Forward masking model

The models described below can be used to replicate (hopefully) the results presented in the JASA article (2005):

A computer model of the auditory nerve response to forward masking stimuli.
By Ray Meddis and Lowel O'mard.

The model was created using AMS (Auditory Modelling System). If you wish to run the model you will need to download the appropriate modelling software. The software is evolving all the time but the version to be found here is the version used to evaluate the model as published in the article (version 1.1.7). If there are problems when running the latest version of the software, you might try to go back in time to this version.

If you have problems with these programs or require further clarification, please contact Ray Meddis (rmeddis@essex.ac.uk). If you are having difficulty with program execution, please zip up the folder you are using and attach it to your email. This can save 48 hrs of delay! Do bear in mind that some of the programs are stochastic and will give a different answer each time. hopefully the broad pattern of results will be maintained but the detail will usually be different.

The computer neural model is given by the *.sim* files *forwardMaskingSPIKE.sim* and *forwardMaskingPROB.sim* with associated *.par* files. You can run these by launching AMS and loading/running the chosen file. The SPIKE version computes individual spikes while the PROB version computes only the probability that a spike will be generated. Single-file versions of the model are present as .spf files.

While the models run in stand-alone mode, the simulations of experiments are controlled by MATLAB programs that invoke the model on each experimental trial with appropriate parameters. MATLAB version 6 or higher is required for this.

There are four main demonstrations controlled by MATLAB programs whose procedures are fully explained in the article. Make the folder the current directory before starting. There is no need to change the MATLAB path.

rate-level

This evaluates the rate-response of the model using tone pips of increasing level. This simulates the results shown in Fig. 2 of the article. The program computes the rate-level function for all three types of fiber and is activated using the command

```
rate_level
```

Two figures are produced:

1. The PSTH of the current stimulus. Note that the program computes a smooth probability function (not spikes which would be slower and add little).

2. The rate-level functions.

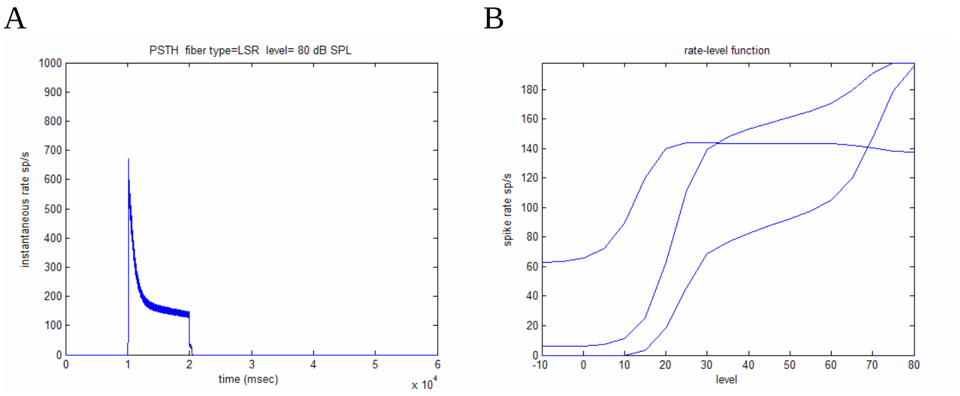


Figure A: PSTH, B: rate-level function for HSR, MSR and LSR fibers.

Forward masking

This evaluates the response of a single AN fiber following stimulation by a masker. This simulates the results shown in Fig. 4 of the paper. The response is computed as a spike probability. The programme is invoked by

```
forward_masking (<fiberType(string)>)
```

where fibertype is ‘HSR’, MSR’ or ‘LSR’. For example:

```
forward_masking (‘HSR’)
```

Two figures are produced:

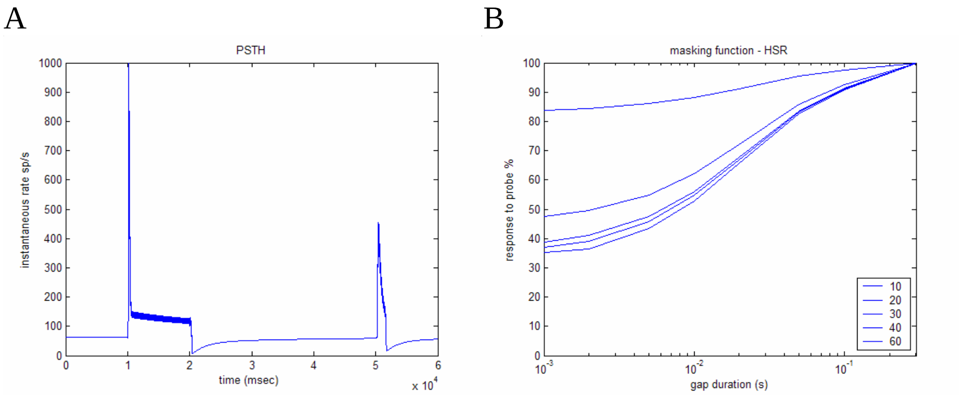


Figure A: PSTH of the single-fiber spike-probability response to the masker-gap-probe stimulus. B: forward masking recovery functions

allThresholdsRelkin

This simulates the experiment by Relkin and Turner featured in Fig. 8 of the paper.

The program is invoked as follows:

```
allThresholdsRelkin(<fiberType (string)>, <list of masker levels>)
```

For example:

```
allThresholdsRelkin('LSR', [ 0:10:90])
```

The result should be four figures:

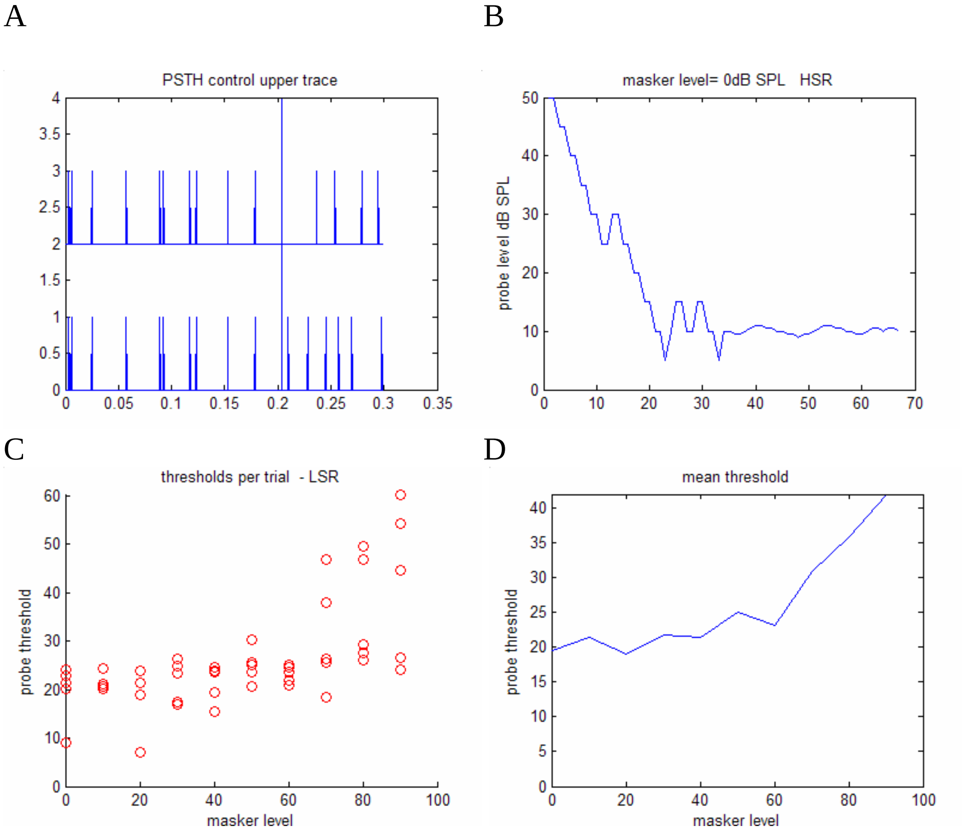


Figure
A: The PSTH for the current test. The upper trace is the AN fiber response to the maskere alone. The lower trace is the response to the masker followed immediately by the probe.
B: The Leavitt up/down path followed while computing the threshold.
C: The threshold obtained for each individual trial.
D: The mean threshold averaged across blocks.

allThresholdsCoincidence

This replicates the results shown in Fig. 9 in the paper. Masked probe thresholds are computed for a range of masker levels and masker-probe gaps. When testing this module, you can obtain the most satisfactory results using a mixture of LSR and HSR fibers. When HSR fibers are used in isolation, a threshold may not be obtained for 80 dB maskers and 5 msec gaps. This is because the fibers are unresponsive and may not produce consistent supra-threshold results even at the highest probe levels.

To invoke the model:

```
[thresholdSummary p allResults] = allThresholdsCoincidence(<fiber
   List>, <masker level list (s)>, <gap duration list (s)>)
```

where < *fiber List* > is a 3-valued vector specifying the number of HSR, MSR and LSR fibers.

`<masker levels dB>: use -100 to switch masker off.`

Example, (10 HSR and 10 LSR fibers):

```
[thresholdSummary p allResults]=allThresholdsCoincidence([10 0 10], [20
   40 60 80 -100], [.005 0.01 0.02  0.04 ])
```

Most of the parameters of the model are set in the program during initialisation and are stored in a cell array called ‘p’ (for parameters). *p* is returned with the results at the end of the program. If you add *p* as a fourth argument in the function call, your cell array *p* will be used rather than the program defaults.

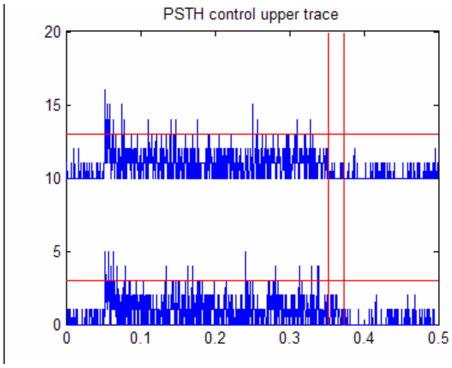
Example result (this run took about 5 hours on my laptop).

```
thresholdSummary =

30.2679  28.375   26.9821  25.3571
52.8571  43.2143  27.5714  26.1071
65.6607  54.7857  30.6429  24.375
82.5179  62.8571  57.625   30.875
21.9821  18.7857  19.2857  20.0893

p=
             numFiberList: [10 0 10]
          maskerLevelList: [20 40 60 80 -100]
          gapDurationList: [0.0050 0.0100 0.0200 0.0400]
     coincidenceCriterion: 3
                       BF: 4000
                  simFile: 'forwardMaskingSPIKE.spf'
         model_AN_latency: 0.0010
           maskerDuration: 0.3000
            probeDuration: 0.0200
    maskerIinitialSilence: 0.0500
             rampDuration: 0.0100
            totalDuration: 0.5000
```

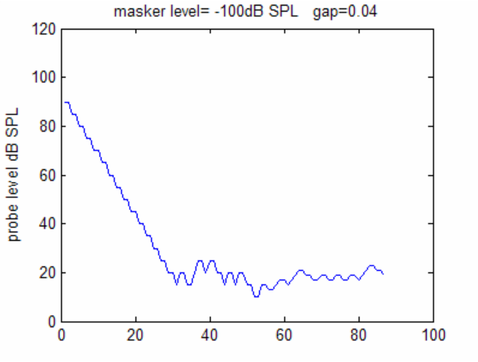
```
                  dt: 1.0000e-005
        PSTHbinWidth: 5.0000e-004
             nBlocks: 4
     startProbeLevel: 90
      startLevelStep: 5
    finalLeavittStep: 2
switchProbeStepSizeAt: 10
 maxLeavittSmallTurns: 14
     maxLeavitTrials: 200
simFileWithRepeatsHSR: 'HSR.spf'
simFileWithRepeatsLSR: 'LSR.spf'


5.8hours to complete

allResults =
{masker level (repl)   ?         gap(1)    gap(2)    gap(3)    gap(4)}
   20.0000    1.0000    0.0400   31.2143   28.1429   23.7143   27.1429
   20.0000    2.0000    0.0400   28.2143   31.9286   31.0714   26.2143
   20.0000    3.0000    0.0400   30.2143   27.5000   29.4286   22.6429
   20.0000    4.0000    0.0400   31.4286   25.9286   23.7143   25.4286
   40.0000    1.0000    0.0400   44.7143   46.8571   19.5714   24.5000
   40.0000    2.0000    0.0400   54.2143   55.7143   27.5714   27.7857
   40.0000    3.0000    0.0400   59.6429   40.9286   38.7143   24.0000
   40.0000    4.0000    0.0400   52.8571   29.3571   24.4286   28.1429
   60.0000    1.0000    0.0400   71.0714   52.7857   31.9286   25.5714
   60.0000    2.0000    0.0400   57.7143   54.5000   20.0714   24.2143
   60.0000    3.0000    0.0400   66.3571   53.7143   28.4286   24.6429
   60.0000    4.0000    0.0400   67.5000   58.1429   42.1429   23.0714
   80.0000    1.0000    0.0400   84.9286   58.5000   52.8571   32.7143
   80.0000    2.0000    0.0400   76.0000   60.3571   63.3571   33.8571
   80.0000    3.0000    0.0400   88.5000   61.3571   62.5714   28.4286
   80.0000    4.0000    0.0400   80.6429   71.2143   51.7143   28.5000
 -100.0000    1.0000    0.0400   23.1429   19.5714   20.9286   22.5000
 -100.0000    2.0000    0.0400   22.4286   17.6429   18.5000   19.0714
 -100.0000    3.0000    0.0400   22.0714   19.7857   19.7857   20.3571
 -100.0000    4.0000    0.0400   20.2857   18.1429   17.9286   18.4286
```

Five figures should result:

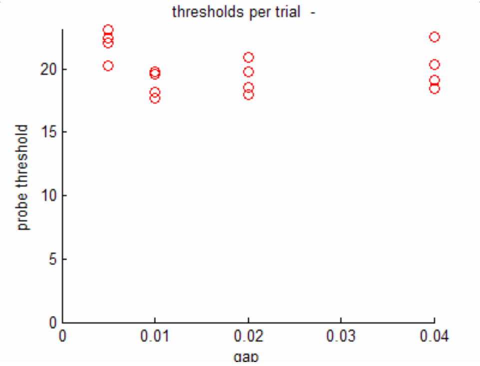
1



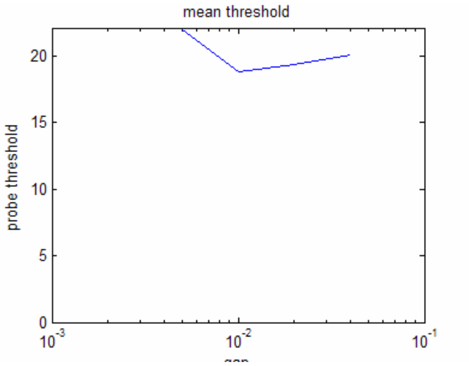
2



3



4



5

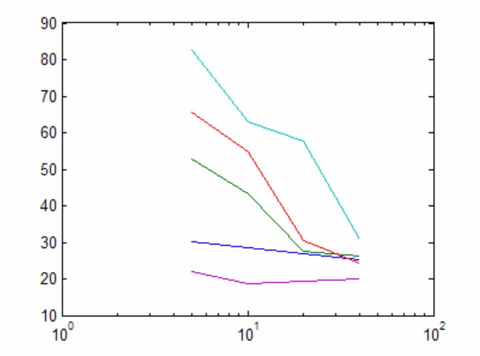
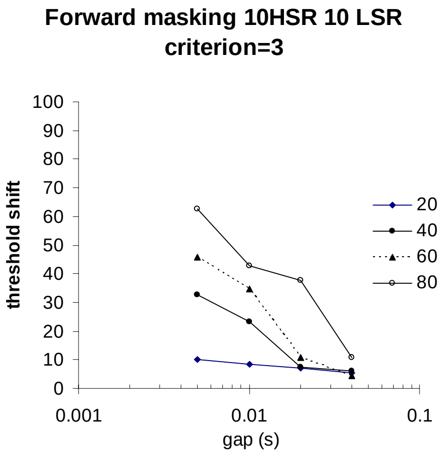


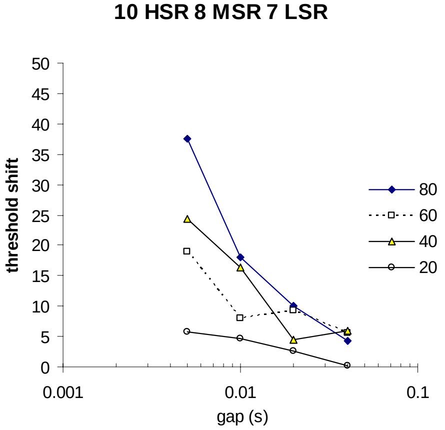
Figure
1. The PSTHs for the probe (lower trace) and the no-probe conditions.
2. The progress of the Leavitt threshold function.
3. The thresholds so far for this masker level.
4. The current average across blocks for the current masker level.
5. The mean thresholds (so far) across all masker levels and gaps.

The Excel spreadsheet in the folder contains the following sets of results.

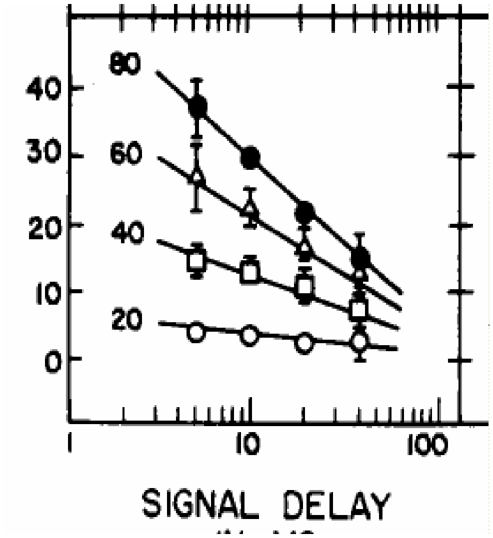
A



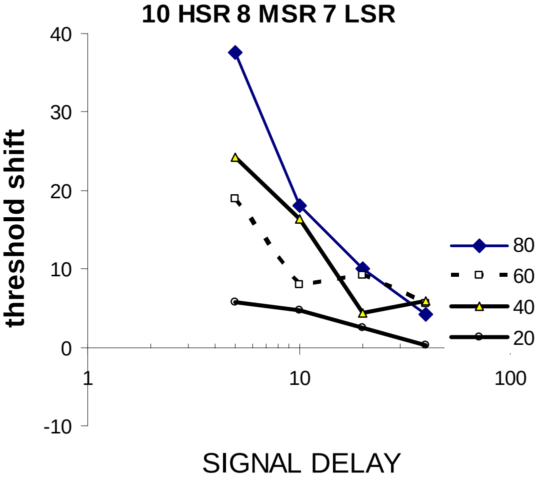
B



C



D



Absolute thresholds are 20 dB SPL. Note changes of scale. B is close to Jesteadt's results.

Replenish rate
The replenish rate (published as 3) can be changed by resenting the p cell array

```
p.REPLENISH_RATE=3;
```

This gives a more realistic results in the sense that the recovery functions do not meet at the 40 msec gap. This is at the expense of a severely reduced saturated firing rate for the HSR fiber. More research is needed!