

Fourier transform methods provide a number of advantages over scanning methods in spectroscopy. Please provide brief answers to the 4 of following questions in **Part A** and 4 of the questions in **Part B**.

Part A. Answer 4 of the following 6 questions:

(1) Name two advantages Fourier methods have over scanning methods.

- 1. Throughput or Jacquinot advantage: Sample is excited with multiple frequencies simultaneously.**
- 2. Multiplex or Fellgett advantage: all frequencies are detected simultaneously.**
- 3. High wavelength accuracy and precision.**

(2) The time between data points in the acquisition of time domain data is often called the "dwell time." What effect on the Fourier transformed spectrum does this time have?

The spectral width.

(3) What characteristic of the Fourier transformed spectrum does the total data acquisition time affect?

The resolution. (also accepted signal to noise ratio as correct).

(4) What are the effects on the experimental measurement of choosing an acquisition time that is too short?

The data is often truncated, which can degrade the signal to noise, and introduces spurious frequencies into spectrum.

(5) Why might you want to multiply time domain data by a decaying exponential function before taking the Fourier transform?

This increases signal to noise at the small expense of some line broadening.

(6) Can you think of a way to increase the resolution of a spectrum using the same (i.e., without taking new) data?

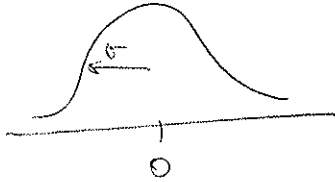
Add additional zeros to the data, doubling or quadrupling the length of the data set before Fourier transformation (this is called zero filling).

Part B.

For 4 of the 6 following waveforms, give the (real or cosine) Fourier transform. Label the waveform that you have drawn. Make your drawings as accurate as possible.

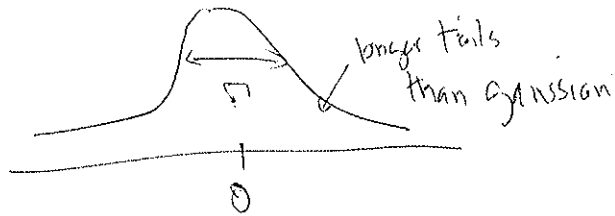
1. Gaussian

FT is also a Gaussian



2. Exponential decay

Lorentzian line shape

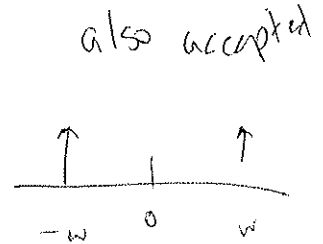
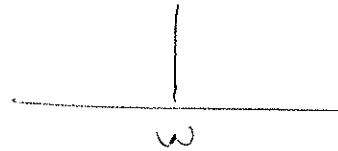
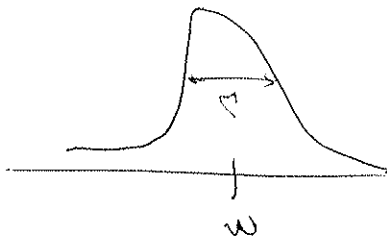


3. Exponentially decaying cosine

4. Cosine

Lorentzian line shape centered at frequency ω of cosine function

Delta function centered at frequency ω of the cosine function

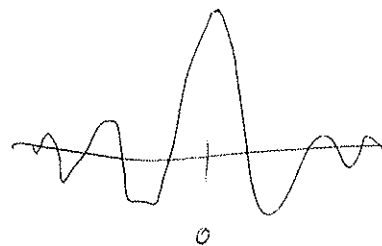
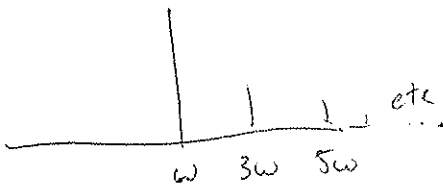


5. Square Wave

6. Rectangular Pulse

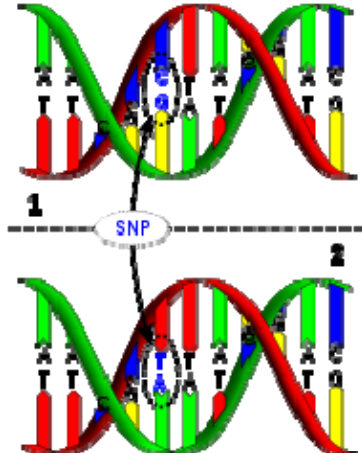
Series of delta functions at $\omega, 3\omega, 5\omega$ of square wave frequency.

Sinc function ($\sin x/x$)



CRIB: Biochemistry Cume, February 14 (2009)

1. SNP is a single change (mutation) at a specific sequence in the genomic DNA derived from a given species (for example humans). SNPs correspond to a collection of such mutations in genomic DNA. **(10 points)**



2. In genomic DNA, exons encode the sequence of amino acid in proteins. Each amino acid is encoded by one or more codons (3 consecutive bases). Informative SNPs in exons correspond to mutations that would change the amino acid sequence of a protein at specific position(s). In some cases, a SNP produces a stop codon in DNA. Such SNPs would lead to production of incomplete proteins during protein synthesis.

Since the genetic code is degenerate, a mutation does not necessarily produce a change in the amino acid sequence of a protein. Such mutations, known as "synonymous or silent mutations", are not informative. **(20 points)**

3. Examples include mutations in regulatory signals dispersed in control segments in genomic DNA. **(10 points)**

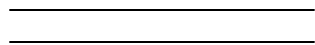
4. In their simplest form, DNA microarrays consist of thousands and thousands microscopic spots of deoxy-oligonucleotides, synthesized on and attached to a matrix (usually glass). The sequenced human genomic DNA is used as a reference for automated chemical synthesis of the deoxy-oligonucleotides on the matrix. Therefore, in DNA microarrays, the DNA sequences in the spots are derived from the reference human genomic DNA. The spots are designed to cover the "unique" sequences that appear in the reference human DNA.

In the experiments, the DNA from an individual is isolated and amplified. Labeled amplified DNA is then hybridized to the DNA microarrays, under optimized conditions. Hybridization to the microarrays would produce signals that are detected and analyzed by automated systems. **(20 points)**

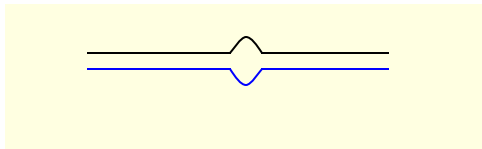
5. (A) DNA hybridization provides a measure of similarity between sequences derived from two different sources. DNA strands with complementary bases will hybridize (will form hydrogen bonds), producing stable double-stranded DNA. Mutated DNA does not form a stable duplex with the target DNA (i.e. DNA in microarrays).

(B) Differences in DNA stability provide the basis for identifying SNPs. If the DNA sequence in a person has one mismatch with the reference DNA, the mismatch defines a mutation (a SNP). Mutated DNA will not form a stable duplex with and hence will not hybridize to specific DNA spots in microarrays. Therefore, mutated sequences will not produce a signal.

(20 points)



Stable



Unstable

6. Over the past decades, evidence has emerged indicating that a substantial portion of variability in drug response is genetically determined. Furthermore, many common diseases in humans are not caused by sequence variations within a single protein (i.e. within a single gene) but arise as a consequence of abnormalities in sequences of several proteins (i.e. several genes). By identifying DNA sequences that harbor SNPs associated with a disease, researchers can begin to identify the proteins and biochemical pathways that might be relevant to understanding the molecular basis of that disease. However, often, only a subset of SNPs may appear in an individual. Consequently, variations within subsets may influence the severity of a disease in human populations.

Furthermore, because of the complexity of combinatorial variations in sequences, individuals may differ in their response to therapeutic agents. Additionally, because of these variations, some individuals may experience adverse side effect to a drug while others might not. In individualized medicine, SNPs are often classified according to protein molecules and hence biochemical pathways that the variations might affect. These classifications are used to determine why individuals may differ in their ability to absorb or clear certain drugs, and to determine why an individual may experience an adverse side effect to a particular drug.

(20 points)

--Answer Key--

**Inorganic Chemistry Cumulative Exam
Purdue University**

Saturday, February 14, 2009

A special exam on hearts and blood for Valentine's Day

- 1A.** Fe in a porphyrin ligand (4 N donors, conjugated, etc.)
1B. Fe^{2+} binds O_2 , then there is a valence tautomerism to an $(\text{Fe}^{3+})\text{--}[(\text{O}_2)^{\cdot-}]$
- 2A.** An Fe_2 center. Both Fe's are Fe^{2+} prior to O_2 binding and Fe^{3+} afterwards, while the O_2 is reduced to $(\text{O}_2)^{2-}$.
2B. A Cu_2 center. Both Cu's are Cu^{1+} prior to O_2 binding and Cu^{2+} afterwards, while the O_2 is reduced to $(\text{O}_2)^{2-}$.
- 3A.** Porphyria
3B. People are unable to place Fe into porphyrins.
3C. Iron supplements
3D. Just some of the many examples: A porphyrin without a metal generates singlet O_2 upon exposure to light. This singlet O_2 is very reactive, toxic, and painful. So people do not want to be exposed to light. So they sleep in boxes (or coffins), wear capes, only come out at night, etc.

No Organic Cume Crib for February 14, 2009
Written by Professor Wei

No Physical Cume Crib for February 14, 2009
Written by Professor Wasserman