CHE 597I: Optimization in Biological Systems
Fall 2004

Instructor: Costas D. Maranas
Office: 112 Fenske
Phone Number: 863-9958
E-mail: costas@psu.edu
Classroom: 101 Fenske
Class Schedule: TR, 1:00-2:15pm
Office Hours: open

Useful Textbooks (suggested):
1. "Optimization in Operations Research," R.L. Rardin, Pearson Education, 1st Ed., (1997).
2. "Systematic Methods of Chemical Process Design," Biegler, L.T., I.E. Grossmann and A.W. Westerberg, & Prentice Hall, (1997)
3. "Engineering Optimization, Methods and Applications", G.V. Reklaitis, A. Ravindran and K.M. Ragsdell, & Wiley, (1983)
4. "Nonlinear and Mixed--Integer Optimization", C.A. Floudas, Oxford Press, (1996)
5. "GAMS: A Users Guide", A. Brook, D. Kendrick and A. Meeraus, The Scientific Press Series, (1992)
6. "Metabolic Engineering : principles and methodologies," G.N. Stephanopoulos, A.A. Aristidou and J. Nielsen, Academic Press, (1998).

Prerequisites:
Basic understanding of linear algebra and working knowledge of a programming language. Contact instructor for more details.

Homework:
Regular homework assignments will be handed out almost every week.

Exam Policy:
One exam close to the end of semester.

Project:
Each student team will be asked to apply the optimization tool that they learned on a particular problem of their choosing, submit a report on the results and present their work in class.

Paper critique:
Each student team will be asked to review/critique one journal paper and present their conclusions in class.

Grading Breakdown:

Homework	20%
Exam	30%
Paper critique	20%
Project	30%

Course Description:
This course will focus on the introduction of fundamentals and applications of mathematical optimization in biological systems. The first part of the course will address optimization theory, solution algorithms and

implementation software. Topics to be covered include nonlinear optimization, linear programming, mixed-integer linear and nonlinear optimization as well as stochastic methods. Emphasis will be placed on understanding the logic of the methods, the key assumptions that underlie them, their comparative merits and shortcomings, and how they can be applied for solving engineering problems. Valuable hands-on experience will be provided on coding optimization models by using the modeling environment GAMS and specialized optimization solvers such as MINOS and CPLEX. The second part of the course will focus on the application of these tools to protein and metabolic engineering problems. Specifically we will address the protein folding problem and protein redesign strategies as well as optimal modifications in metabolic networks for various bioengineering tasks.

Tentative Syllabus:

1. Introduction
    - Historical Perspective
    - Basic Definitions
    - Linear Algebra Overview
    - Convexity Analysis

2. Unconstrained Nonlinear Optimization
    - Optimality conditions
    - Newton's method
    - Truncated Newton's method
    - Quasi-Newton methods (e.g., BSGS)

3. Linear Programming, LP.
    - Formulation
    - Simplex method
    - Examples

4. GAMS (General Algebraic Modeling System)

5. Mixed-Integer Linear Programming, MILP.
    - Formulation and examples
    - Modeling with binary variables
    - Branch and bound solution methods

6. Constrained Nonlinear Programming, NLP.
    - Optimality conditions, KKT

7. Mixed-Integer Nonlinear Programming, MINLP.
    - Formulation challenges
    - Outer Approximation, OA

8. Stochastic Methods
    - Simulated Annealing, SA
    - Genetic Algorithms, GA

9. Optimization Applications in Protein Systems
    - The protein folding problem
    - Protein redesign/optimization
    - Protein docking

10. Optimization Applications in Metabolic Networks
- Performance limits of metabolic networks and gene additions
- Optimal gene knock-out strategies
- Analysis of topological properties