Non-nutritive suck spatiotemporal index in preterm infants: NNS STI

J Wang & S.M. Barlow

University of Kansas

Lawrence, Kansas USA

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1   Part I Background -- Math Fundamentals

1.1   What is STI ?

STI: the spatiotemporal index. Mathematically, STI is the cumulative sum of the standard deviations (SD) for a set of trajectories. STI shows the stability of a sequence of movements. [1,2]

1.2   Data selection

The purpose of non-nutritive suck spatiotemporal index (**NNS STI**) is to compare the suck pressure control profiles among NNS bursts for comparative studies within and among preterm babies. This comparison is based on a set of selected bursts with fixed peak number. For example, for any individual comparison you make, if 5 peaks are selected for the 1st burst, then another 5 peaks must be for the 2nd burst, and always 5 peaks for all the other bursts in this comparison. Figure 1 shows the first 5 peaks from eight bursts, which are called eight trajectories. Selecting the same number of peaks from every burst is necessary to make different sets of trajectories comparable.
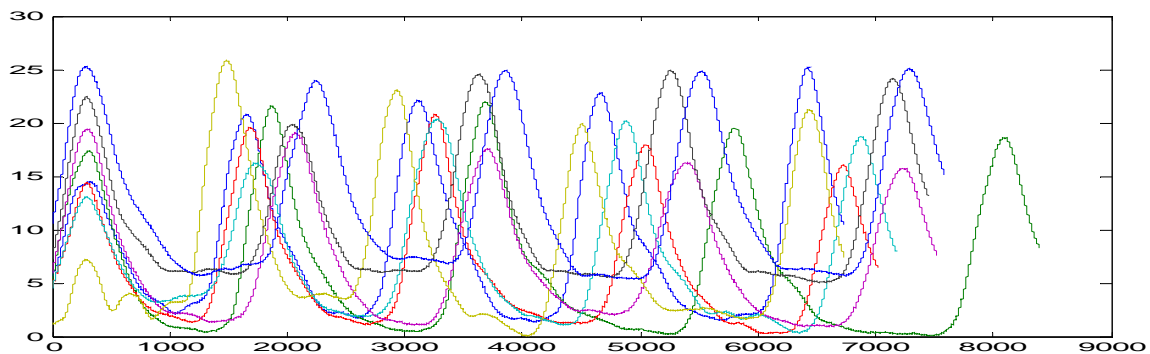

Figure 1: Original data plot

1.3   Data normalization

As shown in Figure 1, the five NNS peaks from different bursts have different length. How could we compare among trajectories with different length? In this section, we need to normalize different trajectories to the same length in order to match valley to valley, and peak to peak of different trials. Figure 2 shows the eight normalized trajectories based on the original data in Figure 1.

Important note: Due to the mathematical requirements of the normalization, the sample number after normalization has to be larger than the maximum non-normalized sample number. For example, in Figure 1, the maximum non-normalized data length is around 8500; while after normalization, all the data are lengthened to 10000.
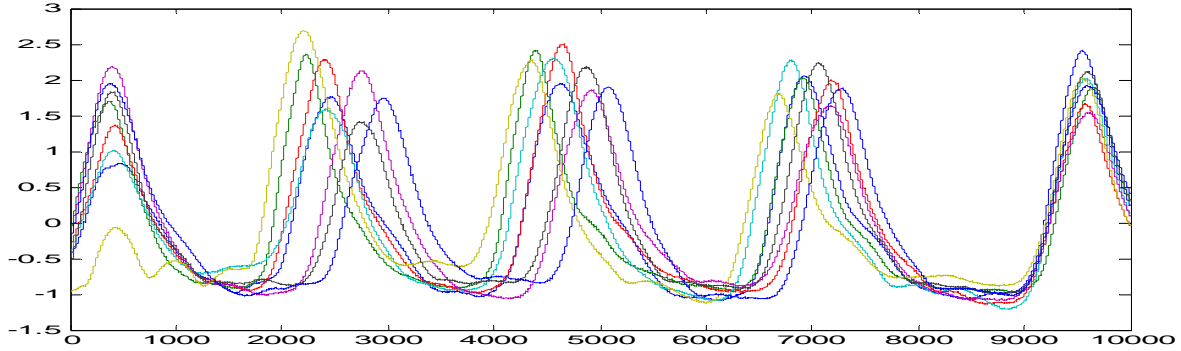

Figure 2: Normalized Data plot.

1.4   SD and STI calculation

Suppose we are given a population x_1, ..., x_N of values. The arithmetic mean of this population is defined as Eq. (1)

$$\overline{x} = \frac{1}{N}\sum_{i=1}^{N} x_i = \frac{x_1 + x_2 + ... + x_N}{N} \tag{1}$$

and the standard deviation(SD) of this population is defined as Eq. (2)

$$\sigma = \sqrt{\frac{1}{N}\sum_{i-1}^{N}(x_i - \overline{x})^2} \tag{2}$$

In our case, as shown in Figure 2, there are eight trajectories, thus an N=8. We will calculate the SD based on eight normalized pressure values for each sample point. 10000 SD values will be calculated for the normalized data. Figure 3 shows the original data, normalized data and standard deviation.

The STI value represents the sum of standard deviation. In order to keep STI simple and neat, we will add SD every 100 samples (which is named as STI step), instead of adding all 10000 SDs.
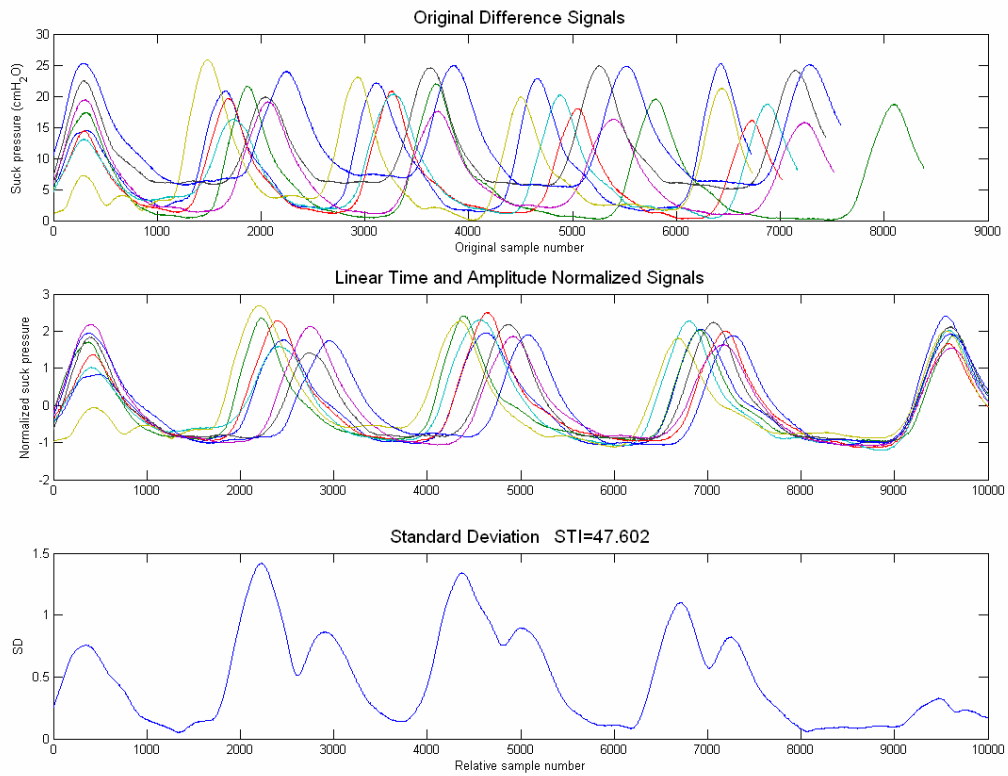
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Figure 3: STI Calculations for NNS skilled preterm infant.

Figure 3 is the STI analysis result for a preterm infant with good suck pressure patterning, with an STI=47.60. Figure 4 shows an example of poor NNS patterning sampled from a preterm infant with respiratory distress syndrome. In this case, the poor suck patterning results in an STI increase to 93.01.
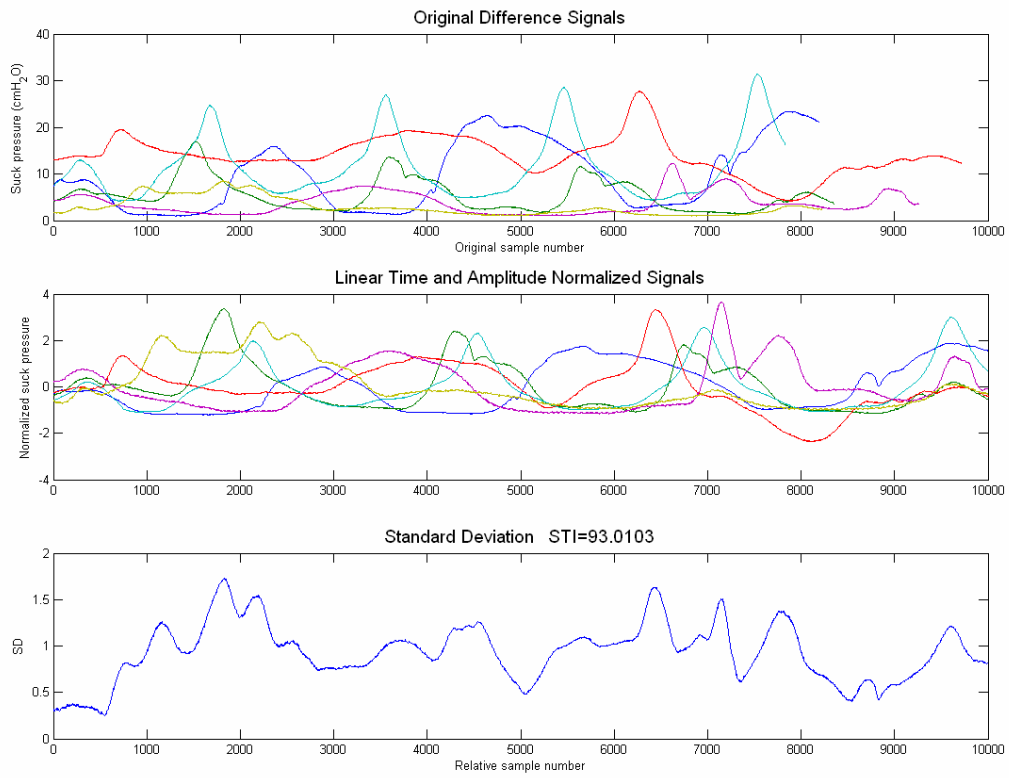
Figure 4:   STI Calculations for NNS impaired preterm infant.

2   Part II User manual

The NNS STI is programmed using LabVIEW. The plots in LabVIEW are hard to export to other file. If a pretty plot like Figure 3 or Figure 4 is desired, a MATLAB code (NormAndOrigPlot.m) needs to be called for STI calculation based on LabVIEW data file.

Important note: All blue are inputs that user needs to tune to do the STI data selection. All purple text are outputs that user needs to keep in mind for data processing thereafter.

2.1   Step 0 Data preparation

The input suck pressure files for NNS STI are ∗.txt file generated from NeoSuck *RT*. Before running NNS STI, suck pressure in blocks should be ready. In **NeoSuck *RT***, go to **Tools**, and then click **Create ASCII Blocks**.

2.2   Step 1 Peak detection

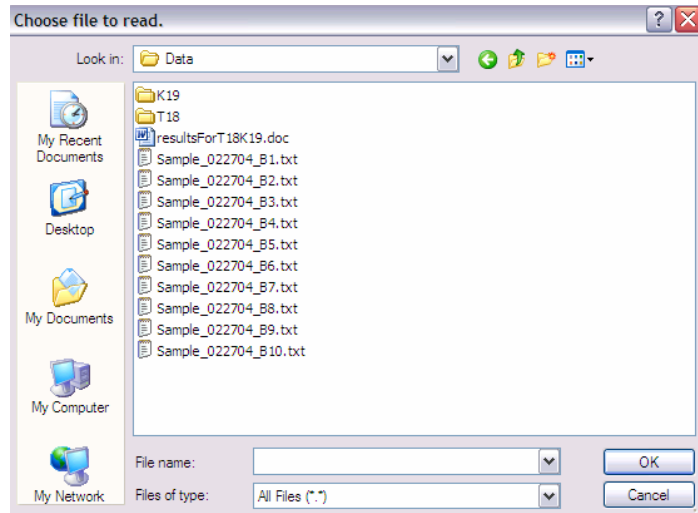Once the NNS STI is opened, the Choose file dialog will pop up for your first block selection.

Figure 5: Choose File Dialog.

After the block is chosen, this block of suck pressure is showed in "Block Suck Pressure" plot. The red line cursor need to be tuned (the red line could be dragged up and down) in order to select the right peaks we want. All recognized peaks are marked by yellow dot.
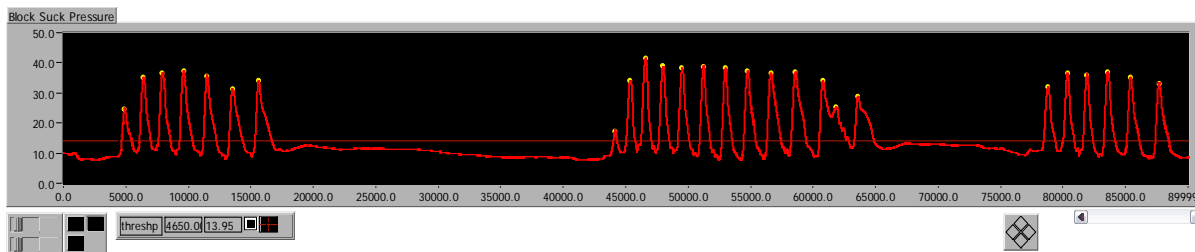
Figure 6: Block Suck Pressure Plot in LabVIEW

2.3   Step 2 Burst detection

Bursts are recognized by setting the distance from the last peak position of the first burst to the first peak position of the next burst. User needs to change the INPUT -- Sample number for distance between bursts until the OUTPUT -- Number of recognized bursts in current block shows the right burst number, if it doesn't display the correct burst number.

2.4   Step 3 Peak shoulder detection and deletion

Peak with peak shoulder looks like the second peak shown in Figure 7. If the distance from peak to its should is less than INPUT -- Sample number from peak to its shoulder, the shoulder will be deleted. For example, the first plot in Figure 7, which the input sample distance set as 300, shows the shoulder as a peak. While in the second plot, the distance is increased to 900, all the shoulders are deleted.
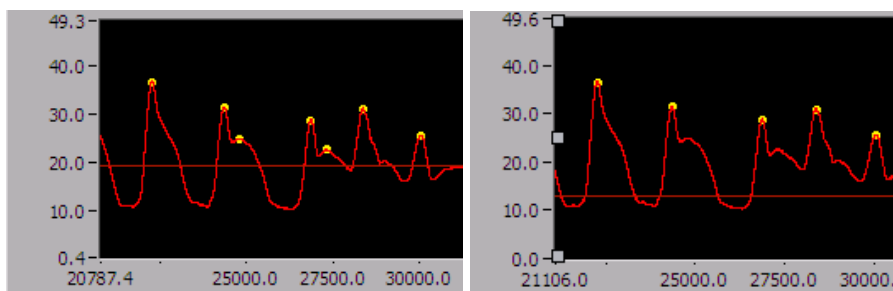

Figure 7: Peaks with Peak Shoulder (left) and Peaks with Peak Shoulder Deleted (right).

2.5   Step 4 Select burst and peaks for SD

Up to now, all the peaks without shoulder and bursts should both be recognized exactly as what user wants them to be.

Remember our SD processing is based on a set of bursts with same peak number. Now it's time to INPUT -- Select burst, and define INPUT -- Select how many peaks you want to compare.

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Normally, INPUT -- Start to 1st Peak doesn't need any tuning. It is defined to set the beginning point of the current burst.

After you input everything, a selected burst with desired peak number will be plotted in "Selected peaks in current burst" as shown in Figure 8.
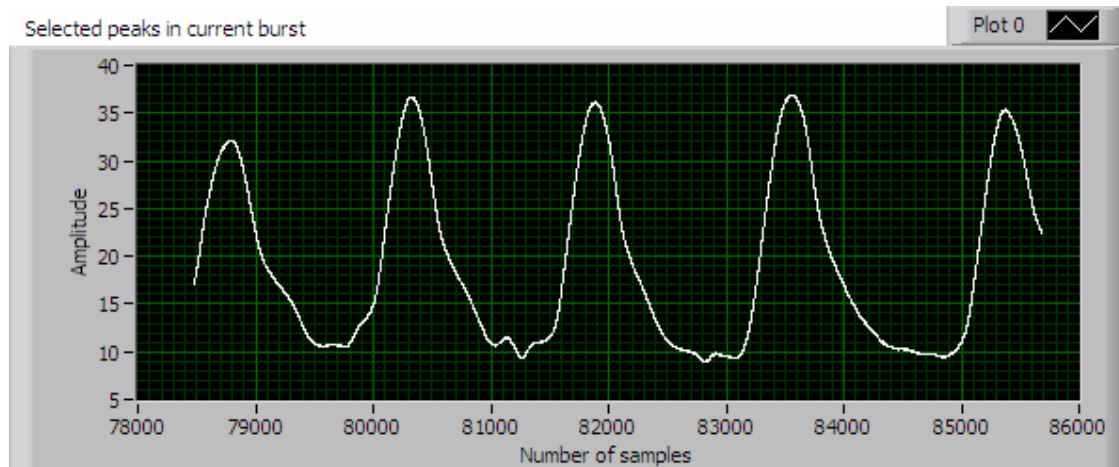

Figure 8: Current Data Selection

OUPUT -- Selected length for comparison must be less than INPUT-Number of points after normalization in step 5 in order to satisfy the mathematical requirement of normalization.

Important note:

- INPUT -- Select burst will be changed every time a new burst is selected; while INPUT -- Select how many peaks you want to compare will keep unchanged for this whole STI processing.

- OUPUT -- Selected length for comparison < INPUT-Number of points after normalization in step 5.

Up to now, a first trajectory selection is finished. The next trajectory will be started by press "Next" (as in Figure 9) button at the right upper corner in Step 1. Even you are selecting the next burst in the same block; you also need to re-select this block file. Then Step 1, Step 2, Step 3 and Step 4 will be repeatedly tuned to get desired data. While there is a trick here, if you are trying to select different bursts from the same block, the only input you need to change is INPUT -- Select burst in step 4.

Figure 9: Next button for starting next burst selection

2.6   Step 5 SD and STI calculation

Again, INPUT-Number of points after normalization (the default is 10000) has to be always larger than OUPUT -- Selected length for comparison in Step 4. Figure 10 shows an example of accumulated five trajectories from LabVIEW.
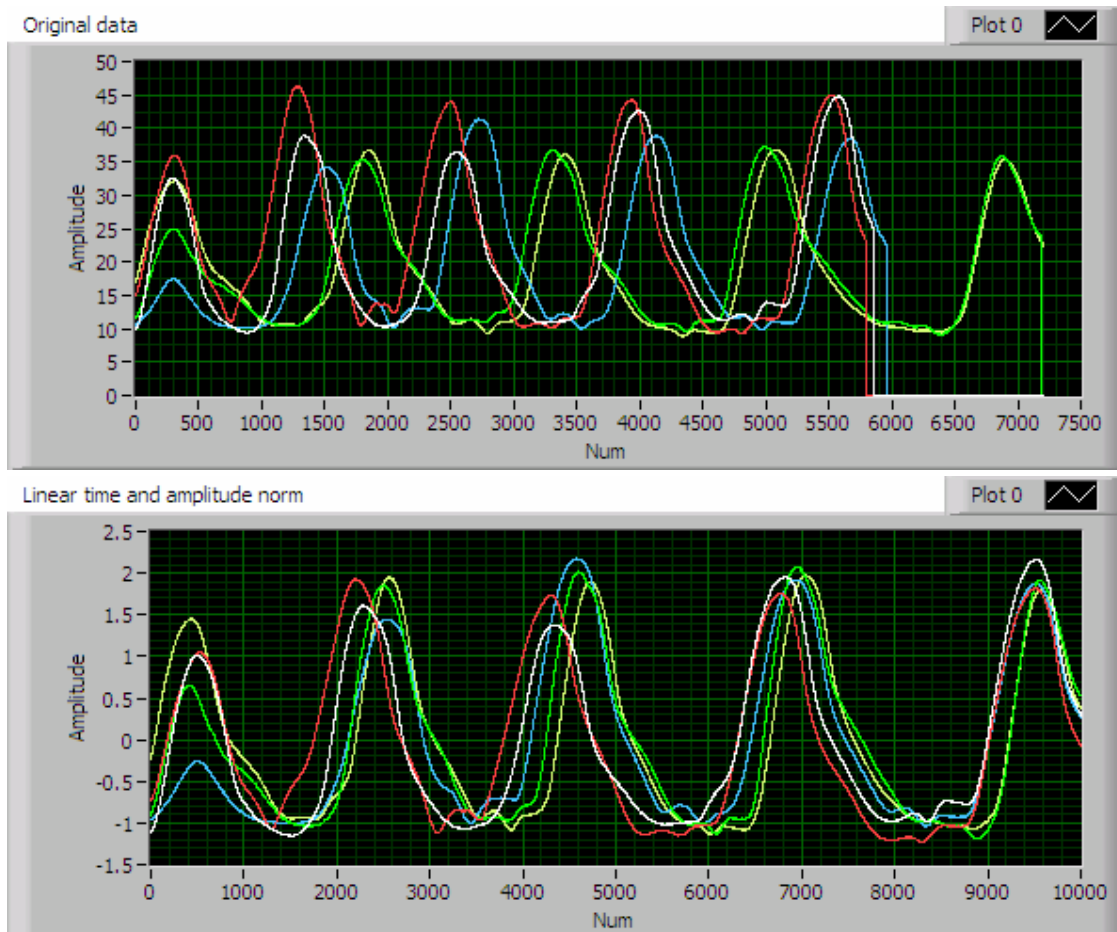

Figure 10: Plots of Original Data and Normalized data

Remember we said in Part I—SD and STI calculation, that in order to keep STI simple and neat, we will just add 100 of 10000 SD values (as in Figure 11). INPUT-SD Step is for picking one SD value for every SD Step samples to add to STI value. Normally this value does need any tuning if the normalized sample points are 10000.
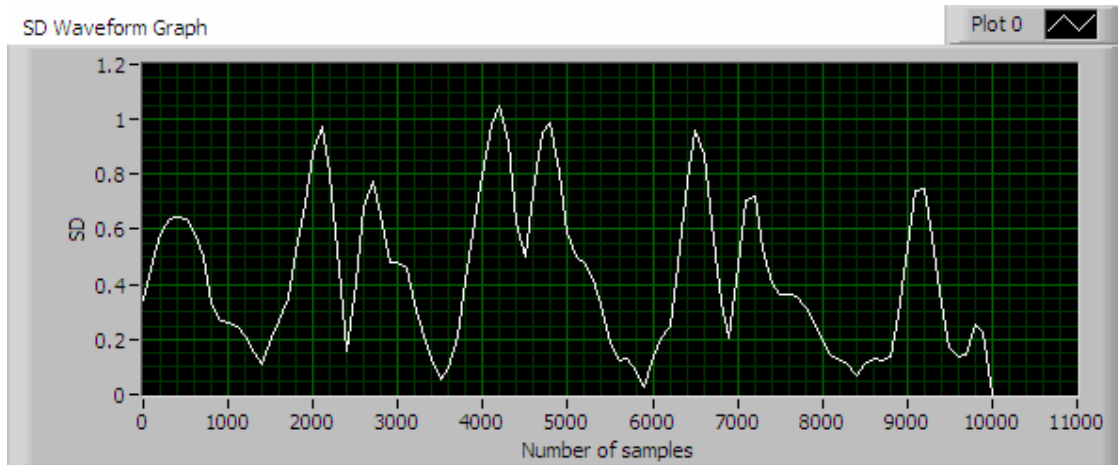
Figure 11: SD Plot with 100 Sample Points

OUTPUT-STI Value showed current STI value after the last burst selection

Normalized Data File Path and Original Data File Path set the path and file name for data file in Figure 10. Those data files are used for pretty processing in MATLAB as well as keeping a data file record for your STI processing.

Figure 12: STOP button

The "STOP and SAVE DATA" button (as in Figure 12) is for stopping the whole program and saving data.

3   References.

[1]   Smith, A. and Zelaznik, H. N. (2004). Development of functional synergies for speech motor coordination in childhood and adolescence. *Dev Psychobiol*, 45:22-33.

[2]   Smith, A., Johnson, M., McGillem, C. and Goffman, L. (2000). On the assessment of stability and patterning of speech movements. *Journal of Speech, Language, and Hearing Research* 43:277-286.

[3]   Poore M, Barlow SM, Wang J, Estep M. (2006). Spatiotemporal index of the human suck in premature infants with a history of severe respiratory distress syndrome. In preparation for *J Early Human Development*.