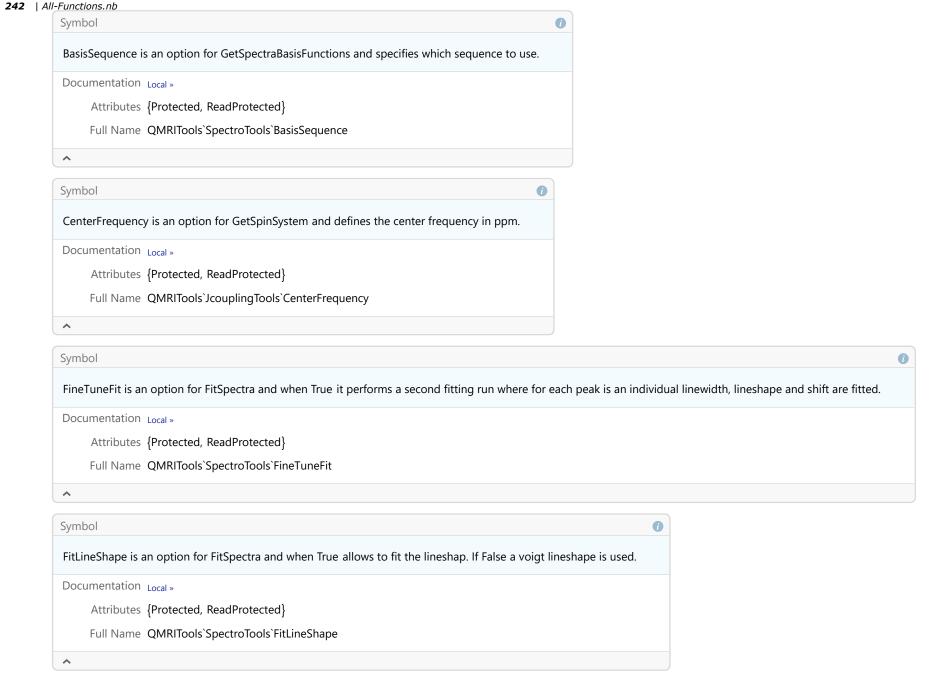
```
Symbol
TimeShiftFid[fid, time, gam] aplies a linebroadening with linewidth gam and a Voigt lineshape to the fid. The time can be obtained using GetTimeRange.
TimeShiftFid[fid, time, {gam, f}] aplies a linebroadening with linewidth gam and a custom lineshape f to the fid (f=0, "Gaussian", f=1 "Lorentzian").
TimeShiftFid[fid, time, gyro, {gam, eps}] aplies a linebroadening with linewidth gam to the fid and a phase eps that results in eps ppm shift of the spectra. The gyro can be obtained with GetGyro.
TimeShiftFid[fid, time, gyro, {gam, eps, f}] aplies a linebroadening with linewidth gam using a custom lineshape f to the fid and a phase eps that results in eps ppm shift of the spectra.
The linewidth gam is given in ms and the spectra shift eps is given in ppm.
   Documentation Local »
Default Definitions SyntaxInformation[TimeShiftFidV] = {ArgumentsPattern \rightarrow {_, _, _, _.}}
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`SpectroTools`TimeShiftFidV
^
```

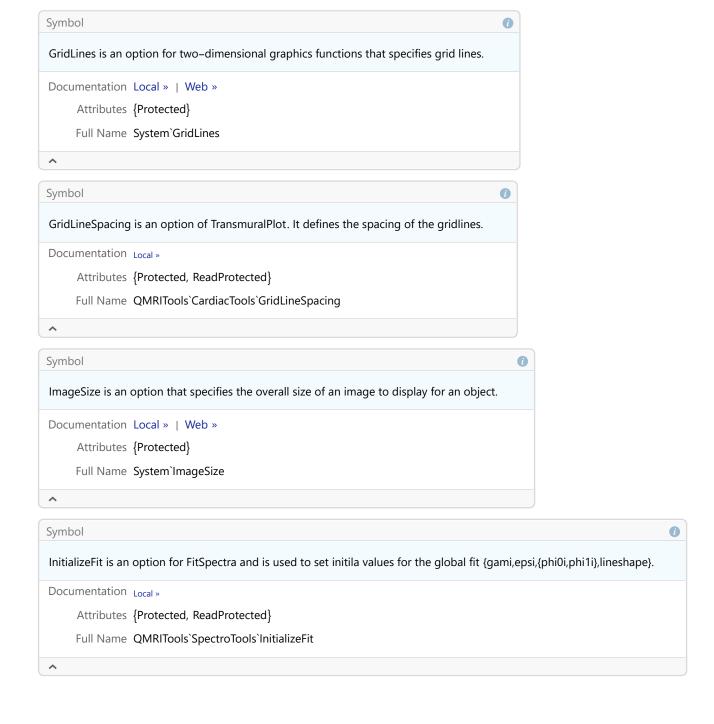
Options

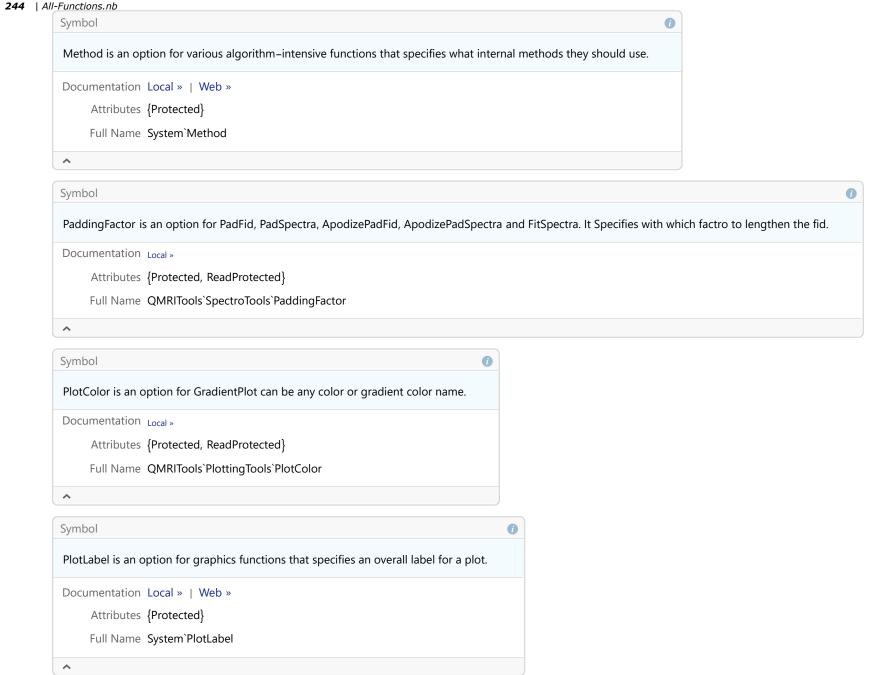
Attributes {Protected}

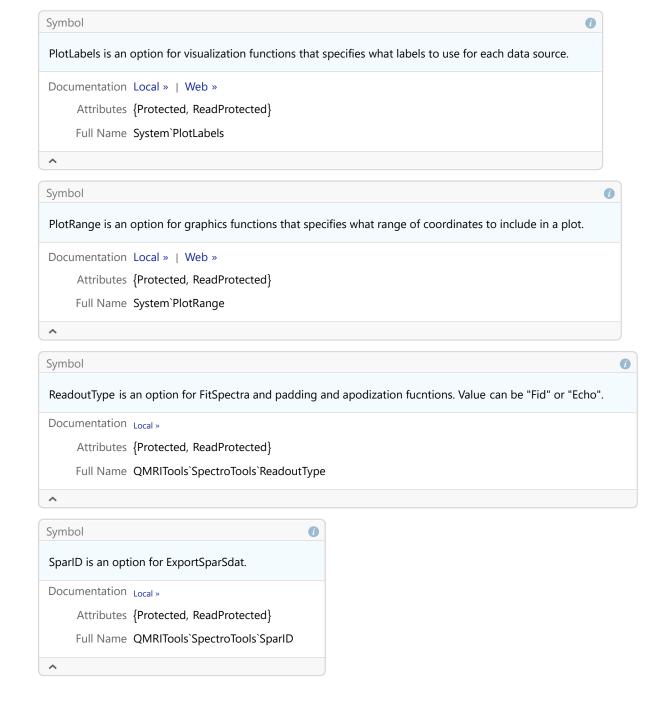
Full Name System`AspectRatio

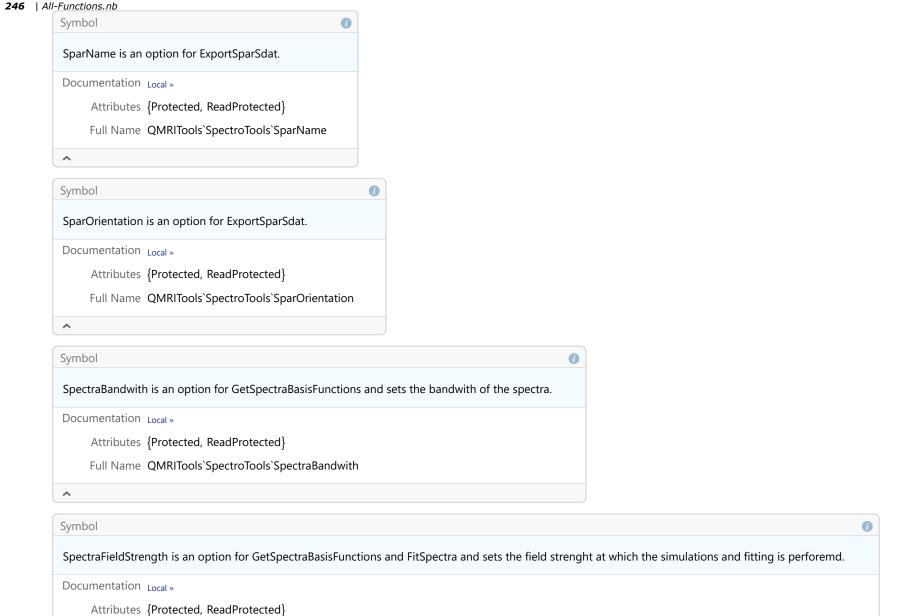






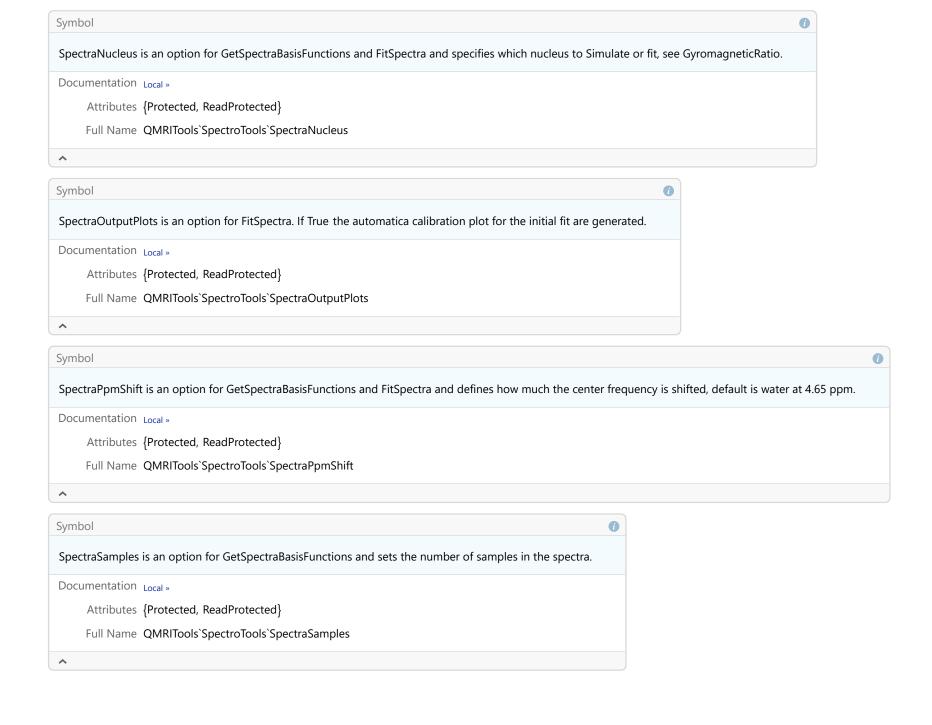


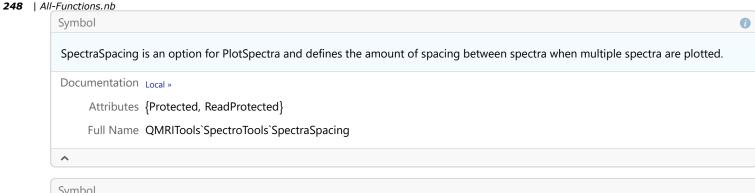


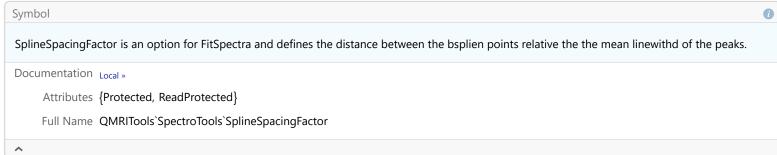


Full Name QMRITools`SpectroTools`SpectraFieldStrength

 \wedge

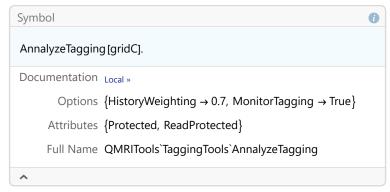






TaggingTools

Functions



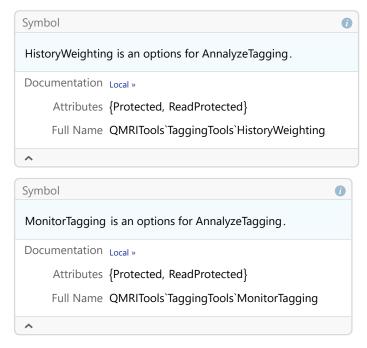
```
CalculateDispacementParameters[{motx, moty}, mask].

Documentation Local »

Attributes {Protected, ReadProtected}

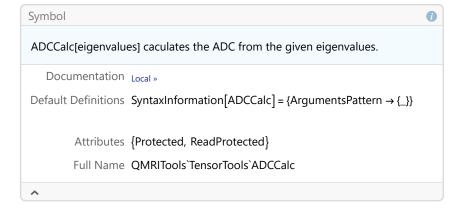
Full Name QMRITools`TaggingTools`CalculateDispacementParameters
```

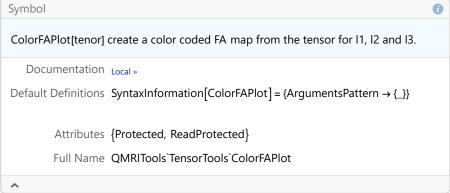
Options



TensorTools

Functions





```
ConcatenateDiffusionData[{{data1, ..., dataN}, {grad1, ..., gradN}, {bval, ..., bvalN}, {vox, ..., voxN}}] concatenates the diffusion data sets.

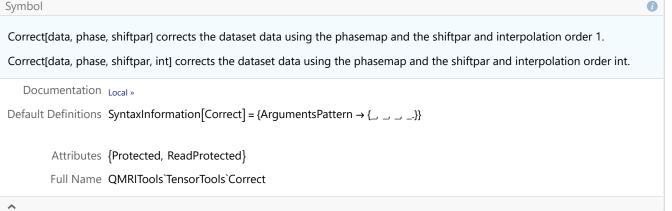
ConcatenateDiffusionData[{data1, ..., dataN}, {grad1, ..., gradN}, {bval, ..., bvalN}, {vox, ..., voxN}] concatenates the diffusion data sets.

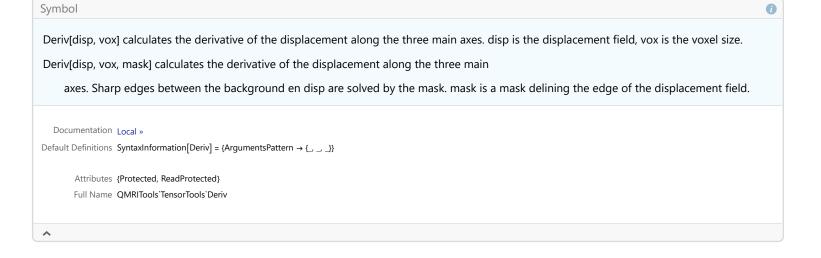
Documentation Local »

Default Definitions SyntaxInformation[ConcatenateDiffusionData] = {ArgumentsPattern → {_, _, _, _, _, _}}}

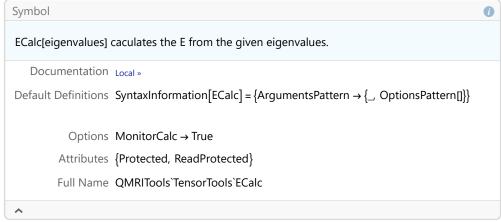
Attributes {Protected, ReadProtected}

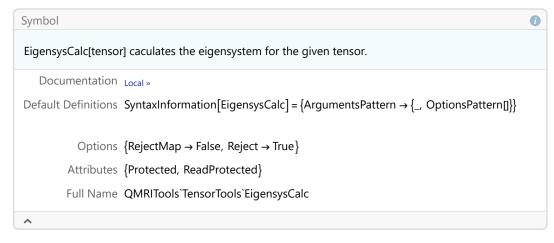
Full Name QMRITools`TensorTools`ConcatenateDiffusionData
```

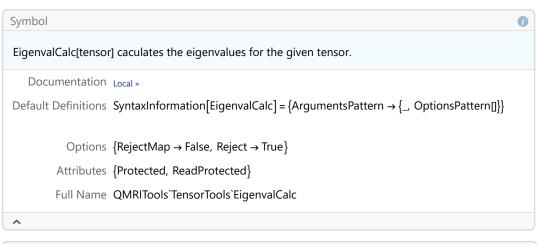


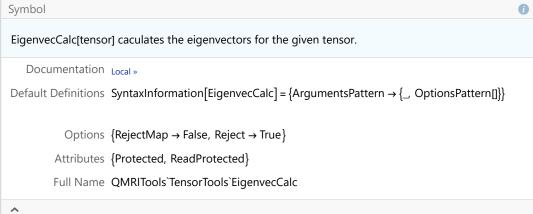


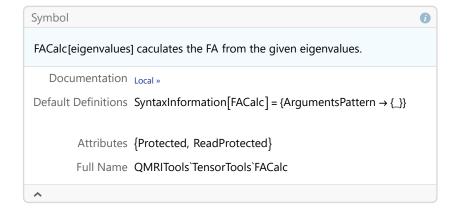
252 | All-Functions.nb Symbol DriftCorrect[data, bval] dirft corrects the data using the signals of the lowest bvalue that has 6 or more unique volumes. For the function to work optimal it is best to have these volumes evenly spread througout thet data and for the first and last volume to have this low bvalue. DriftCorrect[] is based on DOI: 10.1002/mrm.26124. Documentation Local » Default Definitions SyntaxInformation[DriftCorrect] = {ArgumentsPattern → {_, _, _, OptionsPattern[]}} Options {NormalizeSignal → True, UseMask → True} Attributes {Protected, ReadProtected} Full Name QMRITools`TensorTools`DriftCorrect ^



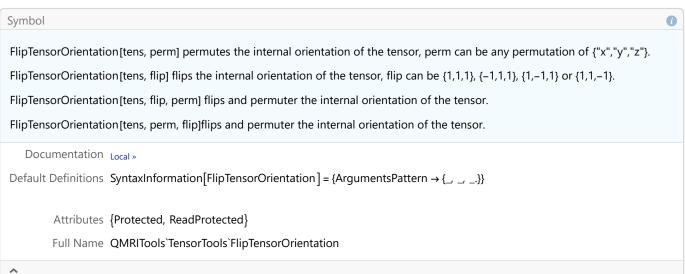








254 | All-Functions.nb Symbol FlipGradientOrientation[grad, perm] permutes the internal orientation of the gradients, perm can be any permutation of {"x","y","z"}. FlipGradientOrientation[grad, flip] flips the internal orientation of the gradients, flip can be {1,1,1}, {-1,1,1}, {1,-1,1} or {1,1,-1}. FlipGradientOrientation[grad, flip, perm] flips and permuter the internal orientation of the gradients. FlipGradientOrientation[grad, perm, flip]flips and permuter the internal orientation of the gradients. Documentation Local » Attributes {Protected, ReadProtected} Full Name QMRITools`TensorTools`FlipGradientOrientation



```
Symbol
ParameterCalc[tensor] caculates the eigenvalues and MD and FA from the given tensor. The parameters are I1, I2, I3, MD and FA. I1, I2, I3, MD are in (10^-3 mm^2/s).
   Documentation Local »
Default Definitions SyntaxInformation[ParameterCalc] = {ArgumentsPattern → {_, OptionsPattern[]}}
          Options Reject → False
        Attributes {Protected, ReadProtected}
        Full Name QMRITools`TensorTools`ParameterCalc
```

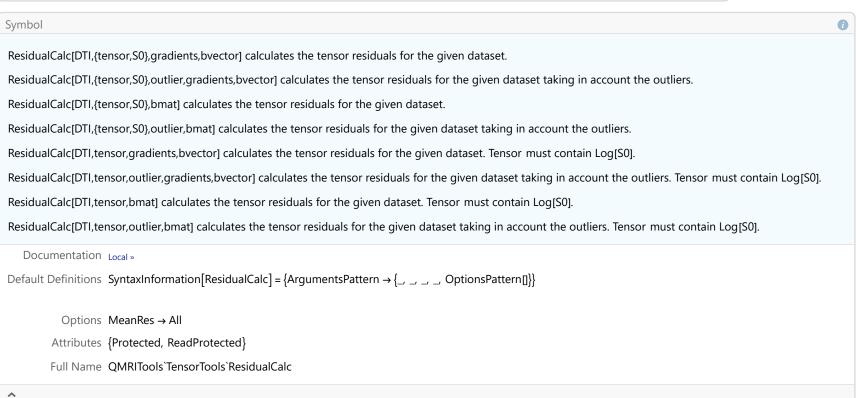
```
RemovelsoImages[data, grad, bval] Romoves the ISO images from the philips scanner from the data. ISO images have g={0,0,0} and b>0.

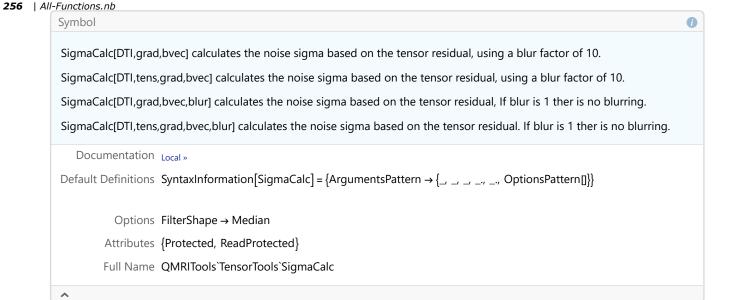
Documentation Local »

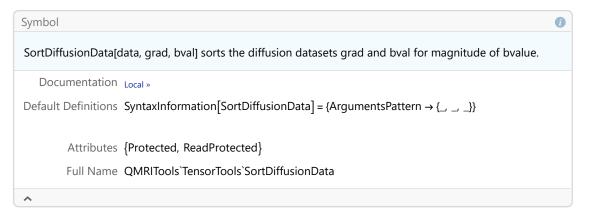
Default Definitions SyntaxInformation[RemovelsoImages] = {ArgumentsPattern → {__ _ _ _ }}

Attributes {Protected, ReadProtected}

Full Name QMRITools`TensorTools`RemovelsoImages
```







Symbol

TensorCalc[data, gradients, bvalue] calculates the diffusion tensor for the given dataset. Allows for one unweighted image and one b value.

Gradient directions must be in the form $\{\{x1,y1,z1\}, ..., \{xn,yn,zn\}\}\$ without the unweighted gradient direction.

bvalue is a singe number indicating the b-value used.

TensorCalc[data, gradients, bvec] calculates the diffusion tensor for the given dataset. allows for multiple unweighted images and multiple bvalues.

allows for differnt tensor fitting methods. gradient directions must be in the form {{x1,y1,z1}, ..., {xn,yn,zn}} with the unweighted direction as {0,0,0}.

bvec the bvector, with a bvalue defined for each gradient direction. b value for unweighted images is 0.

TensorCalc[data, bmatix] calculates the diffusion tensor for the given dataset. allows for multiple unweighted images and multiple bvalues.

bmat is the bmatrix which can be generated usiong Bmatrix.

The bvalue assumed to be is in s/mm² and therfore the output is in mm²/2.

TensorCalc[] is based on DOI: 10.1016/j.neuroimage.2013.05.028 and 10.1002/mrm.25165.

Documentation Local »

 $\label{eq:definitions} Default \ Definitions \ \ SyntaxInformation[TensorCalc] = \{ArgumentsPattern \rightarrow \{_, _, _, OptionsPattern[]\}\}$

Options ➤ MonitorCalc → True ... (6 total)

Attributes {Protected, ReadProtected}

Full Name QMRITools`TensorTools`TensorCalc

^

Symbol



TensorCorrect[tensor, phase, shift, vox] corrects the tensor based on B0 field map. Can perform both translation and rotation of tensor.

Documentation Local »

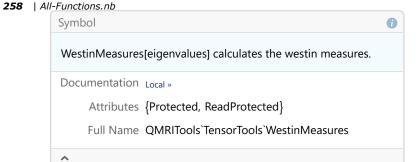
 $\label{eq:definitions} Default \ Definitions \ \ SyntaxInformation[TensorCorrect] = \{Arguments \ Pattern \ \rightarrow \{_, _, _, _, Options \ Pattern \]\} \}$

Options RotationCorrect → False

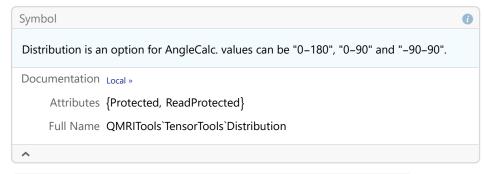
Attributes {Protected, ReadProtected}

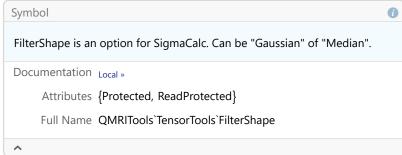
Full Name QMRITools`TensorTools`TensorCorrect

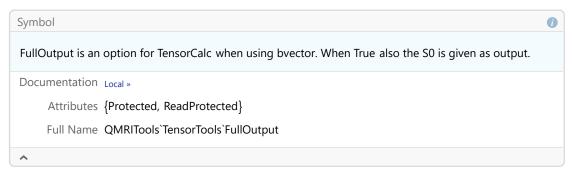
^

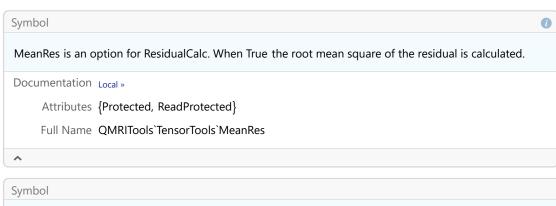


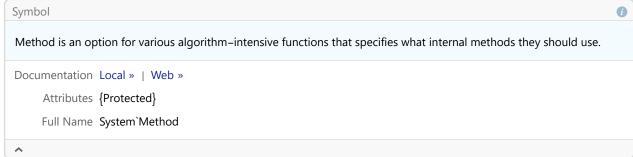
Options

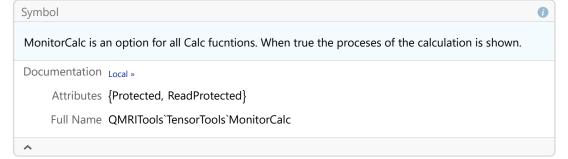




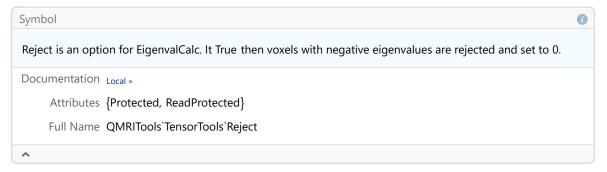


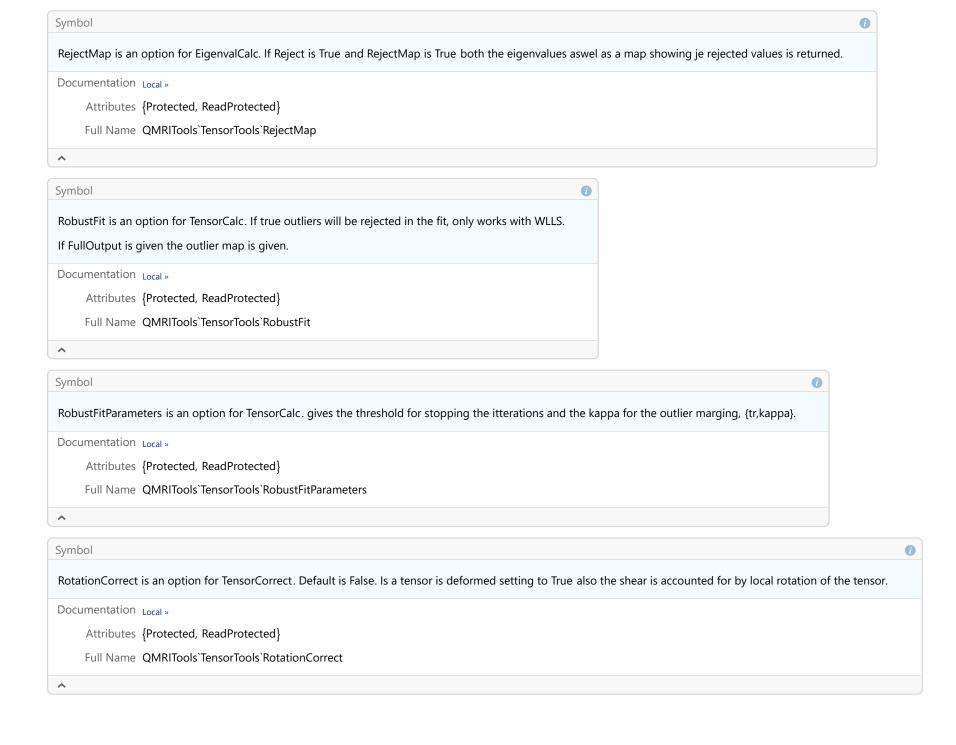




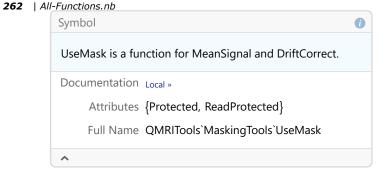






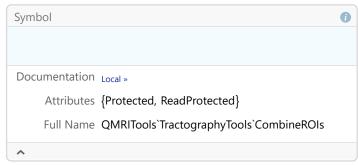


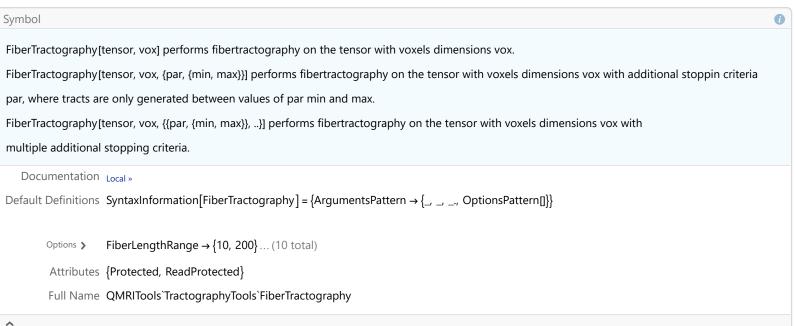


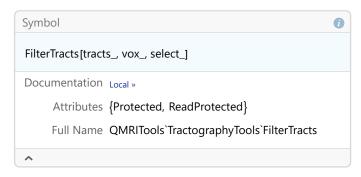


TractographyTools

Functions







Symbol

^

FindTensorPermutation [tensor, vox] performs tractography for all tensor permutations and gives back the one that has the longest tracts.

FindTensorPermutation [tensor, vox, {par, {min, max}}] same but with additional stoppin criteria par, where tracts are only generated between values of par min and max.

FindTensorPermutation [tensor, vox, {{par, {min, max}}, ...}] same but with multiple additional stopping criteria.

Ouput = {permutations, flips, plot}

FindTensorPermutation[] is based on DOI: 10.1016/j.media.2014.05.012.

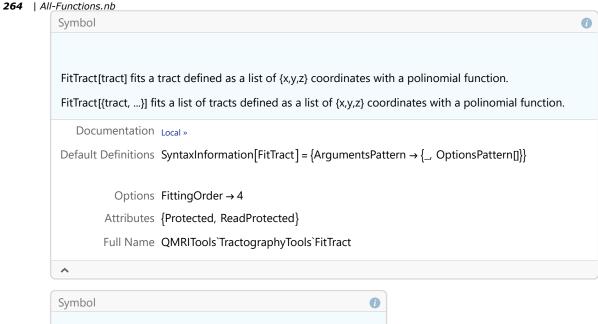
Documentation Local »

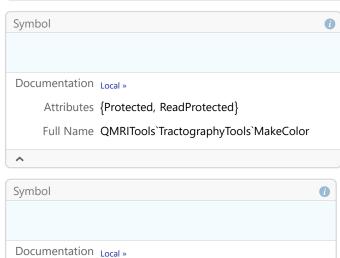
 $\label{eq:definitions} Default \ Definitions \ \ SyntaxInformation[FindTensorPermutation] = \\ \left\{ ArgumentsPattern \rightarrow \left\{ _, _, _, OptionsPattern[] \right\} \right\}$

Options \Rightarrow FiberLengthRange \rightarrow {10, 200}... (7 total)

Attributes {Protected, ReadProtected}

Full Name QMRITools`TractographyTools`FindTensorPermutation

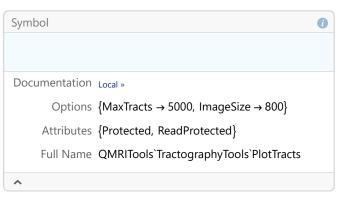


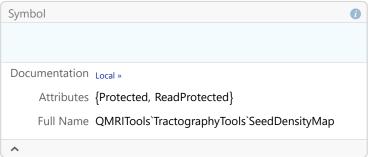


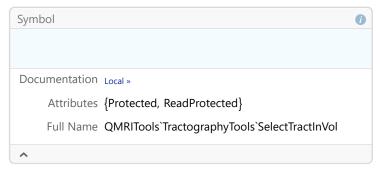
Full Name QMRITools`TractographyTools`PartTracts

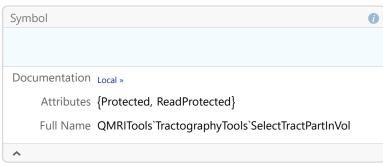
Attributes {Protected, ReadProtected}

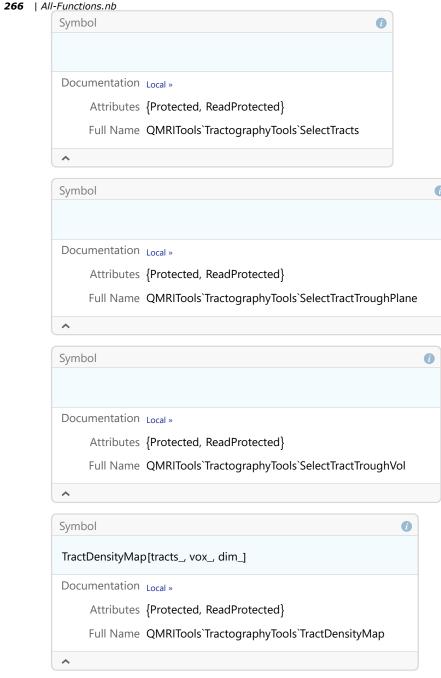
^



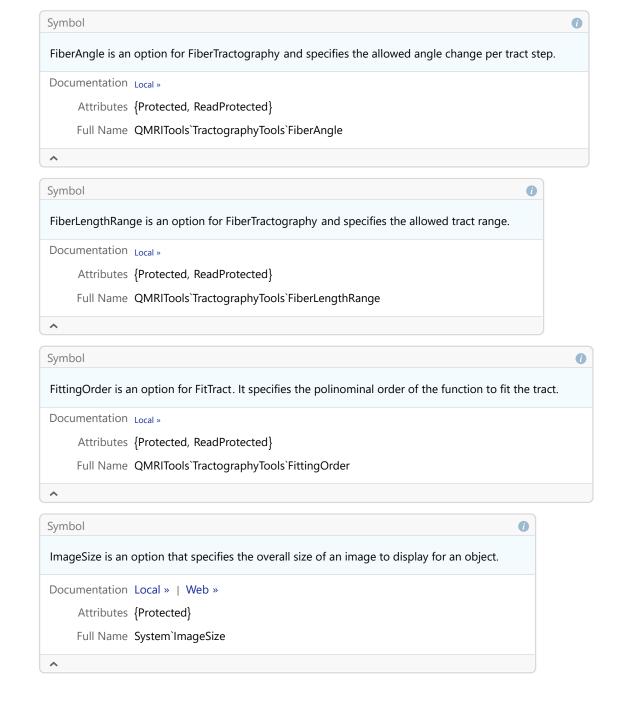






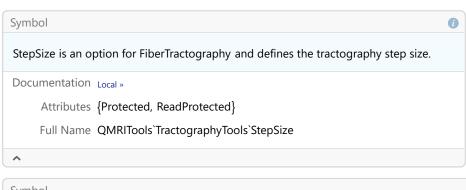


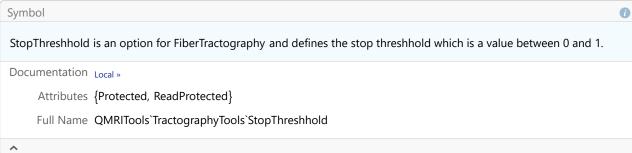
Options



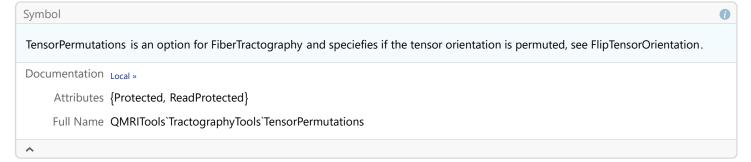


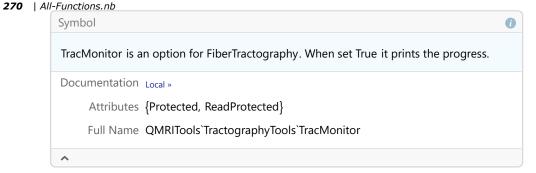
Symbol Method is an option for various algorithm-intensive functions that specifies what internal methods they should use. Documentation Local » | Web » Attributes {Protected} Full Name System`Method ^







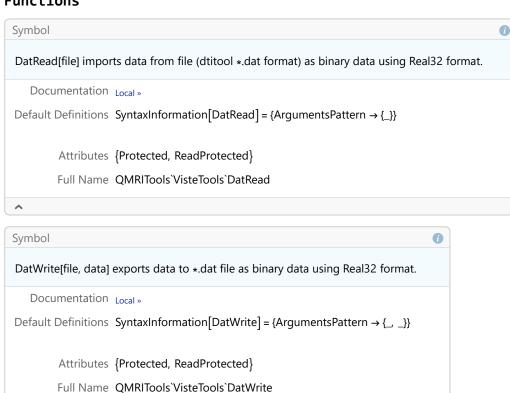




VisteTools

Functions

^



Symbol

^

DTItoolExp[tensor, voxsize] exports tensor to {XX.dat, YY.dat, ZZ.dat, XY.dat, XZ.dat, YZ.dat} and uses XX.dat as background and generates corresponding *dti files.

DTItoolExp[tensor, voxsize, folder] exports tensor to {XX.dat, YY.dat, XZ.dat, XY.dat, XZ.dat, YZ.dat} to the given folder and uses XX.dat as background and generates corresponding *dti files.

DTItoolExp[tensor, voxsize, folder, add] exports tensor to {XX.dat, YY.dat, ZZ.dat, XY.dat, XZ.dat,

YZ.dat} to the given folder and uses XX.dat as background and generates corresponding *dti files adds - add to the filenames.

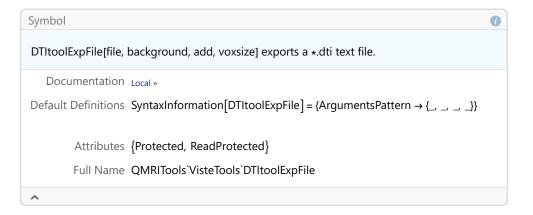
DTItoolExp[back, tensor, voxsize] exports background to back.dat and tensor to {XX.dat, YY.dat, XZ.dat, XY.dat, XZ.dat} and generates corresponding *dti files.

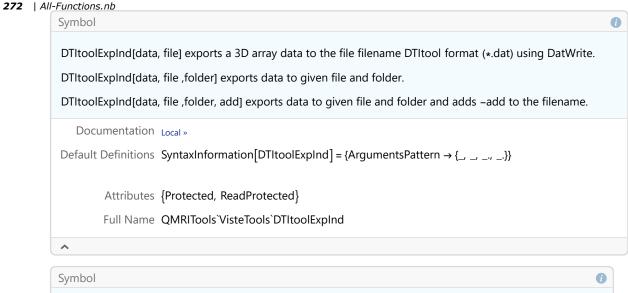
DTItoolExp[back, tensor, voxsize, folder] exports background to back.dat and tensor to {XX.dat, YY.dat, ZZ.dat, XY.dat, XZ.dat, YZ.dat} to the given folder and generates corresponding *dti files.

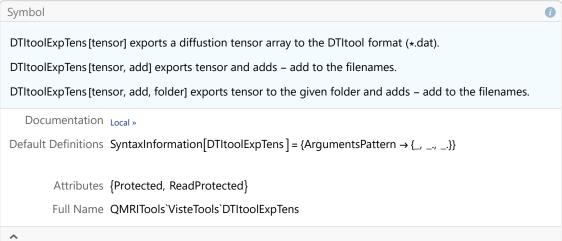
DTItoolExp[back, tensor, voxsize, folder, add] exports background to back.dat and tensor to

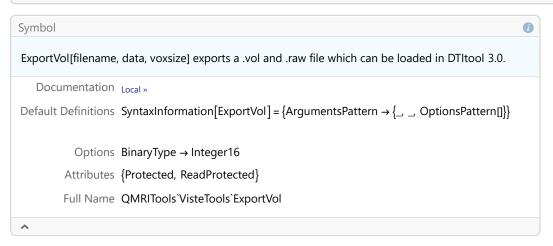
{XX.dat, YY.dat, ZZ.dat, XY.dat, XZ.dat, YZ.dat} to the given folder and generates corresponding *dti files and adds – add to the filenames.

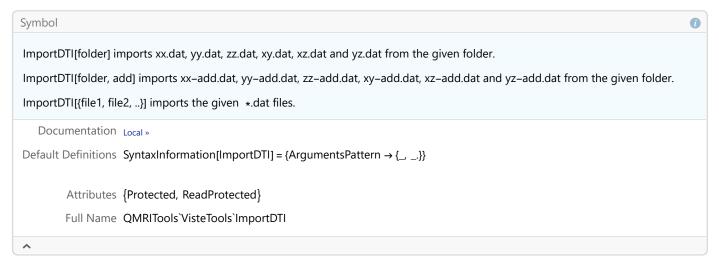
Documentation Local » Default Definitions SyntaxInformation[DTItoolExp] = {ArgumentsPattern \rightarrow {_, _, _, _, _, _}} Attributes {Protected, ReadProtected} Full Name QMRITools'VisteTools'DTItoolExp

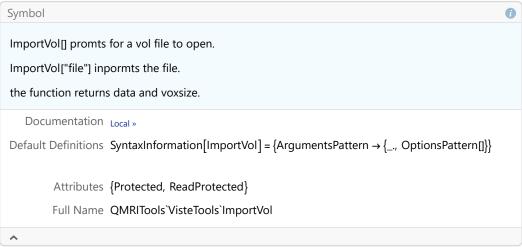


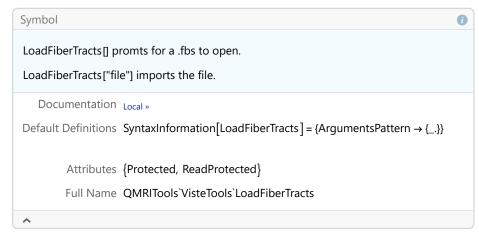












Options

