

## HPSearch2 data file (.mat) structure (numbers shown are examples):

\* curvesettings <1x1 struct> : (parameter information is stored)

```
- time_start: '10-Sep-2013 12:34:56'
- time_stop: '10-Sep-2013 12:35:00'
- dataversion: 2.1000
- curvesettingsfile: 'C:\AAA\BBB\123.456.789.0123.ITD.mat'
- Fs: [4.8828e+004 4.8828e+004] (= [inFs outFS])
- stim <1x1 struct>
    ISI: 120
    Duration: 50
    Delay: 10
    Ramp: 5
    RadVary: 0
    Frozen: 0
    limits: [1x1 struct]
- tdt: <1x1 struct>
    AcqDuration: 80
    SweepPeriod: 90
    TTLPulseDur: 1
    CircuitGain: 1
    HPEnable: 0
    HPFreq: 50
    LPEnable: 1
    LPFreq: 10000
    limits: [1x1 struct]
- channels <1x1 struct>
    InputChannel: 128
    OutputChannelL: 1
    OutputChannelR: 2
- analysis <1x1 struct>
    WindowWidth: 0
    StartTime: 10
    EndTime: 60
    ThresSD: 3
    Raster: 30
    limits: [1x1 struct]
    ThAuto: 0
    Peak: -1
    Sign: -1
    Scale: 0.1
    Threshold: 3.6000
- animal <1x1 struct>
    Animal: '000'
    Unit: '0'
    Rec: '34'
    Date: '2013-09-10'
    Time: '12:34:56'
    Pen: '0'
    AP: '0'
    ML: '0'
    Depth: '0'
    comments: ''

- caldata <1x1 struct>
    freq: [1x50 double]
    DAscale: 5
    mag: [2x50 double]
    phase_us: [2x50 double]
    mindbspl: [101.2345 84.3210]
    maginv: [2x50 double]
- curve <1x1 struct>
    stimtype: 'TONE'
    side: 'BOTH'
    Spont: 1
    Temp: 0
    SaveStim: 0
- stimcache <1x1 struct>
    loopvars: {'ITD' 'NONE'}
    nloopvars: 1
    ntrials: 22
    nreps: 10
    nstims: 220
    curvetype: 'ITD'
    stimtype: 'TONE'
    side: 'BOTH'
    spont: 1
    frozen: 0
    radvary: 0
    LeftON: 1
    RightON: 1
    tvec: [1x2441 double]
    trialRandomSequence: [10x22 double]
    rep: [220x1 double]
    Freq: {220x1 cell} #unsorted#
    ITD: [220x1 double] #unsorted#
    ILD: [220x1 double] #unsorted#
    ABI: [220x1 double] #unsorted#
    BC: [220x1 double] #unsorted#
    sAMp: [220x1 double] #unsorted#
    sAMf: [220x1 double] #unsorted#
    isspont: [220x1 double] #unsorted#
    splval: {220x1 cell} #unsorted#
    rmsval: {220x1 cell} #unsorted#
    atten: {220x1 cell} #unsorted#
    loopvar: [220x2 double] #unsorted#
    depvars: [22x10x2 double] #unsorted#
    depvars_sort: [22x10x2 double] #sorted#
```

\* curvedata <1x1 struct> : (varied paramters and spike timings/counts data are stored)

```
- depvars: [22x10x2 double] #unsorted#
- depvars_sort: [22x10x2 double] #sorted#
- spike_times: {22x10 cell} #sorted#
- spike_counts: [22x10 double] #sorted#
- isspont: [22x10 double] #sorted#
- cancelFlag: 0
```

\* curveresp <22x10 cell> : (waveform data are stored) #sorted#

**HINT:** "a(stimcache.trialRandomSequence(rep,trial), rep) = b" will give you sorted data.

## HPSearch2 binary data file (.dat2) structure (numbers shown are examples):

(How to read): [data, info] = TytoSpan\_readdat2('123.456.789.0123.ITD.dat2')

\* data <220x1 cell> **#unsorted#**

- loopvar: [ 100; NaN ]
- trial: 1
- rep: 1
- datatrace: (waveform data is stored)
- datatraceu: (unfiltered waveform data is stored)

\* info <1x1 struct>

- time\_start: 7.3511e+005
- time\_end: 7.3511e+005
- dataversion: 2.1000
- datafile: 'C:\AAA\BBB\123.456.789.0123.ITD.dat2'
- Fs: [4.8828e+004; 4.8828e+004] (= [inFs; outFS])
- stim <1x1 struct> : (same as .mat file)
- tdt <1x1 struct> : (same as .mat file)
- channels <1x1 struct> : (same as .mat file)
- analysis <1x1 struct> : (same as .mat file)
- animal <1x1 struct> : (same as .mat file)
- caldata <1x1 struct> : (same as .mat file)
- curve/click <1x1 struct> : (same as .mat file)
- stimcache <1x1 struct>: (same as .mat file)
- indev: [1x1 struct]
  - Circuit\_Path: [1x34 double]
  - Circuit\_Name: [1x31 double]
  - Fs: 4.8828e+004
  - Dnum: 1
- outdev: [1x1 struct]
  - Circuit\_Path: []
  - Circuit\_Name: []
  - Fs: 4.8828e+004
  - Dnum: 1
- complete: 0 (0: incomplete data, 1: complete data)
- nread: 205 (number of traces actually recorded)

**NOTE1:** All characters are stored as double (e.g., 'ITD' becomes [73 84 68]).

**NOTE2:** Three-dimensional arrays (e.g., depvars, depvars\_sort) are stored as two-dimensional.

## TytoSpan data file (.mat) structure:

- \* curvesettings <1x1 struct> : (parameter information is stored)
- \* curvedata <1x1 struct> : (varied paramters and spike timings/counts data are stored)
- \* curveresp <22x10 cell> : (waveform data are stored) **#sorted#**

TytoSpan recalculates nreps (number of repetitions) from .dat2 file to minimize unused repetition numbers. If the data is complete (recording is not aborted), then nreps = nreps\_orig. If the data is incomplete (recording is aborted), then the new nreps can be smaller than nreps\_orig. The basic structure of the TytoSpan output data is the same as HPSearch2 data (.mat) file, except for the additional data shown below:

- curvesettings.nreps\_orig (original number of nrep)
- curvedata.isactual: [22x10 double] **#sorted#** (flag to show if this is 'real' or 'dummy' data)