

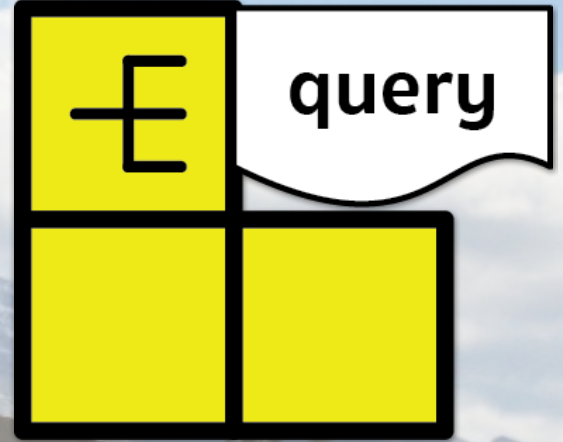
# General Importer

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Mac Win

# BOXsci



Web: <https://sites.google.com/site/matBoxSite/>

## SOP: Importing or updating data in BOXsci

**TASK:** Import variable types of data using a general standard for continuous and discrete data. All meta information is provided in cross-platform spreadsheets.

**SOLUTION:** Use standardized META CSV spreadsheet tables loaded from command line:

```
>> sci_db_import
```

or through SCIBOX menu Tools/Import/sci\_db\_import. The user is prompted to indicate the path to the following META CSVs:

```
<sTable> _metaSubject --- description of subject in the imported sessions
<sTable> _metaSignal --- description of sessions
<sTable> _metaTrialType --- description of trial types, e.g. locomotion, reach, etc
<sTable> _metaTrial --- description of trials
<sTable> _metaEvent --- description of different event types
```

When metaEvent table is present the importer expects to find event MAT file described in sFile, sPath fields of metaEvent.

```
<sTable> _Event --- event table with timestamp events
```

e.g. emgraw\_metaSubject.csv

```
<sTable> _metaEvent : not implemented yet
<sTable> _Event : not implemented yet
```

### USEFUL NOTES:

--- CSVs can be exported from Numbers (Mac) as CSV and from Excel (PC) as "CSV (MS-DOS)". Please, keep only one set of CSVs in the same folder.

--- Since CSV file format stands for comma separated values, it goes without saying that comma should not be used in notes.

--- The most common mistakes are typos. Please use COPY&PASTE for names of files and folder locations. For convenience, please, keep all data files in one folder. It will be easier to change the location information when moved.

### Table Description

In general, the order of field names does not matter, but the exact field names are expected.

Name	Size	Name	Size
emgraw_metaSignal.csv	222 bytes	emgraw_metaSignal.csv	222 bytes
emgraw_metaSubject.csv	61 bytes	emgraw_metaSubject.csv	61 bytes
emgraw_metaTrial.csv	215 bytes	emgraw_metaTrial.csv	215 bytes
emgraw_metaTrialType.csv	60 bytes	emgraw_metaTrialType.csv	60 bytes

emgraw\_metaSubject
Open with Numbers

sSubject	sPrefix	sSession	sNote
RPI_CAT1	RPI1	S1_20120801	

emgraw\_metaSignal
Open with Numbers

sSignalRaw	sSignal	sTable	nDim	sUnit	nGain	nRate
LG	LG	emgraw	1	au	1	10000
MG	MG		1			
TA	TA		1			
Glut	Glut		1			
ST	ST		1			
BF	BF		1			
VL	VL		1			
Sart	Sart		1			

**metaSubject**

**sSubject** --- e.g. 'Sherlock Holmes'  
**sPrefix** --- e.g. 'SH' subject name prefix (usually PROTOCOL ID or INITIALS)  
**sNote** --- subject description

Note: sSession is no longer required.

**metaSignal**

**sSignalRaw** --- expected column or field name in the data file. The order of these signals should match to that in the data file  
**sSignal** --- the corresponding signal name in the database  
**sTable** --- the data table  
**nRate** --- sampling rate  
**sUnit** --- signal unit

Note that referenced MAT files should contain signals organized in the following structure

TABLE.(sSignal) = [nSample x 1], e.g. EMG.TA = [column\_vector]

e.g. EMG.TA = [1 2 3 4 5]'; % note the transpose sign

where

TABLE is the value of field *sTable*

**metaTrialType**

**sTrialType** --- trial type (single word, no spaces)  
**sNote** --- detailed description limited to 255 chars

**metaTrial**

**sFile** --- data file; file extension determines the loader used to import data to BOXsci (e.g.

Name	Size
emgrow_metaSignal.csv	222 bytes
emgrow_metaSubject.csv	61 bytes
emgrow_metaTrial.csv	215 bytes
emgrow_metaTrialType.csv	60 bytes

sTrialType	sNote
loc	Locomotion on the treadmill with FPs

sFile	sPath	sSubject	sSession	bTrial	nTrial	sTrialType
XcatBlock45_emgrow.mat	/Users/sergij/Projects/PRJ - RPI/RPI - Xpecally	RPI_CAT1	S1_20120801	1	1	loc

'TestEMG1.csv' or 'TestKin.c3d')

**sPath** --- location of file on disk  
**sSubject** --- string of subject name  
**sSession** --- 'S1\_YYYYMMDD'  
**bTrial** --- equiv. of deleted trial; consider not importing these trials by running the importer from the Command Window: **sci\_db\_import**('bTrial', "...")  
**nTrial** --- describe the order of trial in the recorded session. This field is used to match information between tables.  
**sTrialType** --- assigns trial types described in **metaTrialType** table

---

<b>idTrial</b>	---	if not empty then replace data in selected idTrials (empty field for automatic id assignment)
<b>tSync</b>	---	table sync (usually =0 for synched tables)
<b>nSampleStart</b>	---	starting sample (use for long files or leave empty for short files)
<b>nSampleEnd</b>	---	the last sample (leave blank for the end of file or short files)
<b>sNote</b>	---	trial description

Note that *metaTrial* should not have *idSession* field, which is generated automatically by the importer.

#### *metaEvent*

<b>sEvent</b>	---	event name (single word, no spaces), e.g. 'on', 'off', 'spike1'
<b>sEventType</b>	---	event type (single word, no spaces), e.g. 'tStamp', 'tPeriod', 'tText', 'tSpike'
<b>sMarker</b>	---	plot symbol, e.g. 'o'
<b>nEdgeColor</b>	---	color of symbol edge, e.g. [1 0 0]
<b>nFaceColor</b>	---	color of symbol face, e.g. [1 0 0]
<b>nMarkerSize</b>	---	symbol size in points
<b>sFile</b>	---	event data file name
<b>sPath</b>	---	event data file location

#### *Event*

<b>tEvent</b>	---	time stamp of event in (s)
<b>sEventType</b>	---	event type (single word, no spaces), e.g. 'tStamp', 'tPeriod', 'tText', 'tSpike'
<b>sSignal</b>	---	signal name that belongs to the same table
<b>bEvent</b>	---	boolean, e.g. true / false
<b>nDuration</b>	---	event duration in (s), e.g. 0

## Notes