P2.5. VEP Spectral Bands For Detecting Alcoholics
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We propose using Visual Evoked Potential (VEP) signals to detect alcoholics. The
studies show that the VEPs of subjects with alcoholism have different spectral
characteristics from those of normal subjects. The VEPs of normal subjects have a
peak at around 100 ms after the stimulus, whereas the VEPs of alcoholics have a
peak at around 200 ms after the stimulus. The difference in the peak times can be
used to discriminate between normal subjects and alcoholics with a high degree of
accuracy.

P2.6. Remote Management Of Patient Care Through Wireless Devices And The Internet
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A real-time health care system has been developed for home-bound patients. It
takes advantage of the Bluetooth wireless communication and Internet
infrastructure. The system includes a microcontroller-based sensing device, a
junction box (VitalPol) and a master control laptop computer. The sensing device
can acquire 4 independent channel vital signals from a patient. The sampling rate
is up to 40KHz and the resolution is 12 bits. The VitalPol is also microcontroller-
based with a Bluetooth card integrated. The master computer contains another
Bluetooth card and is connected to the Internet. The VitalPol collects the
patient's vital signals from the sensing device and routes them to the laptop
through using Bluetooth. The VitalPol contains several RS232, USB and
PCMCIA interfaces so that it can be connected to a host of other medical
devices. DSP was also used to process the signal. System analysis and
management software is developed to parse, monitor and control the sensing
device and the VitalPol. Such a system of devices permits the physician the
ability to manage a patient remotely through the Internet. Patient records can be
stored in database for further analysis and diagnosis. This work was partially
funded through a grant from NASA.

P2.7. Modeling Long-Term HRV And Number Of Degrees-Of-Freedom Of Autonomic Dynamics At SA Node
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Simulations of the dynamics of fluid turbulence and heart rate variability (HRV)
of healthy subjects suggest a cascade mechanism underlying the long-term heart
rate fluctuations. The phase-to-beat interval known as the RR interval (RII) is thus
modeled as the product of 3 cascade components: \( r(t) = \pi_1 \exp(\omega(t)) \) where \( \omega(t) \) is a
gaussian process with mean \( \mu \) and variance \( \sigma^2 \). From the refractory property of
the heart muscle cells, a bounded cascade is assumed. It is sufficient to impose
\( \sigma(t) < \sigma \) for this purpose. The scale invariance of HRV is modeled by allowing
\( \omega(t) \) to vary in dyadic times \( t, (t+1) \) with \( \delta \) = \( t, (t+1) \) \( \leq 2^N \) and \( N \) is the
number of points. We constructed the log-process: \( \gamma(t) = \log(\sigma(t)) \) and its
increment \( \Delta \gamma(t) = \gamma(t+1) - \gamma(t) \) where \( \tau \) is an arbitrary interval. It is shown
that \( \Delta \gamma(t) \sim \log(\omega(t)/\omega(t+1)) \) and thus \( \sigma(t) \) can be estimated directly from the
measured data \( r(t) \). Moreover, bounded cascade is unique in that the product
\( r(t) = \prod_{i=1}^{N} \omega(t+i) \) will reach a limit in large \( N \). This property together with the
known number of cascade components are required to reproduce the HRV pattern.
Considering \( \omega(t) \) as the degree-of-freedom (DOF) in dynamical system term, the
limiting \( \Delta \) defines the "dimension" of the autonomic dynamical system at the
sino-atrial node. Based on the absolute moment of the increment process,
\( \Delta(t) = \exp(\Delta \gamma(t)) \), the asymptotic model is found when \( \Delta \to 1 \) (Figure 1).

P2.8. The Influence Of Metatarsophalangeal Joint On Gait Pattern And Corresponding Compensatory Strategy
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Up to now, the influence of flexion of metatarsophalangeal (MP) joints on gait and
their corresponding compensatory strategies taken by subjects when their MP joints
are flexed have not been reported. To make it clear, it will be useful for physical
therapy, prosthesis design and gait planning for bipedal. The purpose of this study
is to investigate the effect of flexing MP joint on gait pattern and the responses of the subjects when their MP joints
are flexed. Five healthy young subjects were instructed to walk at their preferred
speed on level pathway with and without MP joints flexion, which were
accomplished by constraining MP joints using two specialized shoes with
high sole stiffness and some bandages. The apparent differences can be seen
between the angular displacements and velocities of each joint for subjects with
and without constraint, but the experiment differences were found about the shape
of motion of hip and ankle joints except for knee. When the MP joints are
constrained, the other joints will make some compensatory efforts. Apparent
multi-joint coordination motion compensatory strategy is employed when the
MP joints are constrained, which means that the hip, knee and ankle joints make
corresponding compensatory efforts. But their compensatory contributions are
different: the knee and ankle joints do dominate compensatory functions. Due to
the contributions of all joints, the subjects with constrain of MP joints can also
walk in a gait pattern close to the normal. The variation of average speed and
stride length are less than 5%.

P2.9. The Hierarchical Collective Motions Method: Simulations Of Large Molecules
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Several obstacles stand in the way of performing atom-level computer
simulations of biological macromolecules. First of all, the large number of atoms
and the need for high accuracy make the simulations extremely computationally
intensive. Second, large molecules are highly dynamic and characterized by multiple time scales spanning many orders of magnitude.
Unfortunately, most of the interesting phenomena take place over the course of
the long time scales, while the timescales are of the order of the small time scales.
Most of the interesting interactions of biomolecules involve a few slow, large-scale collective motions of many atoms. If these
interactions are not properly modeled, the simulations will fail. In this study, we
have devised a new method, called the Hierarchical Collective Motions (HCM)
method, to extract this information. It consists of running short simulations on small, overlapping segments of the molecule,
then analyzing the resulting information, eliminating small, uninteresting motions, and defining a new set of variables. Next, the
segments are joined into larger and larger segments, and the information from the previous simulations is used to
new simulations at the coarser level. The analysis, elimination, and
renormalization procedure is repeated until only one segment, encompassing the
whole molecule, remains. Results obtained from simple model systems will be
presented.

P2.10. Metabolic Pre-Conditioning Of Cultured Cells: Generating Resistance To Detrimental Effects Of Plasma
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Understanding the regulation of hepatic lipid metabolism is important for several
biotechnological applications involving liver cells. For example, hepatic-based
liver devices are exposed to patient's plasma or blood. Thus, maintaining a stable hepato-cellular function during plasma exposure is critical to the successful development of liver assist systems. Previously, we found that hepatocytes exposed to plasma accumulate intracellular lipids and exhibit a decline in the expression of liver specific functions. Second, the effect of insulin pre-conditioning and amino acid supplementation on the accumulation of lipids and the expression of hepatic specific functions of rat hepatocytes exposed to plasma. While hepatocytes cultured in high insulin (500 pg/mL) medium accumulated large quantities of triglycerides during subsequent plasma exposure, culture in low insulin (50 pg/mL) medium markedly prevented lipid accumulation, but without insulin, but increased with amino acid supplementation. Thus, hepatic lipid metabolism during plasma exposure can be modulated by medium pre-conditioning and supplements added to plasma. Metabolic flux analysis was used to quantify the changes in lipogenic fluxes and pathways within the cells in response to pre-conditioning and amino acid supplementation. We found that low insulin pre-conditioning increased lipid oxidation through the TCA cycle, which was enhanced with amino acid supplementation.