# Yokogawa MEG Reader Toolbox for MATLAB

### **Revision 1.4**

## **Specifications**

2011.05.06

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This toolbox is written for MATLAB version 7.5 (R2007b) onwards.

This toolbox must not be used for clinical applications. If MEG data are processed by this toolbox, they should not be later employed for clinical and/or diagnostic purposes.

## This toolbox consists of following functions:

Category	Function name	Purpose
Read MEG data	getYkgwData	Get measurement data.
Read MEG header	getYkgwHdrSystem	Get information about system.
	getYkgwHdrChannel	Get information about channel.
	getYkgwHdrAcqCond	Get information about data acquisition condition.
	getYkgwHdrEvent	Get information about trigger event.
	getYkgwHdrCoregist	Get information about coregistration.
	getYkgwHdrDigitize	Get information about digitization.
	getYkgwHdrSubject	Get information about subject.
	getYkgwHdrBookmark	Get information about bookmark.
	getYkgwHdrSource	Get information about analyzed sources.
Read MRI	getYkgwMriHdr	Get information about header of MRI file (*.mri).
Others	getYkgwVersion	Get information about version of this toolbox.

getYkgwData

This function retrieves the measurement data of whole channels by the specified file path and sample range.

data getYkgwData(

filepath, start\_sample, sample\_length

);

Arguments:

string [in] File path filepath

[in] Start sample or trial(frame) number for retrieving data. start\_sample double

The start number corresponding to each acquisition type is as follows : - Continuous Raw : Start sample number for retrieving data. (0 origin) - Evoked Average : Start sample number for retrieving data. (0 origin) - Evoked Raw : Start frame number for retrieving data. (1 origin)

When both start\_sample and sample\_length are omitted, you can get data of whole samples.

double [in] Sample length for retrieving data. sample\_length

The number of samples or trials(frames) corresponding to each acquisition type is as follows:

- Continuous Raw : Number of samples for retrieving data. - Evoked Average: Number of samples for retrieving data. - Evoked Raw : Number of trials(frames) for retrieving data. When this parameter is omitted or is specified as 'Inf',

you can get data from start\_sample to the end of sample(frame).

Return values:

matrix(double) [out] double matrix of measurement data.

Row: number of channels (whole channel), Column: number of samples

Unit of the each channel depends on channel type as follows:

[Tesla] MagnetoMeter AxialGradioMeter [Tesla] PlanarGradioMeter [Tesla] ReferenceMagnetoMeter [Tesla] ReferenceAxialGradioMeter [Tesla] ReferencePlanarGradioMeter [Tesla] TriggerChannel [Volt]

EegChannel [Volt] \*This has already been reflected EEG gain EcgChannel [Volt] \*This has already been reflected ECG gain

EtcChannel [Volt] NullChannel [Volt]

getYkgwHdrSystem

This function retrieves information of the system.

system\_info getYkgwHdrSystem(

filepath

);

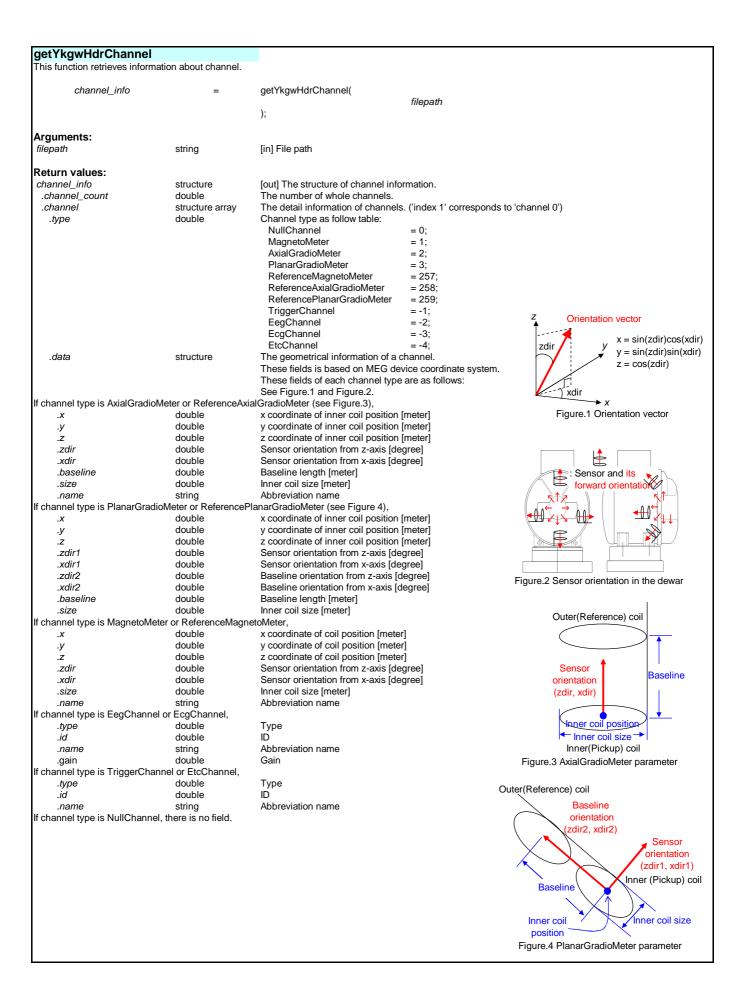
Arguments:

filepath string [in] File path

Return values: system\_info

[out] The structure of system information. double Data version .version .revision double Data revision .system\_id double System ID .system\_name string System name .model\_name string Model name

structure



getYkgwHdrAcqCond

This function retrieves information about data acquisition condition.

acq\_cond = getYkgwHdrAcqCond(

filepath

);

Arguments:

filepath string [in] File path

Return values:

acq\_cond structure [out] The structure of information about data acquisition condition.

.acq\_type double Acquisition type

AcqTypeContinuousRaw = 1; AcqTypeEvokedAve = 2; AcqTypeEvokedRaw = 3;

If acquisition type is AcqTypeContinuousRaw,

.sample\_rate double Sampling rate [Hz]

.sample\_count double The number of samples which were actually acquired [sample]

.specified\_sample\_count double The number of samples which were specified before starting acquisition [sample]

If acquisition type is AcqTypeEvokedAve or AcqTypeEvokedRaw,

.sample\_rate double Sampling rate [Hz]

frame\_length double Frame length (The number of samples per one trial) [sample]

\_pretrigger\_length double Pretrigger length (The number of samples before trigger per one trial) [sample]

.average\_count double The number of trials(frames) which were actually acquired [trial]

.specified\_average\_count double The number of trials(frames) which were specified before starting acquisition [trials]

.multi\_trigger structure The structure of multi trigger information.

.enable boolean Is multi trigger mode ? (true : multi trigger mode)

.count double Number of multi triggers

List of multi trigger mode, this structure array is set to empty.)

.enable boolean Is current multi trigger set to enable ? (true : enable)

.code double Event code (1 origin)

.name string Event name

.average\_count double The number of trials(frames) which were actually acquired [trial]

.specified\_average\_count double The number of trials(frames) which were specified before starting acquisition [trials]

getYkgwHdrEvent

This function retrieves information about trigger event.

event = getYkgwHdrEvent(

filepath

);

Arguments:

filepath string [in] File path

Return values:

event structure array [out] The structure array of trigger event corresponding to each trial.

.sample\_no double Sample number of current event (0 origin)

.code double Event code (1 origin)

.name string Event name

```
getYkgwHdrCoregist
This function retrieves information about coregistration.
             coregist
                                                        getYkgwHdrCoregist(
                                                                                              filepath
Arguments:
filepath
                                   string
                                                        [in] File path
Return values:
coregist
                                   structure
                                                        [out] The structure of information about coregistration.
  .done
                                   boolean
                                                        Is coregistration done ? (true : done)
  .mri_type
                                   double
                                                        MRI type
                                                          NoMriFile
                                                                                              = 0;
                                                          NormalMriFile
                                                                                              = 1:
                                                          VirtualMriFile
                                                                                              = 2:
 .mri_file
                                   string
                                                        File path of MRI file (*.mri)
                                                        File path of HPI(Head Position Indicator) file (*.mrk)
  .hpi_file
                                   string
                                                        4 x 4 matrix which transforms MEG device coordinate to MRI coordinate [meter]
                                   matrix(double)
  .meg2mri
                                                          usage: [xmri, ymri, zmri, 1]' = coregist.meg2mri * [xmeg, ymeg, zmeg, 1]'
  .mri2meg
                                   matrix(double)
                                                        4 x 4 matrix which transforms MRI coordinate to MEG device coordinate [meter]
                                                          usage: [xmeg, ymeg, zmeg, 1]' = coregist.meg2mri * [xmri, ymri, zmri, 1]'
                                   structure array
                                                        The structure array of HPI(Head Position Indicator)
  .hpi
   .meg_pos
                                   matrix(double)
                                                        HPI position [x, y, z] on MEG device coordinate [meter]
                                   matrix(double)
                                                        HPI position [x, y, z] on MRI coordinate [meter] (Before coregistration, this field is set to [0,0,0])
   .mri_pos
    .label
                                                         HPI label as follows:
                                   strina
                                                          'LPA' : Left PreAuricular
                                                          'RPA'
                                                                   Right PreAuricular
                                                                   Center PreFrontal
                                                          'CPF'
                                                          'I PF'
                                                                 · Left PreFrontal
                                                          'RPF'
                                                                 : Right PreFrontal
  .model
                                   structure
                                                         The structure of conductor model.
   .type
                                   double
                                                        Conductor model type
                                                          UNKNOWN_MODEL
                                                                                              = -1:
                                                          NO_MODEL
                                                                                              = 0;
                                                          SPHERICAL_MODEL
                                                                                              = 1;
                                                          LAYERED_MODEL
If Conductor model type is SPHERICAL_MODEL,
                                                        x coordinate of spherical center position on MRI coordinate [meter]
                                   double
   .CX
                                   double
                                                        y coordinate of spherical center position on MRI coordinate [meter]
   .cv
                                   double
                                                        z coordinate of spherical center position on MRI coordinate [meter]
   .CZ
                                   double
                                                        radius of spherical conductor on MRI coordinate [meter]
    radius
If Conductor model type is LAYERED_MODEL,
                                                        Coefficient 'ax' of planar equation 'ax * x + ay * y + az * z = c'
                                   double
                                                        Coefficient 'ay' of planar equation 'ax * x + ay * y + az * z = c'
Coefficient 'az' of planar equation 'ax * x + ay * y + az * z = c'
Coefficient 'c' of planar equation 'ax * x + ay * y + az * z = c'
   .ay
                                   double
   .az
                                   double
                                   double
getYkgwHdrDigitize
This function retrieves information of the digitization.
             digitize
                                                        getYkgwHdrDigitize(
                                                                                              filepath
                                                        );
Arguments:
                                                        [in] File path
filepath
                                   string
Return values:
digitize
                                   structure
                                                        [out] The structure of information and points about digitization.
  .info
                                                        The structure of information about digitization.
                                   structure
    .digitizer_file
                                   string
                                                        File path of digitizer file
                                                        Is matching done? (true : done)
   done
                                   boolean
    .meg2digitizer
                                                        4 x 4 matrix which transforms MEG coordinate to Digitizer coordinate.
                                   matrix(double)
                                                        4 x 4 matrix which transforms Digitizer coordinate to MEG coordinate.
   .digitizer2meg
                                   matrix(double)
  .point
                                   structure array
                                                        The structure of point data about digitization.
   .nam
                                   string
                                                        Point name
                                   double
                                                        x-coordinate on digitizer coordinate [meter]
   .x
                                   double
                                                        y-coordinate on digitizer coordinate [meter]
   .y
   .z
                                   double
                                                        z-coordinate on digitizer coordinate [meter]
```

getYkgwHdrSubject This function retrieves information of the subject. subject getYkgwHdrSubject( filepath Arguments: string filepath [in] File path Return values: subject [out] The structure of subject information. .id string .name string Name string Birthday .birthday string Sex .sex .handed Handed string getYkgwHdrBookmark This function retrieves information about bookmark. bookmark getYkgwHdrBookmark( filepath ); Arguments: string [in] File path filepath Return values: bookmark structure array [out] The structure array of bookmark information. .sample\_no double Sample number of bookmark .label double Label of bookmark .comment string Comment of bookmark getYkgwHdrSource This function retrieves information of the sources. getYkgwHdrSource( source filepath ); Arguments: filepath string [in] File path Return values: [out] The structure array of analyzed source information. structure array source Note: Sources are arranged in order of estimated time. Type of source .type double DipoleModel = 1; . DistributedSourceModel = 2; .time double Analyzed Time [second] from 1970.1.1 .sample\_no double Time sample index of source .channel\_list row vector(double) Channel number (0 origin) list which used to estimate .model structure The structure of conductor model. .type double Conductor model type UNKNOWN\_MODEL NO\_MODEL = 0;SPHERICAL\_MODEL = 1; LAYERED\_MODEL = 2: If Conductor model type is SPHERICAL\_MODEL, x coordinate of spherical center position on MEG coordinate [meter] double .cy double y coordinate of spherical center position on MEG coordinate [meter] .cz double z coordinate of spherical center position on MEG coordinate [meter] .radius double radius of spherical conductor on MEG coordinate [meter] If Conductor model type is LAYERED\_MODEL, Coefficient 'ax' of planar equation 'ax \* x + ay \* y + az \* z = c' Coefficient 'ay' of planar equation 'ax \* x + ay \* y + az \* z = c' double .ax

Coefficient 'az' of planar equation 'ax \* x + ay \* y + az \* z = c'
Coefficient 'c' of planar equation 'ax \* x + ay \* y + az \* z = c'

double

double

double

.av

.az .c

.algorithm	structure	The structure of conductor algorithm.		
.magnetic_field_calc	double	Algorithm of magnetic field calculation		
0 – –		BiotSavartLaw = 1;		
		SarvasLaw = 2;		
		MagneticDipoleLaw = 3;		
.variable_restraint	double	Algorithm of variable restraint		
	4042.0	NoRestraint = 0;		
		PositionRestraint = 1;		
		DirectionRestraint = 2;		
		IntensityRestraint = 3;		
.optimization	double			
.opumization	double	Algorithm of optimization		
		GradientAlgorithm = 1;		
		LeadFieldReconstructionAlgorithm = 2;		
		ManualSetAlgorithm = 3;		
		UserAlgorithm = 4;		
filter	structure	The structure of spectral filter setting.		
.hpf , .lpf	structure	The structure of high-pass / low-pass filter setting.		
.enable	boolean	Does this filter enable?		
.cutoff_frequency	double	Cutoff frequency [Hz]		
.window_type	double	Window type		
		NoWindow = $0$ ;		
		HanningWindow = 1;		
		HammingWindow = 2;		
.width	double	Filter width		
.bpf, .bef	structure	The structure of band-pass / band-eliminate filter setting.		
.enable	boolean	Does this filter enable?		
.low_frequency	double	Low frequency [Hz]		
.high_frequency	double	High frequency [Hz]		
.window_type	double	Window type		
.width	double	Filter width		
.moveave	structure	The structure of moving average setting.		
.moveave .enable	boolean	Does this filter enable?		
.width	double	Filter width		
.baseadi	structure	The structure of baseline adjustment setting.		
		Does this filter enable?		
.enable	boolean			
.type	double	Type of baseline adjustment		
		PretriggerBaselineAdjust = 0;		
		PosttriggerBaselineAdjust = 1;		
		AllRangeBaselineAdjust = 2;		
		ExplicitBaselineAdjust = 3;		
.start_time	double	Start time [millisecond]		
.end_time	double	End time [millisecond]		
.gof	double	Goodness-of-fit (GOF)		
.correlation	double	Corrlation Coefficiency		
.label	double	Label		
.comment	string	Comment		
.total_intensity	double	Total intensity of sources		
.dipole_count	double	Number of dipole sources		
.dipole_list	structure array	The structure array of dipole sources		
.X	double	x coordinate of dipole position on MEG coordinate [meter]		
.y	double	y coordinate of dipole position on MEG coordinate [meter]		
.y .Z	double	z coordinate of dipole position on MEG coordinate [meter]		
.zdir	double	Dipole orientation from z-axis [degree]		
.xdir	double	Dipole orientation from z-axis [degree]		
	double	· · · · · · · · · · · · · · · · · · ·		
.intensity	double	Dipole intensity (moment) [Ampere Meter]		

#### getYkgwMriHdr This function retrieves header information of specified mri file (\*.mri). mri\_header getYkgwMriHdr( filepath Arguments: [in] File path filepath string Return values: mri\_header structure [out] The structure of mri header information. .data\_style double Data style (0 : DICOM, others : Polhemus) The structure of conductor model. .model structure Is conductor model defined? (true: defined) .done boolean double Conductor model type .type UNKNOWN\_MODEL = -1: NO MODEL = 0;SPHERICAL MODEL = 1; LAYERED\_MODEL = 2: If Conductor model type is SPHERICAL\_MODEL, x coordinate of spherical center position on MRI coordinate [meter] double .cy double y coordinate of spherical center position on MRI coordinate [meter] double z coordinate of spherical center position on MRI coordinate [meter] .cz .radius double radius of spherical conductor on MRI coordinate [meter] If Conductor model type is LAYERED\_MODEL, Coefficient 'ax' of planar equation 'ax \* x + ay \* y + az \* z = c' double .ax Coefficient 'ay' of planar equation 'ax \* x + ay \* y + az \* z = c' Coefficient 'az' of planar equation 'ax \* x + ay \* y + az \* z = c' double .av double .az Coefficient 'c' of planar equation 'ax \* x + ay \* y + az \* z = c'double C The structure of point data about picked HPI. .hpi structure array Is pick-up of a HPI point done? (true: done) .done boolean HPI position [x, y, z] on MRI coordinate [meter] .mri\_pos double .label string HPI label as follows: 'LPA' : Left PreAuricular 'RPA' Right PreAuricular 'CPF' : Center PreFrontal 'LPF' : Left PreFrontal 'RPF' : Right PreFrontal .image\_parameter structure The structure of image parameters. vector(double) 1 x 2 row vector, minimum and maximum of image values .intensity .initial color 1 x 2 row vector, minimum and maximum of initial brightness vector(double) vector(double) 1 x 2 row vector, minimum and maximum of current brightness .color The structure of normalized HEAD coordinate system ( LPA(x-), RPA(x+), nasion(y+) ). See Figure.5. .normalize structure .done Is HEAD coordinate system defined ? ( true : defined ) boolean .mri2normalize matrix(double) 4 x 4 matrix which transforms MRI coordinate to HEAD coordinate [meter] usage: [xhead, yhead, zhead, 1]' = mri\_header.normalize.mri2normalize \* [xmri, ymri, zmri, 1]' The structure of point data about HEAD fiducial points. .point structure array .done boolean Is pick-up of a HEAD fiducial point done? (true: done) Name of HEAD fiducial points. string .name x coordinate of a HEAD fiducial point on MRI coordinate [meter] double .X y coordinate of a HEAD fiducial point on MRI coordinate [meter] double .y double z coordinate of a HEAD fiducial point on MRI coordinate [meter] .z The structure of BESA fiducial information. besa fiducial structure The structure of point data about BESA fiducial points. .point structure array .done boolean Is pick-up of a BESA fiducial point done? (true: done) double x coordinate of a BESA fiducial point on MRI coordinate [meter] .x double y coordinate of a BESA fiducial point on MRI coordinate [meter] .y double z coordinate of a BESA fiducial point on MRI coordinate [meter] Head Anterior Posterior nasion Anterior Right Left Posterior Foot Figure.5 Normalized HEAD coordinate system

getYkgwVersion
This function retrieves version of this toolbox.

getYkgwVersion; ykgw\_ver

Arguments: none

Return values:

ykgw\_ver .version .major

[out] structure of toolbox version toolbox version major.minor[.build[.revision]] toolbox major version

string double double double toolbox minor version .minor toolbox build version .build .revision toolbox revision version release date yyyy.mm.dd .date string