Computational Toxicology

The application of computer technology and mathematical / computational models to analyze, model and/or predict potential toxicological effects from:

- Chemical structure (parent compound or metabolites)
- Inference from similar compounds
- Exposure, bioaccumulation, persistence (biomonitoring data)
- Differential indicators or patterns related to exposure
- Networks of biological pathways affected by the chemical

Environmental Pollutants

Therapeutics

To further understand mechanisms of toxicity: by organ, organism, and/or disease specific relationship

To explain why certain individuals are more susceptible to toxic insults

Highlight points:

1. 150 students – over 5 years
2. 4 hr credit course
3. Individual projects
4. Independent study
5. Honors research
6. Internships at FDA

Key methods

- Chemical fragment or structural similarities (structural alerts)
- Categorization or grouping
  - Analogs, categories based on mechanism, mode of action
- QSARs
- Biological pathway perturbations

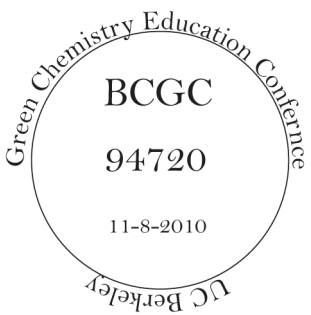
Information about the curriculum:

- **Tool Box Creation**
  - A combination of free on-line resources and commercial software
  - Converting chemical and biologic data into usable formats
  - Student proficiency exercises
- **Environmental or therapeutic challenge**

  2010 student example
  - Create *in silico* methods to identify and prioritize chemicals of concern that may increase the risk of human breast cancer
  - Solve chemical disease-related issues in new ways
- **Tutorials and resources**
  - Toxicology tutorials for non-toxicology majors
  - Software tutorials and user manuals
  - Extensive links to software, datasets, environmental and chemical information
- **UC Berkeley computer laboratory**
  - College of Natural Resources; Geospatial Innovation Facility (GIF); Mulford Hall
  - Full administrative and technical support

Notes

- Current developing practices for filling data gaps has long history with validation
- Physico-chemical properties accurately predicted
- Databases linking chem-biol interactions are limited in scope and size
  - Genotoxicity linked to carcinogenicity generally accurate predictions
  - Non-genotoxic carcinogenicity more complex
- QSARs always limited by applicability domain (chemical space) of training sets
- Interactions with bio-pathways important to identify targets and mechanisms



Dale E. Johnson, PharmD, PhD
UC Berkeley
Department of Nutritional Science and Toxicology
233 Morgan Hall
Berkeley, CA 94720

510-316-1197
daleejohnson@sbcglobal.net

Where to find resources:

Toxicology Tutorials
http://sis.nlm.nih.gov/enviro/toxtutor.html

National Center Comp Tox
http://www.epa.gov/ncct/

European Comp Tox
http://ecb.jrc.ec.europa.eu/qsar/