Contents

1 What is Biostatistics?
3 Degrees Offered
4 Programs Offered / Requirements
4 Master of Science and Master of Public Health Programs
   Requirements of the Master’s Program
   Selected Course Plans
   Joint Master’s Programs
6 The PhD Program
   Requirements
   Selected Course Plans
   Candidacy and Dissertation
12 Interdepartmental Concentrations
14 Admission
16 Financial Support and Tuition
17 Courses
23 Faculty
Graduate study in biostatistics prepares students for a wide variety of careers that involve the application of statistical and mathematical methods to the design and analysis of health, biomedical, and biological studies. Career opportunities for individuals with master’s and doctoral degrees are found in government, pharmaceuticals and other private industries, medical research institutions, and universities. A doctoral degree in biostatistics also prepares the students for a teaching position at a university. There is a very strong demand for graduates of biostatistics programs, and graduates of our program routinely have their choice of a variety of attractive job offers.
Biostatistics concerns the development and application of statistical and mathematical methods to the design and analysis of studies in public health, biological, and biomedical research.

To contribute to the discovery and use of knowledge in the health field, a biostatistician must have considerable knowledge of health problems and of statistical techniques, including their theoretical foundations and their application to the processing and interpretation of data from health studies. Thus, each student’s program includes training in both the “bio,” or life science, and “statistics” portions of biostatistics. These two components of training complement each other.

The specific objectives of the statistics portion of a student’s training are that the student be well-versed in the application of basic techniques and have a thorough understanding of the theory behind these techniques. To implement these objectives, a wide range of courses are offered on statistical theory and application. Statistical computing is an important focus in the applied course work.

A specific objective for training in a “bio” area is to ensure that the biostatistics student develops enough knowledge for effective collaboration with scientists in that area.

Currently, faculty, staff, and students in the Department of Biostatistics are engaged in the design and analysis of studies on the effects of exercise and medical treatment on the cardiovascular system, on clinical and basic research projects involving cancer, on the role of PET scans in the diagnosis of Alzheimer’s disease and other forms of dementia, on the control of diabetes, on methods for assessing the health of workers relative to exposure to contaminants, and on mapping the genes for adult-onset diabetes and several eye disorders. Biostatistics personnel are participating in the analysis and interpretation of studies on the cancer-causing potential of compounds in animals, on the treatment of osteoporosis, and on the care of burned patients. Biostatistics personnel are also involved in collaborative research on other basic medical, environmental, and epidemiologic programs. In addition, there is emphasis within the department on research on biostatistical methodology for surveys, laboratory experiments, data management, clinical trials, genetic studies, and epidemiologic studies.
Degrees Offered

Residential MPH, MS, and PhD Programs

The residential graduate curriculum in biostatistics includes three degree programs: Master of Public Health (MPH), Master of Science (MS), and Doctor of Philosophy (PhD). The MPH program is administered through the School of Public Health; the MS and PhD programs are administered through the Horace H. Rackham School of Graduate Studies. The statistics portions of all of these programs include courses in biostatistical theory and methods. The “bio” part of the MPH program consists of a core program in public health and includes a broad exposure to public health fields. The “bio” part of both the MS and PhD programs consists of a concentration in a single cognate area to which statistics may be applied. This area may be selected from departments within the School of Public Health such as epidemiology; from areas such as physiology or human genetics, which involve courses offered by the U-M Medical School; or from other areas such as psychology, biology, sociology, or economics. Thus, a student has considerable flexibility in planning an individual program of study.

During the 2006–2007 academic year, 29 teaching faculty members have academic appointments in the Department of Biostatistics, 25 of whom have their primary appointment in the department. Information on the faculty, including their research interests and educational background, is given later in this brochure. During the fall term of 2006, 137 graduate students are expected to enroll, 45 in the PhD program, 42 in the MS program, and two in the MPH program. There will also be 48 graduates in the non-residential MS program in Clinical Research Design and Statistical Analysis, discussed next.

Non-residential MS Program in Clinical Research Design and Statistical Analysis

In addition to its regular degree programs, the Department of Biostatistics also offers an MS Program in Clinical Research Design and Statistical Analysis in a non-residential On-Job/On-Campus (OJ/OC) format. Students in this program come to the School for one four-day weekend per month for 18 months. The program provides a means for health-care professionals who are involved in clinical research to develop expertise in research design and statistical analysis appropriate to such research while remaining in their current employment. The program is not intended to be a substitute for the MS or MPH programs in biostatistics and in particular does not prepare students for doctoral study in biostatistics. For further information about this program, please contact:

Roderick Little, PhD
Director
OJ/OC MS Program in Clinical Research Design and Statistical Analysis
Department of Biostatistics
University of Michigan School of Public Health
1420 Washington Heights
Ann Arbor, MI 48109-2029

Or call 734.615.9817, or visit the program web site at www.sph.umich.edu/biostat/programs/clinical-stat/.

The OJ/OC MS program is not described further in this brochure.
The MS and MPH Programs

Requirements of the Master’s Programs
Both the MS and MPH programs consist of 48 credit hours and are designed to be completed in four terms (two years). The two programs have identical requirements in biostatistics and epidemiology but differ in their other requirements. The requirements for both programs include the following (or equivalent course work):

A. Core courses in Biostatistics (22 credit hours)

<table>
<thead>
<tr>
<th>Course</th>
<th>Cr. hrs.</th>
<th>Title</th>
<th>Usual term</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bios 601</td>
<td>4</td>
<td>Probability and Distribution Theory</td>
<td>Fall, year 1</td>
</tr>
<tr>
<td>Bios 602</td>
<td>4</td>
<td>Biostatistical Inference</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 650</td>
<td>4</td>
<td>Applied Statistics I: Linear Regression</td>
<td>Fall, year 1</td>
</tr>
<tr>
<td>Bios 651</td>
<td>3</td>
<td>Applied Statistics II: Generalized Linear Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 653</td>
<td>3</td>
<td>Applied Statistics III: ANOVA and Linear Mixed Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 699</td>
<td>4</td>
<td>Analysis of Biostatistical Investigations</td>
<td>Winter, year 2</td>
</tr>
</tbody>
</table>

B. Electives in Biostatistics or Statistics (12 credit hours)

At least 12 credit hours of electives are required in addition to the core courses. They may be selected from biostatistics courses at the 600/800 level or from statistics courses at the 500/600 level.

Electives need to be formal courses defined as graded courses taught in a lecture format. Bios 600 and Bios 605 cannot be counted toward this requirement.

C. Epidemiology Requirement

All students in the School of Public Health are required to demonstrate competency in biostatistics and epidemiology. The epidemiology requirement may be satisfied in any one of the following ways:

1. Completing Epidemiology 503 (winter) or 600 (fall).
2. For students with a background in epidemiology, completing Epidemiology 601 (winter).
3. Taking and passing the Epidemiology 503 exemption examination.
4. Completing Epidemiology 516 and any necessary prerequisites to that course.

The fourth option (Epidemiology 516) is available to MS students but not MPH students.

D1. MS students only. Cognate requirements

MS students must complete at least 9 hours of course work in a cognate area. This should consist of a coherent set of courses in an area (or in related areas) of application of biostatistics; the courses should be approved for graduate credit and may be from more than one department. Cognate courses should be primarily applied as opposed to mathematical/statistical in nature. For example, courses in areas such as mathematics, statistics, operational research, computer science, econometrics, and psychometrics would most likely not qualify as cognate courses. Courses from other departments in public health or in areas such as genetics, biology, psychology, economics, and many other similar areas will likely qualify as cognate courses. Courses in bioinformatics that are biological or experimental in nature would typically count toward the cognate, whereas those that are more quantitative or technical would not. Courses taken to satisfy the epidemiology requirement count toward the cognate requirement. Faculty advisors can provide guidance and recommend approval of cognate courses. If questions arise on review by the Student Administration Office, the Curriculum Committee will make the final decision.

Waivers of cognate requirements. It is possible to have cognate courses taken in a graduate program elsewhere recognized and to receive a partial or complete waiver. It should be noted, however, that if the previously taken courses were applied toward a degree, the required credit hours for the UM degree will not be reduced. A waiver of cognate requirements should be discussed with your advisor and must be approved by the Curriculum Committee and all requests must go through the department’s Student Administration Office.

D2. MPH students only. Breadth, integration, and capstone requirements

All MPH students in the School of Public Health are required to take course work for the breadth and integration of knowledge, and a capstone activity. BIOS 699, one of the core biostatistics courses,
serves for integration of knowledge and as the capstone activity in biostatistics. To satisfy the breadth requirement, MPH students in biostatistics are required to take at least 3 public health–related courses each of at least 2 hours of credit. One of these courses must be in epidemiology and the other two must be from two other departments (not biostatistics, statistics, or mathematics). These courses are usually from the School of Public Health, but, for example, could also include courses from the School of Public Policy, the Department of Economics, or the School of Natural Resources, if they are appropriately oriented towards public health. Including the general epidemiology requirement, at least 12 credit hours of such course work are required. Each student’s program must be approved by the biostatistics curriculum committee in order to assure that the course work is related to public health.

Courses for a Student Intending to Complete Graduate Study with a Master’s Degree

Students can complete the master’s program in two years. Table 1 gives the standard sequence of courses for master’s students.

Table 1: A sample sequence of courses* for MS students

<table>
<thead>
<tr>
<th>Fall, year 1</th>
<th>Cr. hrs.</th>
<th>Winter, year 1</th>
<th>Cr. hrs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bios 600**</td>
<td>0-1</td>
<td>Bios 602</td>
<td>4</td>
</tr>
<tr>
<td>Bios 601</td>
<td>4</td>
<td>Bios 651</td>
<td>3</td>
</tr>
<tr>
<td>Bios 650</td>
<td>4</td>
<td>Bios 653</td>
<td>3</td>
</tr>
<tr>
<td>Epid/Cognate*</td>
<td>3-4</td>
<td>Epid/Elective*</td>
<td>3</td>
</tr>
<tr>
<td>Total</td>
<td>11-13</td>
<td>Total</td>
<td>13</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fall, year 2</th>
<th>Cr. hrs.</th>
<th>Winter, year 2</th>
<th>Cr. hrs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>3 electives*</td>
<td>9</td>
<td>Bios 699</td>
<td>4</td>
</tr>
<tr>
<td>Epid/Cognate*</td>
<td>3-4</td>
<td>1-2 electives*</td>
<td>3-6</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Epid/Cognate*</td>
<td>3</td>
</tr>
<tr>
<td>Total</td>
<td>12-13</td>
<td>Total</td>
<td>10-13</td>
</tr>
</tbody>
</table>

*The timing of electives and cognates may be freely interchanged. For an MPH degree, electives and cognates should be selected to satisfy the breadth requirement in D2 above.

**Optional course offered one week before the fall term. The purpose is to review basic statistical concepts and tools and to introduce the SPH computer network and statistical software.

Courses for a Master’s Student Planning to Continue for a PhD Degree

This section describes a program of study for students who are planning to continue on to the PhD program. The PhD degree includes a cognate requirement, which is fulfilled by the cognate courses in the MS program. Students in the MPH program must also take courses that satisfy the PhD cognate requirement.

Before advancement to candidacy, a PhD student must pass the Qualifying Examinations (see pages 10–12). The following program of study will enable a student to take the Qualifying Examinations at the completion of the master’s program, and to complete the PhD course requirements in one additional year.

To prepare for the Qualifying Examinations, a student should take the core courses for the master’s degree and the following required courses from the PhD program:

<table>
<thead>
<tr>
<th>Course</th>
<th>Cr. hrs.</th>
<th>Title</th>
<th>Usual term</th>
</tr>
</thead>
<tbody>
<tr>
<td>Math 451</td>
<td>3</td>
<td>Advanced Calculus I</td>
<td>Fall or Winter</td>
</tr>
<tr>
<td>Stat 610</td>
<td>3</td>
<td>Mathematical Statistics I</td>
<td>Fall</td>
</tr>
<tr>
<td>Stat 611</td>
<td>3</td>
<td>Mathematical Statistics II</td>
<td>Winter</td>
</tr>
</tbody>
</table>

A sample master’s program for students who intend to continue into the PhD program is presented in Table 2. Stat 610 and Stat 611 fulfill six of the required 12 credit hours of electives in the master’s program, although they do not fulfill requirements for electives in the PhD program. Students planning to continue in the PhD program have less flexibility for the choice of electives since Stat 610 and Stat 611 must be included in this program of study. Students who have taken an advanced calculus course (Math 451 or its equivalent) may be exempted from the requirement and choose an elective in its place.
**The PhD Program**

**Requirements of the PhD Program**

The PhD degree requires successful completion of:

- **Course work:**
  1. Core courses
  2. Electives in biostatistics and statistics
  3. Epidemiology requirement
  4. Electives in a cognate area
  5. Qualifying Examinations in theory and applications

- **Dissertation:**
  6. Presentation of proposal for research, including an extensive literature review
  7. Research
  8. Writing of the dissertation
  9. Oral defense

After successful completion of the course work and the Qualifying Examinations, the student is advanced to candidacy and begins work on his/her dissertation.

Students entering with a relevant master’s degree in biostatistics or statistics are likely to have completed several of the courses required for the PhD program. For this reason, we outline two programs of study: one for students with a relevant master’s degree and one for students without a relevant master’s degree. Each student should determine the details of the program of study after consultation with his/her faculty advisor.

**Courses for a PhD Student Starting from a Relevant Master’s Degree**

This program is designed to enable a student to take the Qualifying Examinations at the end of year one. The student would then achieve candidacy and be able to concentrate full time on dissertation research.

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**Table 2: A sample sequence of courses* for MS students intending to continue in the PhD program**

<table>
<thead>
<tr>
<th>Fall, year 1</th>
<th>Cr. hrs.</th>
<th>Winter, year 1</th>
<th>Cr. hrs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bios 600**</td>
<td>0-1</td>
<td>Bios 602</td>
<td>4</td>
</tr>
<tr>
<td>Bios 601</td>
<td>4</td>
<td>Bios 651</td>
<td>3</td>
</tr>
<tr>
<td>Bios 650</td>
<td>4</td>
<td>Bios 653</td>
<td>3</td>
</tr>
<tr>
<td>Epid/Cognate*</td>
<td>3-4</td>
<td>Epid/Math 451***</td>
<td>3</td>
</tr>
<tr>
<td>Total</td>
<td>11-13</td>
<td>Total</td>
<td>13</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fall, year 2</th>
<th>Cr. hrs.</th>
<th>Winter, year 2</th>
<th>Cr. hrs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stat 610</td>
<td>3</td>
<td>Bios 699</td>
<td>4</td>
</tr>
<tr>
<td>2 Electives*</td>
<td>6</td>
<td>Stat 611</td>
<td>3</td>
</tr>
<tr>
<td>Epid/Cognate*</td>
<td>3-4</td>
<td>Epid/Cognate*</td>
<td>3</td>
</tr>
<tr>
<td>Total</td>
<td>12-13</td>
<td>Total</td>
<td>10</td>
</tr>
</tbody>
</table>

**Spring/Summer, year 2**

- Qualifying Exams

*This represents a minimal program of study for an MS degree. The timing of electives and cognates may be freely interchanged.

**Optional elective offered one week before the fall term. The purpose is to review basic statistical concepts and tools, and to introduce the SPH computer network and statistical software.

*** Math 451 is also offered in the fall or spring term.

**Joint Master’s Program**

Students in a joint master’s program between biostatistics and another area of study have the same core courses as students with a single major in biostatistics. However, they are required to complete only three elective courses in biostatistics (nine credit hours).
Typically, a student entering with a relevant master’s degree will have had the following courses or their equivalents:

- **Bios 601** Probability and Distribution Theory
- **Bios 602** Biostatistical Inference
- **Bios 650** Applied Statistics I: Linear Regression
- **Math 451** Advanced Calculus I

One or two electives in biostatistics or statistics.

This accelerated program is not possible unless the student has already completed the first three courses listed above. Math 451 can be taken in the first term of year one, if necessary.

**A. Core Courses (19 credit hours)**

<table>
<thead>
<tr>
<th>Course</th>
<th>Cr. hrs.</th>
<th>Title</th>
<th>Usual term</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prior to taking the Qualifying Examinations:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stat 610</td>
<td>3</td>
<td>Mathematical Statistics I</td>
<td>Fall, year 1</td>
</tr>
<tr>
<td>Stat 611</td>
<td>3</td>
<td>Mathematical Statistics II</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 651</td>
<td>3</td>
<td>Applied Stat. II: Generalized Linear Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 653</td>
<td>3</td>
<td>Applied Stat. III: ANOVA and Linear Mixed Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 699</td>
<td>4</td>
<td>Analysis of Biostatistical Investigations</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Prior to achieving candidacy:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bios 680*</td>
<td>3</td>
<td>Stochastic Processes</td>
<td>Year 2</td>
</tr>
</tbody>
</table>

*or a course in probability for which Bios 601 or its equivalent is a prerequisite

**B. Electives (15 credit hours)**

It is assumed that students entering with a relevant Master’s degree will have taken equivalent courses that will enable them to be exempted from three to six hours of this requirement.

Electives may be selected from biostatistics at the 600/800 level, from statistics at the 500/600 level, or with approval of the Candidacy Committee, from courses taught in other departments. At least 12 of these hours should be in formal courses and 9 of the 12 hours should be at the 800 level in biostatistics or 600 level in statistics. A formal course is defined to be a graded course that is taught in a lecture format.

**C. Epidemiology Requirement**

All students in the School of Public Health are required to demonstrate competency in biostatistics and epidemiology. The epidemiology requirement may be satisfied in any one of the following ways:

1. Completing Epidemiology 503 (winter) or 600 (fall).
2. For students with a background in epidemiology, completing Epidemiology 601 (winter).
3. Taking and passing the Epidemiology 503 exemption examination.
4. Completing Epidemiology 516 and any necessary prerequisites to that course.

The fourth option (Epidemiology 516) is available to MS students but not MPH students.

**D. Cognate requirement**

PhD students must complete at least 9 hours of course work in a cognate area. This should consist of a coherent set of courses in an area (or in related areas) of application of biostatistics; the courses should be approved for graduate credit and may be from more than one department. Cognate courses should be primarily applied as opposed to mathematical/statistical in nature. For example, courses in areas such as mathematics, statistics, operational research, computer science, econometrics, and psychometrics would most likely not qualify as cognate courses. Courses from other departments in public health or in areas such as genetics, biology, psychology, economics, and many other similar areas will likely qualify as cognate courses. Courses in bioinformatics that are biological or experimental in nature would typically count toward the cognate, whereas those that are more quantitative or technical would not. Courses taken to satisfy the epidemiology requirement count toward the cognate requirement. Faculty advisors can provide guidance and recommend approval of cognate courses. If questions arise on review by the Student Administration Office, the Curriculum Committee will make the final decision.
Waivers of cognate requirements. It is possible to have cognate courses taken in a graduate program elsewhere recognized and to receive a partial or complete waiver. It should be noted, however, that if the previously taken courses were applied toward a degree, the required credit hours for the UM degree will not be reduced. A waiver of cognate requirements should be discussed with your advisor and must be approved by the Curriculum Committee, and all requests must go through the department’s Student Administration Office.

In Table 3, we present a possible sequence of courses and examinations for a student entering with a relevant master’s degree. Prior to registering for this sequence, the student should confirm with his or her faculty advisor that he or she has adequate prior course work. Also, the student should discuss with his or her faculty advisor the possibility of receiving exemptions from the courses listed above. Bios 820 or 990 in the last term is an individually-tailored readings course in the area of biostatistics in which the student would like to do the literature review.

<table>
<thead>
<tr>
<th>Course Cr. hrs.</th>
<th>Title</th>
<th>Usual term</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bios 601 4</td>
<td>Probability and Distribution Theory</td>
<td>Fall, year 1</td>
</tr>
<tr>
<td>Bios 602 4</td>
<td>Biostatistical Inference</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Stat 610 3</td>
<td>Mathematical Statistics I</td>
<td>Fall, year 2</td>
</tr>
<tr>
<td>Stat 611 3</td>
<td>Mathematical Statistics II</td>
<td>Winter, year 2</td>
</tr>
<tr>
<td>Bios 650 4</td>
<td>Applied Statistics I Linear Regression</td>
<td>Fall, year 1</td>
</tr>
<tr>
<td>Bios 651 3</td>
<td>Applied Statistics II Generalized Linear Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 653 3</td>
<td>Applied Statistics III ANOVA and Linear Mixed Models</td>
<td>Winter, year 1</td>
</tr>
<tr>
<td>Bios 699 4</td>
<td>Analysis of Biostatistical Investigations</td>
<td>Winter, year 2</td>
</tr>
<tr>
<td>Math 451 3</td>
<td>Advanced Calculus I</td>
<td>Year 1</td>
</tr>
</tbody>
</table>

Prior to achieving candidacy:

- Bios 680* 3 | Stochastic Processes | Year 2

Courses for a PhD Student Starting without a Relevant Master’s Degree

This program does not assume any relevant course work for a student entering the PhD program. Prior to registering for courses the student should discuss with his/her advisor the specific courses that should be taken.

A. Core Courses (34 credit hours)

B. Electives (15 credit hours)

At least 15 credit hours of electives are required. They may be selected from biostatistics at the 600/800 level, from statistics at the 500/600 level, or with approval of the Candidacy Committee, from courses taught in other departments. At least 12 of these hours should be in formal courses, 9 of the 12 hours should be at the 800 level in biostatistics or 600 level in statistics. A formal course is defined to be a graded course that is taught in a lecture format.
C. Epidemiology requirement
All students in the School of Public Health are required to demonstrate competency in biostatistics and epidemiology. The epidemiology requirement may be satisfied in any one of the following ways:

1. Completing Epidemiology 503 (winter) or 600 (fall).
2. For students with a background in epidemiology, completing Epidemiology 601 (winter).
3. Taking and passing the Epidemiology 503 exemption examination.
4. Completing Epidemiology 516 and any necessary prerequisites to that course.

The fourth option (Epidemiology 516) is available to MS students but not MPH students.

D. Cognate requirement
PhD students must complete at least 9 hours of course work in a cognate area. This should consist of a coherent set of courses in an area (or in related areas) of application of biostatistics; the courses should be approved for graduate credit and may be from more than one department. Cognate courses should be primarily applied as opposed to mathematical/statistical in nature. For example, courses in areas such as mathematics, statistics, operational research, computer science, econometrics, and psychometrics would most likely not qualify as cognate courses. Courses from other departments in public health or in areas such as genetics, biology, psychology, economics, and many other similar areas will likely qualify as cognate courses. Courses in bioinformatics that are biological or experimental in nature would typically count toward the cognate, whereas those that are more quantitative or technical would not. Courses taken to satisfy the epidemiology requirement count toward the cognate requirement. Faculty advisors can provide guidance and recommend approval of cognate courses. If questions arise on review by the Student Administration Office, the Curriculum Committee will make the final decision.

Waivers of cognate requirements. It is possible to have cognate courses taken in a graduate program elsewhere recognized and to receive a partial or complete waiver. It should be noted, however, that if the previously taken courses were applied toward a degree, the required credit hours for the UM degree will not be reduced. A waiver of cognate requirements should be discussed with your advisor and must be approved by the Curriculum Committee, and all requests must go through the department’s Student Administration Office.

In Table 4 we present a possible sequence of courses and examinations for students entering without a relevant master’s degree.

Table 4: A sample sequence of courses* for a PhD student entering without a relevant master’s degree

| Table 4: A sample sequence of courses* for a PhD student entering without a relevant master’s degree |
|---------------------------------------------------|---------------------------------------------------|
| Fall, year 1 | Cr. hrs. | Winter, year 1 | Cr. hrs. |
| Bios 600 | 0-1 | Bios 602 | 4 |
| Bios 601 | 4 | Bios 651 | 3 |
| Bios 650 | 4 | Bios 653 | 3 |
| Epid/Cognate* | 3-4 | Math 451 | 3 |
| Total | 11-13 | Total | 13 |

| Fall, year 2 | Cr. hrs. | Winter, year 2 | Cr. hrs. |
| Stat 610 | 3 | Bios 680 | 3 |
| 2 electives* | 6 | Stat 611 | 3 |
| Epid/Cognate* | 3-4 | Bios 689 | 4 |
| Epid/Cognate* | 3 |
| Total | 12-13 | Total | 13 |

Spring/Summer, year 2

| Qualifying Examinations |

*This represents a minimal program of study for the PhD degree. The timing of electives and of cognates may be freely interchanged. These courses also allow a student to receive a master’s degree at the end of the second year. Three additional electives would be taken in year three for a total of 15 credit hours of electives. Bios 820 or 980, an individually tailored reading course in the area of biostatistics in which the student would like to do the literature review, is particularly recommended.
Candidacy and Dissertation

The Qualifying Examinations

The Qualifying Examinations are given during a two-day period and consist of one six-hour theory exam and one six-hour applications exam. Each exam will consist of six questions, all of which should be attempted. Both exams will be closed-book; the problems do not require a computer. All examination questions focus on material that a person with a PhD in biostatistics is expected to know, regardless of subsequent specialization. The examinations encompass material in the core mathematical statistics, probability, and applied statistics courses in the PhD program in biostatistics. The general level of the Qualifying Examinations is characterized by the following reading and topics lists:

**Guidelines for the Theory Examination**


While it is not possible to provide an exhaustive list, the following list of topics is offered as a guideline for the types of questions that are asked on the theory exam:

**Probability and Distribution Theory**

- Probability calculations (marginal, conditional, expectations, etc.)
- Distributions of functions of random variables
- Properties of common discrete and continuous exp. family dns, univariate and multivariate
- Generating functions (moment generating functions, characteristic functions, probability generating functions)
- Inequalities
- Convergence concepts
- Limit theorems (strong and weak laws of large numbers, central limit theorem)

**Inference**

- General principles (sufficiency, ancillarity, consistency, completeness, etc.)
- Point estimation (UMVU, method of moments, estimating equations, maximum likelihood, conditional and quasi-likelihood)
- Interval estimation (construction of confidence intervals and Bayes credibility intervals)
- Classical hypothesis testing (UMP tests, likelihood ratio tests, Type I and II errors, score and Wald tests, power/sample size calculations), loss functions
- Asymptotic distribution theory (Delta method, regularity conditions)

**Maximum Likelihood**

- Properties
- Calculations
- Numerical algorithms (scoring, EM, etc.)
- Variance estimation

**Bayes**

- Bayes’ theorem, Bayesian credibility intervals, Bayesian hypothesis testing, conjugate priors, empirical Bayes

**Guidelines for the Applications Examination**


While it is not possible to provide an exhaustive list, the following list of topics is offered as a guideline for the types of questions that are asked on the applications exam:
**Linear Regression**
- Assumptions, model diagnostics, goodness-of-fit measures
- Estimation/prediction/hypothesis testing/interval estimation
- Model formulation and interpretation of parameters
- Other modeling issues—variable selection, multicollinearity, transformations, interaction, multiple comparisons
- ANOVA/ANCOVA for regression

**Mixed Models/Repeated Measures**
- Formulation of mean and covariance structures, parameter interpretation
- Estimation and inference for fixed and random effects
- Estimation methods (ML, REML, GEE)
- Model assumptions, goodness-of-fit
- ANOVA for mixed models
- Unbalanced and missing data

**Generalized Linear Models**
- Assumptions
- Link functions for standard exponential family distributions
- Estimation/hypothesis testing/interval estimation
- Interpretation of parameters
- Diagnostics/goodness-of-fit
- Models for ordinal data
- Chi-squared tests for contingency tables

**Experimental Design**
- Design of randomized and observational studies
- Analysis plans that account for design features
- Power/sample size calculations

As a rule, students must be admitted to the biostatistics PhD program before taking the Qualifying Examinations. This rule may be waived in exceptional circumstances, subject to written consent of the Admission and Candidacy Committees.

The Qualifying Examinations are not individualized to the student. They are prepared and graded by the members of the Candidacy Committee.

The Qualifying Examinations are offered once each year, in June.

A student who has passed neither the theory nor applied examination must take both examinations during the same two-day examination period. If a student passes one examination and fails the other, and the student wishes to continue in the PhD program, then the student must retake the failed examination but need not retake the passed examination.

If a student fails either the theory examination twice or the applied examination twice, the student will not be allowed to continue in the PhD program.

Except for special cases, full-time PhD students entering without a relevant master’s degree must take the Qualifying Examinations within two-and-a-half years of entering the program, while students entering with a relevant master’s degree must take them within one year of entering the program. The requirements for part-time students are pro-rated, so that, for example, a half-time student entering with a relevant master’s degree will be required to take the Qualifying Examinations within two years. A student retaking a Qualifying Examination must retake it the next time it is offered. If a student wishes to delay the examinations, he or she must submit a written request to the Candidacy Committee, with justification for the delay (such as additional cognate courses in the student’s program, illness, or necessity of taking remedial mathematics courses).

**Advancement to Candidacy**
Advancing to candidacy requires passing the Qualifying Examinations and completing the required course work. Once these requirements are met, the student should apply for candidacy by submitting the Candidacy Requirements form to the chair of the Candidacy Committee. The Candidacy Committee then makes the final decision regarding advancement.

**Dissertation Committee**
In accordance with Rackham Graduate School regulations, the dissertation committee must have at least four members, with at least two from within and at least one from outside the Department of Biostatistics. A member whose research interests are closely aligned with those of the student is the committee chair, unless this member is from outside the department, in which case this member and a member from with-
in the department are designated as co-chairs. The dissertation committee is selected by mutual agreement between the student and committee members and is nominated to the dean of the graduate school by the chair of the department. The committee directs and reviews the student’s doctoral research, conducts the oral defense of the dissertation, and decides whether or not the dissertation is approved.

Each candidate for the PhD degree in biostatistics is required to give a seminar presenting a proposal for the dissertation research with an extensive review of literature within 18 to 24 months of the date at which they reach candidacy.

**Dissertation Content**
The dissertation research must be a creative and significant original contribution to the field of biostatistics. The research may involve the development of new biostatistical methodology or it may consist of the innovative application of available procedures to important biomedical problems.

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### Interdepartmental Concentrations

After admission to one of the five departments in the School, students can also apply for admission to an Interdepartmental Concentration (IC). ICs offer the opportunity to deepen a student’s understanding of public health topics that have major implications for society as a whole today. The curriculum is designed to be accessible to all public health students without extending training time toward the degree. Faculty from all five departments within the School as well as affiliated faculty from other University of Michigan schools and colleges participate in these exciting programs. The School of Public Health offers ICs in Global Health, Public Health Genetics, and Reproductive and Women’s Health. A supplemental application is required for admission to ICs, and spaces in each IC are limited.

### IC in Global Health

Designed to provide an opportunity to study public health issues in global health in a multidisciplinary framework, this IC helps students develop knowledge and skills related to problems, programs, policies, and practices that are altering public health risks in the context of expanding globalization. Students in this IC learn about diverse global processes that are affecting public health throughout the world. They also examine environmental, cultural, and economic processes that transcend national and continental boundaries and that affect exposure and behavior risks, and they explore health promotion opportunities. The curriculum consists of 12 credit hours of course work: three core courses, one elective, a summer internship, and a seminar. Because the course work extends over four semesters of enrollment, students who have been admitted to a program requiring fewer than four semesters will not be able to participate.
IC in Public Health Genetics
Advances in genetics are occurring at a pace that challenges our collective ability to respond to the many social, legal, ethical, and public health policy implications of this information. The IC in Public Health Genetics provides an opportunity for public health professionals to gain an understanding of the effects of genes on health and disease and to apply genetic information to public health practice. As a student in this IC, you will learn to understand how genes, together with the environment and behavior, influence health. The curriculum is composed of 12 credit hours of course work: three core courses and one elective. The elective will be chosen to emphasize the specific applications of your interests and to supplement the degree requirements of your department.

IC in Reproductive and Women’s Health
The fields of reproductive health and women’s health are challenging and transforming traditional public health approaches to fertility and population change, maternal and child health, and women’s health. As a student in this IC you will learn to approach reproductive and women’s health from a multidisciplinary perspective and to understand how to apply your departmental training to this content area. You can study public health problems, programs and policies related to contraception, emerging reproductive technologies, social and ethical issues in reproduction, maternal health and pregnancy outcomes, and other aspects of women’s health. The curriculum includes four courses, among them a two-term integrative seminar course taken in the first year of study and one elective course.
Admission

Admission Procedures
Application forms for admission to the MPH, MS, and PhD programs are available online. The MPH program is administered by the School of Public Health, while the MS and PhD programs are administered by the Horace H. Rackham School of Graduate Studies. Please be sure to complete the correct application form for the degree you wish to pursue. Students applying for an MPH must submit a School of Public Health application form at http://www.sph.umich.edu/admissions/; applicants to the MS and PhD programs must submit a Rackham application, which can be found at http://www.rackham.umich.edu/Admis.

An applicant to the MPH program should return the application form to the School of Public Health, while an applicant to the MS and PhD programs should return portions of the application form to the Rackham School and portions to the Department of Biostatistics. Please refer to the application form for details. Official transcripts of all previous college and university work and three letters of recommendation also are required.

All applicants must submit scores from the Aptitude Test of the Graduate Record Examination taken within the past five years. Applications for the test, together with the examination fee, must be received by the Educational Testing Service several weeks before the test date. The GRE may be taken at one of any number of test centers throughout the United States and several other countries. For those with access to a computer, the GRE may also be taken “on-line” at times most convenient to the applicant. Information about the test is available from:

Educational Testing Service
P.O. Box 6000
Princeton NJ 08541-6000
609.771.7670

To schedule call 1.800.GRE.CALL.
For information through the GRE Web site visit http://www.gre.org.

Completed applications should be received in the department by February 1, since decisions related to funding favor applications received by the deadline. Late applications will be considered for admission and financial support as space permits.

Admission Requirements
Master’s Programs (MS or MPH)
A bachelor’s degree from an accredited college or university is required of all applicants. The minimum mathematics prerequisite for admission is three semesters of calculus, a course in matrix or linear algebra, and an introductory course in statistics or biostatistics or the equivalent. It is recommended that students who have not had recent exposure to these prerequisites review these topics, particularly, but not limited to, multivariable calculus and matrix algebra. Additional mathematics courses, such as Advanced Calculus and Numerical Analysis, and knowledge of a computer programming language such as C or FORTRAN are helpful but not required. Courses in the life or behavioral sciences are also desirable but not required. The minimum grade point average required for admission is 3.0 on a 4.0 scale, and successful applicants must have demonstrated an ability to earn grades of B or better in mathematics and statistics courses.

Students with inadequate preparation in mathematics or statistics may be admitted conditionally to the master’s programs. Courses in calculus, matrix or linear algebra, or in introductory biostatistics will not be counted toward the credits needed to fulfill the degree requirements and must be complete before starting the program.

PhD Program
In addition to the requirements for admission to the master’s programs given above, admission to the PhD program requires at least a B+ average in any previous graduate work. It is generally expected that applicants show a combined score of 1100 on the verbal and quantitative components of the Aptitude Test of the Graduate Record Examination (GRE) and a combined score of 1200 on the quantitative and analytical components of the GRE. More recent GRE scores reporting an analytical writing measure
Admission

scored 0 to 6 are generally expected to show skill at the level of 4.5 or above for admission to the PhD program. Many students applying to the PhD program already have a master’s degree in biostatistics or statistics. However, particularly well-qualified students with a relevant bachelor’s degree and a strong academic record may be admitted directly to the PhD program.

Students from Abroad

The Department of Biostatistics welcomes applications from qualified students from countries other than the United States. Many admitted students are offered support in the form of research or teaching assistantships. Prior to admission, unsupported students from abroad must furnish evidence of sufficient financial support to cover the cost of the entire period of study. Students must also demonstrate prior to admission a satisfactory proficiency in the English language as measured by the Test of English as a Foreign Language (TOEFL) or by the English Proficiency Test of the English Language Institute (ELI) of the University of Michigan. A proficiency test score of 600 or above on the paper-pencil TOEFL, of 250 or above on the computer-based TOEFL, or 85 or above on the ELI test, indicating an ability to carry a full academic course load, is preferred. A score of 560–600 on the paper-pencil TOEFL, of 220–250 on the computer-based TOEFL, or 80–84 on the ELI test, indicating an ability to take a three-quarters academic course load, is accepted with the understanding that the student will need to take additional training in the English language while enrolled and may have to spend an extra term of study to complete the program.

Faculty Advisor

Each student is assigned a faculty advisor. The faculty advisor assists the student in the planning of the student’s program of study. When a PhD candidate forms a dissertation committee, the chair of the committee serves as the student’s advisor.

Exemptions/Credits Based on Previous Course Work

Prior equivalent course work may be used to receive exemption from course requirements (core, electives, or cognate) in any of the programs described. The student should discuss the possibility of receiving exemptions with his/her faculty advisor. Upon approval of the faculty advisor, a formal request for exemptions from a requirement should be submitted to the department’s Student Administration Office. The request will then be forwarded to the appropriate departmental committee for review.

Up to six hours of credit may be obtained for relevant course work at the graduate level provided that the courses were not taken to fulfill the requirements of another degree program. After approval by the department (see preceding paragraph), a petition for this credit must be submitted to the School of Public Health for the MPH degree and to the Rackham School of Graduate Studies for the MS and PhD degrees.

The department requires that all requests for exemptions/credits based on previous course work be submitted to the Student Administration Office no later than the last day of classes for the student’s first fall term. Please be advised that you may be required to provide courses materials such as a syllabus, course description, etc.

Grades

The passing range for grades is from A+ to C-. Graduate students are required to maintain a B average to remain in good standing and to graduate. No course with a grade below C- is credited towards satisfaction of departmental requirements.
Financial Support and Aid in Biostatistics

Financial support is available in several forms for well-qualified applicants: fellowships, research assistantships, graduate student instructorships, and complete and partial tuition scholarships.

Fellowships are available for outstanding applicants. Fellowships provide both tuition support and a monthly stipend, and may provide additional support, for example, to attend a scientific meeting. Fellowship support frees the awardee to concentrate entirely on his/her studies. Support is available from federally funded training grants in cancer research, biostatistics, and statistical genetics administered within the department, as well as from a variety of other School of Public Health and University sources. Fellowships are also available for students from historically underrepresented populations, including those from educationally or economically disadvantaged backgrounds.

The Department of Biostatistics provides research assistantships to well-qualified applicants. Graduate Student Research Assistants (GSRAs) typically work on one or more funded research projects with a faculty member. Many such projects are conducted in collaboration with medical or public health investigators; others are for the development of statistical methods with biostatistics faculty as principal investigators.

The Department of Biostatistics also provides well-qualified applicants with employment as Graduate Student Instructors (GSIs). GSIs run lab sessions, hold office hours, and grade homework and exams. Most GSIs assist in introductory biostatistics courses taken by non-majors. GSIs arrive in Ann Arbor in late August to take part in a Graduate Student Instructor orientation.

GSRA and GSI support is offered on a 50% basis, corresponding to approximately 14 or 20 hours work per week. All Fellows, GSRAs, and GSIs receive a monthly stipend, health insurance, and a full tuition waiver for the terms they are working. For GSRAs and GSIs, the stipend for 2005–2006 is $1,790.75 per month.

To apply for financial support at the time of admission, simply fill out the item on the application form indicating preference for different types of financial support. A student should consult his or her advisor concerning financial support after admission.

Tuition and Fees

The tuition structure at the University of Michigan is two-tiered, with separate resident and non-resident rates. Eligibility to pay resident tuition is determined by the University based on criteria set forth in the University’s Residency Classification Guidelines. For more information, or to request a copy of the guidelines, please contact the Residency Classification Office, 1514 LSA Building, University of Michigan, Ann Arbor MI 48109-1382, telephone 734.764.1400.

Tuition and fees for a term are payable at registration or in installments during the term. The number and dates of the installments are specified in advance for each term. Tuition and fees are subject to change without notice by action of the Regents of the University. The following is the tuition as of fall 2005:

- Michigan resident, per term $8,020
- Michigan non-resident, per term $14,814
- PhD candidate (resident and non-resident), per term $4,743

(PhD candidate refers to a student who has been advanced to candidacy)
Courses

**For Non-Majors**

**503. Introduction to Biostatistics**
Fundamental statistical concepts related to the practice of public health: descriptive statistics; probability; sampling; statistical distributions; estimation; hypothesis testing; chi-square tests; simple and multiple linear regression; one-way ANOVA. Use of the computer in statistical analysis.

**510. Statistical Computer Program Packages**
Students learn use of several widely-used statistical computer-program packages such as BMDP, SAS, and SPSS. Emphasis placed on relative merits of these packages with respect to types of statistical analyses they perform and their methods of data management.

**513. Application of Regression Analysis to Public Health Studies**
This course provides a broad overview of statistical methods (linear, logistics, Poisson, and Cox regression) at an applied level. The course is meant to be a single follow-up course to Biostat 503/553 for SPH students who are not interested in going on to Biostat 560.

**523. Biostatistical Analysis for Health-Related Studies**
A second course in applied biostatistical methods and data analysis. Concepts of data analysis and experimental design for health-related studies. Emphasis on categorical data analysis, multiple regression, analysis of variance, and covariance.

**553. Applied Biostatistics**
Fundamental statistical concepts related to the practice of public health: descriptive statistics; probability; sampling; statistical distributions; estimation; hypothesis testing; chi-square tests; simple and multiple linear regression; one-way ANOVA. Taught at a more advanced mathematical level than Biostat 503. Use of the computer in statistical analysis.

**560. Statistical Methods in Epidemiology**
Statistical methods commonly used in environmental epidemiology. Emphasis on choosing appropriate statistical methods and subsequent interpretation. Topics include probability, measures of association and risk, sample size calculations, SMR and PMR analysis, logistic regression, and survival analysis.
For Majors

578. Practical Projects
Practical projects in consultation and statistical analysis of data in research studies with health investigators. Course requirements include an approved practical work experience related to biostatistics in consultation with a faculty advisor. May be elected more than once. Enrollment limited to biostatistics majors with at least two full terms of prior registration.

600. Introduction to Biostatistics
The purpose of this course is to review basic applied statistical concepts and tools and to introduce the SPH computer network and statistical software.

601. Probability and Distribution Theory
Fundamental probability and distribution theory needed for statistical inference. Probability, discrete and continuous distributions, expectation, generating functions, limit theorems, transformations, sampling theory.

602. Biostatistical Inference
Fundamental theory that is the basis of inferential statistical procedures. Point and interval estimation, sufficient statistics, hypothesis testing, maximum likelihood estimates, confidence intervals, criteria for estimators, methods of constructing test and estimation procedures.

605. Introduction to SAS Statistical Programming
This course provides incoming master’s students in biostatistics with basic experience in SAS programming for data set creation and manipulation, an introduction to SAS macros, and SAS matrix manipulation.

610. Readings in Biostatistics
Independent study in a special topic under the guidance of a faculty member. May be elected more than once. Enrollment is limited to biostatistics majors.

615. Statistical Computing
Statistical computing and its applications in biostatistical techniques. Use of computational algorithms to generate random numbers, calculate univariate statistics, perform multiple and nonlinear regression, and find maximum likelihood estimates. Enables students to understand numerical results produced by a computer and to design Monte Carlo simulation studies. In parallel, students learn concepts of efficient programming and usage of biomedical computer programs.

617. Theory and Methods of Sample Design
Theory underlying sample designs and estimation procedures commonly used in survey practice.

619. Clinical Trials
This course is designed for individuals with a strong quantitative background who are interested in the scientific, policy, design, and management aspects of clinical trials. Topics include types of clinical research, bias and random error, study design, ethics, treatment allocation, randomization and stratification, quality control, power and sample size, group sequential monitoring, cross-over designs, and meta-analysis.

630. Statistical Methods in Biological Assay
Logic of biological assay; dosage response curves; quantitative and quantal responses; parallel line and slope-ratio assays; simplified estimators; sequential assays; problems of design.
642. Introduction to Functional MRI
This course presents the basic skills to design and analyze functional magnetic resonance imaging (MRI) experiments. We start by reviewing the basis Matlab and Unix skills necessary to manipulate image data. Next we introduce the principles of MRI and the nature of the Blood Oxygenation Level Dependent (BOLD) effect, including artifacts that corrupt the BOLD signal. We cover blocked and event-related designs and how to optimize statistical power of a design. We cover subject safety issues and practicalities of subject preparation and use of the paradigm presentation software E-prime. We review basic statistics and the statistical tools of functional neuroimaging. We cover each step of analysis, preprocessing, model fitting, model diagnosis and finally statistical inference. When appropriate, the class will take place in a computing lab and lectures will have a “hands-on” component.

645. Time Series Analysis with Biomedical Applications
Introduction to statistical time series analysis with an emphasis on frequency domain (spectral) methods and their applications to biomedical problems. Topics include: autocorrelation, stationarity, autoregressive and moving average processes, power spectra, periodograms, spectral estimation, linear filters, complex demodulation, autoregressive integrated moving average (ARIMA) models, cross-correlation, cross-spectra, coherence, time and frequency domain linear regression. The methods will be illustrated in applications to various areas of public health and medical research such as environmental health, electrophysiology, and endocrinology.

646. Data Analysis in Molecular Biology
The course will cover statistical methods used to analyze data in experimental molecular biology. The course will primarily cover topics relating to gene expression data analysis, but other types of data, such as genome sequence data, which are sometimes analyzed in concert with expression data will also be covered.
664. Special Topics in Biostatistics
This master’s level seminar is designed to provide an extensive review of a number of substantive methods and skill areas in biostatistics. Readings, discussion, and assignments are organized around issues of mutual interest to faculty and students. Reviews and reports on topics are required in the areas selected. May be elected more than once.

666. Statistical Models and Numerical Methods in Human Genetics
Current statistical methodologies used in human genetics including basic concepts in human genetics, sampling designs in human genetics, gene frequency estimation, classical segregation analysis and ascertainment. linkage analysis, the polygenic/multifactorial model, and complex segregation analysis. Numerical techniques frequently employed in human genetics will also be considered.

675. Survival Time Analysis
Concepts and methods for analyzing survival time data obtained from following individuals until occurrence of an event or their loss to follow-up. Survival time models, clinical life tables, survival distributions, mathematical and graphical methods for evaluating goodness of fit, comparison of treatment groups, regression models, proportional hazards models, censoring mechanisms.

680. Applications of Stochastic Processes
Conditional distributions, probability generating functions, convolutions, discrete and continuous parameter, Markov chains, medical and health related applications.

682. Applied Bayesian Inference

685. Elements of Nonparametric Statistics
First half covers theory and applications of rank and randomization tests: sampling and randomization models, randomization t-test, Wilcoxon rank sum and signed rank tests, Kruskal-Wallis test, asymptotic result under randomization, relative efficiency. Second half covers theory and applications of nonparametric regression: smoothing methods, including kernel estimators, local linear regression, smoothing splines, and regression splines, methods for choosing the smoothing parameter, including unbiased risk estimation and cross-validation, introduction to additive models.

690. Health Applications of Multivariate Analysis
Techniques of multivariate analysis related to health and biomedical problems. Emphasis on computational techniques and programs with health examples. Tests of significance for one, two or more populations; general linear model; multivariate analyses of variances and covariances; correlation procedures; principal components and discriminant analyses.

695. Analysis of Categorical Data
Regression models for the analysis of categorical data: logistic, probit and complementary log-log models for binomial random variables; log-linear models for cross-classifications of counts; regression models for Poisson rates; and multinomial response models for both nominal and ordinal responses. Model specification and interpretation are emphasized, and model criticism, model selection, and statistical inference are cast within the framework of likelihood based inference.

699. Analysis of Biostatistical Investigations
Identifying and solving design and data analysis problems using a wide range of biostatistical methods. Written and oral reports on intermediate and final results of case studies required.

800. Seminar in Biostatistics
Presentations and discussions of current consulting and research problems. May be elected more than once. Enrollment limited to biostatistics majors.
### 803. Biostatistics in Cancer Seminar
The purpose of this class is to describe biostatistical research that is occurring in collaboration with cancer researchers and to provide exposure to the field of cancer research. Activities include seminars on statistical methods in cancer, presentations of articles from statistical literature, discussion of cancer clinical trial protocols and grant proposals, and visits to research laboratories. Students formally in the training program are expected to enroll in this course every semester. The course is open to other students, and it is expected that others might like to participate. It is open to both PhD and MS students.

### 815. Advanced Topics in Computational Statistics
Modern numerical analysis for statisticians. Combination of theory and practical computational examples illustrating the current trends in numerical analysis relevant to probability and statistics. Topics chosen from numerical linear algebra, optimization theory, quadrature methods, splines, and Markov chains. Emphasis on newer techniques such as quasi-random methods of integration, the EM algorithm and its variants, and hidden Markov chains. Applications as time permits to areas such as genetics and medical imaging.

### 820. Readings in Biostatistics
Students assigned special topics for literature study under guidance of individual faculty members. May be elected more than once. Enrollment limited to biostatistics majors.

### 830. Advanced Topics in Biostatistics
Advanced training in biostatistical methods primarily for doctoral students. Format will include lectures, readings, presentations, and discussions in an area of special interest to students and faculty, such as stopping rules and interim analysis in clinical trials, conditional and unconditional inference and ancillarity, or nonparametric regression.

### 840. Advanced Topics in Data Analysis
Alternative methods of data analysis useful when data do not fulfill unusual assumptions of statistical tests. Using articles from the literature, students learn methods of data analysis more robust than usual methods and how to choose among them. Focuses on comparison of groups, ANOVA, and regression.

### 845. Advanced Topics in Times Series Analysis
Advanced theory of stationary univariate and multivariate time series. Additional advanced topics such as analysis of non-stationary, non-linear, and/or categorical time series; time-frequency analysis; and statistical methods based on the wavelet transform or related transforms. Application of methods to time series data sets from health research.

### 850. Research in Biostatistics
Research on selected topics involving the application of statistical methods to health problems. May be elected more than once. Enrollment limited to biostatistics majors.

### 851. Linear Statistical Models (Stat 642)
Theory of multivariate normal distribution, distribution of quadratic forms, Cochran’s theorem, Gauss-Markov theorem, general linear hypothesis, experimental design models, Wishart distribution.

### 866. Advanced Topics in Genetic Modeling
Advanced topics in quantitative genetics with emphasis on models for gene mapping, pedigree analysis, reconstruction of evolutionary trees, and molecular genetics experiments, computational mathematics, and statistical techniques such as Chen-Stein Poisson approximations, hidden Markov chains, and the EM algorithm introduced as needed.

### 870. Analysis of Repeated Measurements
Mixed model analysis of variance; multivariate profile analysis; linear mixed effects models with unbalanced designs, time-varying covariates, and structured covariance matrices; maximum likelihood (ML), restricted maximum likelihood (REML), and Bayes estimation and inference; nonlinear mixed effects models.
875. Advanced Topics in Survival Analysis
Lectures and readings from the literature on advanced topics in survival analysis. Covers regression for censored data, general event-history data and models, competing risks. Statistical, mathematical, and probabilistic tools used in survival analysis are extended for these general problems.

880. Statistical Analysis with Missing Data
Statistical analysis of data sets with missing values. Pros and cons of standard methods such as complete-case analysis, imputation. Likelihood-based inference for common statistical problems, including regression, repeated-measures analysis, and contingency table analysis. Stochastic censoring models for nonrandom nonresponse. Computational tools include the EM algorithm, the Gibbs’ sampler, and multiple imputation.

885. Nonparametric Statistics
Theory and techniques of nonparametrics and robustness. M-estimation, influence function, bootstrap, jackknife, generalized additive models, smoothing techniques, penalty functions, projection pursuit, CART.

890. Multivariate Statistical Models (Stat 640)
Derivation of multivariate techniques: multivariate estimation, criteria for testing linear hypothesis, tests for additional information, testing covariance matrices, factor analysis, growth curves, and elementary time series.

895. Analysis of Multivariate Categorical Data
Probability models for two-way tables; multi-factor, multi-response framework; product multinomial distribution theory; Taylor series estimates of variance, weighted least squares and Wald statistics; constraint equations; models for characterizing interactions; step-wise variable selection; factorial designs with multinomial responses; repeated measurement experiments; log-linear models; paired-choice and bioassay experiments; life-table models.

990. Dissertation/Pre-Candidacy
Election for dissertation work by doctoral student not yet admitted to status as a candidate.

995. Dissertation Research for Doctorate in Philosophy
Election for dissertation work by doctoral student who has been admitted to status as a candidate.
Faculty

Goncalo Abecasis
Associate Professor. Identification and characterization of genes determining human variation and disease.
BSc in genetics, University of Leeds, 1997
DPhil in human genetics, University of Oxford, 2000

The focus of my research is the identification and characterization of genes determining human variation and disease. Statistical methods and software developed in my research group facilitate the analysis of very large datasets, where thousands of individuals may be measured at tens of thousands of genetic markers and are currently used in >1000 laboratories around the world. Our gene mapping methods can be used to map discrete traits or quantitative traits in families or in unrelated individuals.

My group has also helped lay the groundwork for genome-wide association studies, by investigating the patterns of genetic variation in detail and helping to build detailed catalogs of genetic variation including millions of variants.

We are actively involved in a number of genetic mapping projects. We are collaborating with scientists at the Kellogg Eye Center to identify genes that contribute to susceptibility to age-related macular degeneration and other ocular disorders, with scientists at the Department of Dermatology to identify genes that contribute to psoriasis susceptibility, and with scientists at the National Institute on Aging to identify genes that contribute to aging related changes.

Selected Publications

Mousumi Banerjee
Research Associate Professor. Survival analysis; tree-based methods; competing risks; applications in cancer.
BS in statistics, Indian Statistical Institute, 1986
MS in statistics, Indian Statistical Institute, 1988
PhD in statistics, University of Wisconsin-Madison, 1994

My methodological research interest is in tree-based methods for survival data. This is motivated by the need of clinical researchers to define interpretable prognostic classification rules both for understanding the prognostic structure of data and for designing future clinical trials. I also work on statistical models and methods for analyzing competing risks data. In this context, I have been particularly interested in situations where the exact cause of death is only partially known. Finally, I am interested in longitudinal data methods, with a focus on model diagnostics and goodness of fit procedures.

My applied research has focused on studies of cancer surveillance. I am engaged in research using data from population-based cancer registries to investigate disparities in patterns of cancer care and outcomes, with an emphasis on racial and ethnic disparities.

Selected Publications
Michael Boehnke
Professor. Statistical genetics, genomics, and genetic epidemiology.
BA in mathematics, University of Oregon, 1977
PhD in biomathematics, UCLA, 1983

Knowledge of the chromosomal location of a disease-predisposing variant may permit improved genetic counseling, and represents an important step towards the isolation and cloning of the gene, better understanding of disease etiology, and the eventual treatment and prevention of the disease. Recent advances in human genetics owing to the sequencing of the human genome and the genomes of model organisms, the identification of a substantial fraction of human genetic variation, and the increasing annotation of the human gene sequence make this a particularly exciting area of research. My methodological work includes development of study designs and methods of statistical analysis for genetic linkage and association studies. I am particularly interested in developing methods relevant to the common familial diseases. These complex diseases include essentially every human disease with substantial impact on the public’s health.

My primary applied project is FUSION: the Finland-United States Investigation of NIDDM Genetics study. In this large, multicenter study, we seek to identify genetic variants that predispose to adult-onset diabetes, or which influence variability in diabetes-related quantitative traits. We have carried out genome scan linkage analysis in >800 Finnish families ascertained through diabetic sibling pairs, and are fine-mapping regions of chromosomes 6, 11, 14, 20, and 22. We recently identified variants near the alternate promoter of the HNF4A gene that appear to increase diabetes risk and that partially explain our linkage result on chromosome 20. I am cofounder of the International Type 2 Diabetes Linkage Analysis Consortium, a collaboration of nearly all groups seeking to identify genetic variants that predispose to adult-onset diabetes. I also am collaborating in genomewide association study of bipolar disorder. Graduate students working under my direction are involved in each of these projects.

Selected publications


Thomas Braun
Assistant Professor. Phase I trial design; permutation and resampling methods; group randomized trials.
BBA in actuarial science, University of Wisconsin–Madison, 1990
MS in biostatistics, University of Washington, 1996
PhD in biostatistics, University of Washington, 1999

My theoretic areas of research include Bayesian approaches to the design of studies designed to find efficacious and nontoxic cumulative dosing treatment schedules of new cytotoxic agents. I also work on statistical methods for the analysis of clustered binary outcomes, especially when the cluster size influences the mean and/or variance of each individual outcome. Last, I continue to examine alternatives to large-sample approximations, such as permutation and resampling methods, and their accuracy in small samples.

My applied area of research deals with bone marrow transplantation and the associated co-morbidity from graft-versus-host disease (GVHD). Most importantly, I am pursuing statistical methodology useful for quantifying a graft-versus-leukemia effect from observed rates of GVHD and leukemia relapse, which is challenging as the two outcomes are correlated competing risks.
Selected Publications


**Morton B. Brown**

*Professor: Clinical trials, categorical data analysis; statistical computing, robust methods and model fitting.*

BA in mathematics, McGill University, 1962  
PhD in mathematics, Princeton University, 1965

There are two distinct thrusts to my research, one methodological and the other applied. The methodological work focuses on the development of practical methods for data analysis. Examples of these are: 1) tests for location and scale that are less sensitive to the underlying assumptions, such as normality and homogeneity of variances; and 2) estimation of parameters in loglinear models when some observations are incomplete and the probability of nonresponse is related to the response that would have been given (i.e., when there is nonignorable nonresponse). The applied thrust includes the development of statistical methods and/or models in response to problems in clinical trials, medicine or biology. Examples of such problems are: 1) a statistic to test for differences between groups when the outcome is continuous and there are dropouts from the study; 2) improved (more robust) methods that will be used for the analysis of assays of hormones; (3) methods to identify patterns of secretion of hormones into the blood, such as pulses or cycles; and (4) models of secretion of one hormone as a function of the secretion of a second hormone.

Selected Publications


McClure LA and Brown MB (2006) A likelihood approach to analyzing clinical trial data when treatments favor different outcomes. *Contemporary Clinical Trials* [published online].

**Richard G. Cornell**

*Professor Emeritus. Adaptive clinical trials and decision analysis.*

BA in mathematics, University of Rochester, 1952  
MS in statistics, Virginia Polytechnic Institute, 1954  
PhD in statistics, Virginia Polytechnic Institute, 1956

My research is motivated by the need for new methodology for the design and analysis of medical and public health investigations. This has grown out of involvement in studies on topics such as the evaluation of burn care, extracorporeal membrane oxygenation (ECMO) treatment for neonates with respiratory distress, the treatment of diabetes, and the transmission of HIV infection. I have a continuing interest in decision analysis, which has grown out of the need to evaluate screening tests for cancer and other diseases.

Selected Publications


**Michael Elliott**

*Assistant Professor. Design and analysis of observational studies.*

BA in mathematics, University of Chicago, 1985  
MS in biostatistics, University of Michigan, 1997  
PhD in biostatistics, University of Michigan, 1999

My methodological research focuses on the design and analysis of observational studies. I am developing model-based Bayesian approaches that complement traditional design-based analyses of complex sample survey data, and considering new methods for combining information from disparate surveys such as the Centers for Disease Control’s Behavioral Risk Factor Surveillance System (BRFSS) and the National Center for Health Statistics’ National Health...
Interview Survey (NHIS). I have addressed the U.S. Census undercount issue, developing hierarchical Bayesian models to combine census, follow-up survey, and demographic analysis data. I also have interest in missing and latent variable data structures. I am using such approaches to model repeated time-to-event measures, and am currently extending “second generation structural equation models” that incorporate growth curve measures for both continuous and categorical covariates. More recently I have considered “potential outcome” models to estimate causal effects in a variety of diverse settings, including longitudinal clinical trials and toxicology studies. My applied interests are in the areas of injury control, including injuries to children in passenger vehicles and workers in industrial accidents. I am also considering the application of latent variable models to psychological affect data and hormone production patterns, and nutrition and obesity in pediatric populations.

Selected Publications


Andréj Galecki

Associate Research Scientist. Research Associate Professor, Institute of Geronotology. Computational methods for analyzing correlated and over dispersed data.

MS in applied mathematics, Technical University of Warsaw (Poland), 1977
Physician Diploma in medicine, Medical Academy of Warsaw, 1981
PhD in epidemiology, Institute of Mother and Child Care in Warsaw, 1987

My primary interests lie in developing computational methods for analyzing correlated and over-dispersed data, which are frequently encountered in many fields of application, such as pharmacokinetic and pharmacodynamic (PK/PD) studies, longitudinal studies, survey sampling and gene mapping in genetics studies. A class of models often considered in this context are hierarchical or mixed-effects models. These models are an extension of the regression models whereby random effects are introduced to describe between-subject variation. My particular interests related to mixed effects models lie in:

1) An extension of mixed models which allows between-subject variation to be modeled as a mixture of underlying distributions. This type of model can be applied to interval and composite gene mapping of quantitative and qualitative trait loci in experimental animal crosses.

2) Computational methods for advanced PK/PD population studies. Here models are often expressed as a solution of a system of ordinary differential equations. To address these problems a new SAS/IML NLMEM macro has been developed and successfully used to analyze existing data. Specific application of these models occurs in population studies when intravenous glucose tolerance test (IVGTT) studies are used to evaluate glucose metabolism in patients.

3) Modeling covariance structure in the presence of two or more repeated factors. A class of models proposed in Galecki, 1994, has been implemented in PROC/MIXED, which is part of commercial statistical software SAS, starting with version 6.12. The proposed class of covariance structures is especially useful for the analysis of several outcomes measured over time.

My other research interests involve a wide range of methodological and practical aspects of research on the elderly, including study design and conducting study itself. I am involved in a number of large NIH-funded projects including analysis cores at the Claude D. Pepper Older Americans Independence Center and Genetics of Age-Sensitive Traits in Mice Program project.

Selected Publications

Debashis Ghosh

Associate Professor. Computational molecular biology; bioinformatics; recurrent failure time data; survival analysis; nonparametric methods; clustering and classification problems.

BA in mathematics, statistics, economics and French studies, Rice University, 1995
MS in biostatistics, University of Washington, 1997
PhD in biostatistics, University of Washington, 2000

My research interests can be broadly grouped into two areas, the first involving bioinformatics and the second involving cancer research. With respect to the first area, these include methods for the analysis of high-dimensional genomic data, inference for oncogenic pathways, and integration across multiple sources of genomic data. I also have other bioinformatic interests in modeling of sequence-activity relationships for MHC-class molecules and analysis of banding patterns in infectious disease epidemiology.

A major goal of the application bioinformatics in cancer research is to generate new biomarkers that will serve as novel diagnostic or screening procedures in cancer. Towards that end, I am also interested in the development of statistical methods for modeling biomarker data, combining biomarkers, modeling progression in cancer studies and analysis of data from cancer epidemiologic studies. This has led to an interest in the use of techniques from computer science, termed machine learning, and their application in biostatistical settings.

Selected Publications


Brenda W. Gillespie

Assistant Professor and Associate Director, CSCAR. Survival analysis; clinical trials.

BA in mathematics, Earlham College, 1972
MS in statistics, Ohio State University, 1975
PhD in statistics, Temple University, 1989

My research interests are in the area of censored data and clinical trials. One research interest concerns the application of categorical regression models to the case of censored survival data. This technique is useful in modeling the hazard function (instead of treating it as a nuisance parameter, as in Cox proportional hazards regression), or in the situation where time-related interactions (i.e., non-proportional hazards) are present. Another field of interest is the analysis of crossover trials with censored data. I have developed (with M. Feingold) a set of nonparametric methods for testing and estimation in this setting. Our methods out-perform previous methods in most cases.

Selected Publications


Timothy Johnson
Research Associate Professor. Longitudinal and time series modeling.
BS in mathematics, University of California, 1984
MS in mathematics, University of California, 1986
PhD in biostatistics, University of California, 1997

My research interests are in Bayesian methods and applied statistics; particularly as applied to endocrinology and the radiological sciences. I am interested in the analysis of hormonal time series data and diagnostic medicine, in particular ROC analysis and diagnostic imaging. My other areas of interest include mixture models, latent variable models, Bayesian model choice, nonparametric Bayesian methods, and Bayesian clustering/classification.

Selected Publications

Jack Kalbfleisch
Professor. Chair of Biostatistics. Statistical methods and theory; survival analysis; analysis of event history and longitudinal studies; design and analysis of clinical trials.
BSc honors in math and physics, University of Waterloo, 1966
MMath in statistics, University of Waterloo, 1967
PhD in statistics, University of Waterloo, 1969

One of my primary research interests is in the development of models and methods for analyzing failure time or event-history data. Applications of this work arise in many areas including epidemiology, medicine, demography, and engineering. In event-history data, interest centers on the timing and occurrence of various kinds of events, such as, for example, repeated infections or recurrences of disease, or sequences of events that occur through the study period. I have been particularly interested in situations in which only partial data or data subject to sampling bias are available.

In many applications, mixture models provide a natural way to describe heterogeneity in a population, and I am interested in various aspects of modeling and analyzing mixtures. This research has included work on algorithms for fitting nonparametric mixtures and on methods for testing the order of a finite mixture, a problem arising in various applications in genetics.

A third area of interest relates to the use of resampling or bootstrapping techniques when an estimating function or equation forms the basis for inference. By estimating directly the distribution of the estimating function itself, it is possible to develop methods for resampling that are computationally less demanding than the usual bootstrap methods and, in many instances, also exhibit better properties. Extensions of these methods to time series or martingale type estimating equations are the subject of current investigations.

Selected Publications

Hyungjin Myra Kim
Adjunct Assistant Professor. Outcomes analysis and health services research.
BA in biology, University of Hawai, Manoa, 1986
MA in biostatistics, University of California, Berkley, 1988
ScD in biostatistics, Harvard University, 1995

My primary appointment is at the Center for Statistical Consultation and Research, where I do statistical consulting for the University of Michigan faculty, staff, and graduate students; collaborate on research proposals; and offer workshops. My main collaborators are from the Health Services Research and Development Department at the Veterans
Administration Hospital. Naturally, my current research efforts are in the fields of decision analyses, outcomes research, health services research, and various forms of telemedicine research. Some of my recent collaborative work includes evaluation of health burden in women with breast hypertrophy and development of an automated risk-adjusted mortality model for intensive care units using a large database. I also work with a radiation oncologist to compare disease specific as well as general quality of life in head- and neck-cancer patients treated with different types of radiation therapy. I am also interested in cost-effectiveness analyses of various diagnostic modalities.

Selected Publications


Sinan Kehagias

Assistant Professor. Bayesian variable selection; clustering; nonparametric bayes; wavelets; bioinformatics; DNA microarray analysis.

BS in statistics, Pusan National University, 1999
MS in statistics, Texas A & M University, 2003
PhD in statistics, Texas A & M University, 2006

I am interested in Bayesian nonparametric approaches for the analysis and modeling of high-throughput data and of biological systems. In particular, I develop model-based Bayesian methods for the analysis of genomics and proteomic data. My research has focused on development of Bayesian variable selection methods for clustering high-dimensional data with an unknown number of components. The method has been successfully used for the identification of new biomarkers and the discovery of new subtypes in cancers.

My other work in bioinformatics includes the wavelet-based method for proteomic data and Bayesian methods to refine the search for DNA regulatory motifs by integrating gene expression and genome sequence data.

Selected Publications


Anant M. Kshirsagar

Professor Emeritus. Multivariate analysis; design of experiments and Markov renewal theory.

MSc in statistics, Bombay University, 1951
PhD in statistics, Manchester University, 1961
DSc in statistics, Manchester University, 1976

One of my research interests is in the extension of growth curve models, which arise in longitudinal data analysis useful in biometry and medical science. Another interest is in the SAS-oriented analysis of mixed traditional replication designs useful in industry. Also, I am interested in mixed linear models, as well as multivariate techniques, especially estimation of chance of miscalculation.

Selected Publications


James M. Lepkowski

Associate Professor. Survey sampling and analysis of categorical data.

BS in mathematics, Illinois State University, 1970
MPH in biostatistics, University of Michigan, 1976
PhD in biostatistics, University of Michigan, 1980

My research interests are in new survey sampling methods and applications across a range of disciplines. I work in a multidisciplinary research environment involving collaboration of statisticians and social, psychological, economic, and political scientists at the Institute for Social Research; substantive research interests are naturally diverse. These include, but are not limited to, health; health care quality and access; health care coverage; epidemiology of chronic conditions; public health; education, gender, labor force participation, and economic status; race and discrimination in higher education; epidemiology of hypertension and stroke risk factors in African Americans; vitamin A deficiency; and cataract and blinding eye conditions. My methodological research activities at present include telephone sampling methods, methods for compensating for missing survey data, and methods to analyze survey data that take the complexity of the survey sample design into account.

My research is centered at the Survey Methodology Program at the Institute for Social Research, a program seeking to improve the cost-effectiveness of survey methods used in practice. My program research interests include survey and sample design, questionnaire design, interviewer behavior, respondent cognition, response errors, coding errors, nonresponse, noncoverage, estimation procedures, compensating for missing data, privacy and confidentiality, and data archiving. This program is linked to the Joint University of Maryland–University of Michigan Program in Survey Methodology in College Park, Maryland. The Joint Program offers degrees in survey methodology to current and future employees in the Federal Statistical System. The Survey Methodology Program is now home to the Rackham Interdepartmental Program in Survey Methodology, offering MS and PhD degrees in survey methodology.

Selected Publications


Roderick J.A. Little

Richard D. Remington Collegiate Professor.

Incomplete data; sample surveys; Bayesian statistics; applied statistics.

BA in mathematics, Cambridge University, 1971
MSc in statistics and operational research,
University of London, 1972
PhD in statistics, University of London, 1974

A primary research interest is the analysis of data sets with missing values. Many statistical techniques are designed for complete, rectangular data sets but, in practice, biostatistical data sets contain missing values, either by design or accident. As detailed in my book with Rubin, initial statistical approaches were relatively ad-hoc, such as discarding incomplete cases or substituting means, but modern methods are increasingly based on models for the data and missing-data mechanism, using likelihood-based inferential techniques. Another interest is the analysis of data collected by complex sampling designs involving stratification and clustering of units. Since working as a statistician for the World Fertility Survey, I have been interested in the development of model-based methods for survey analysis that are robust to misspecification, reasonably efficient, and capable of implementation in applied settings. Statistics is philosophically fascinating and diverse in application. My inferential philosophy is model-based and Bayesian, although the effects of model misspecification need careful attention. My applied interests are broad, including mental health, demography, environmental statistics, biology, economics, and the social sciences, as well as biostatistics.

Selected Publications


**Bhramar Mukherjee**

*Assistant Professor. Bayesian semiparametric methods; statistical methods for sampling schemes; experimental design; applications in epidemiology.*

BSc in statistics, Presidency College, 1994
MStat in applied statistics and data analysis, Indian Statistical Institute, 1996
MS in mathematical statistics, Purdue University, 1999
PhD in statistics, Purdue University, 2001

In terms of statistical methods, my research interests are Bayesian semiparametric methods, experimental design, statistical methods for case-control and other outcome-dependent sampling schemes, studies of gene-gene and gene-environment interaction, missing data and measurement error in case-control studies. The central theme in my research program has been to illustrate the advantage of using Bayesian techniques for flexible, hierarchical modeling of epidemiological data. Epidemiology is a science which progresses by accumulation of evidence, and the Bayesian paradigm offers many natural solutions to complex problems encountered in modern epidemiology. Currently, I am working on case-control studies of gene-environment interaction and family based case-control studies. I am interested in Bayesian nonparametric techniques, especially involving the Dirichlet process prior. Foundational issues related to any choice-based sampling scheme interest me greatly.

*Selected Publications*


Ghosh M and Mukherjee B. Data adaptive sequential design for case-control studies. To appear in *Statistica Sinica*.

**Susan Murray**

*Associate Professor. Survival analysis; missing data issues; quality-of-life research; sequential methods.*

BA in statistics, Rice University, 1990
BA in mathematical sciences, Rice University, 1990
BA in English, Rice University, 1990
MS in biostatistics, Harvard University, 1992
ScD in biostatistics, Harvard University, 1994

My current research interests touch on topics in nonparametric survival analysis, missing data issues, quality-of-life research, and sequential monitoring of survival endpoints. These interests often converge. For instance, in survival analysis missing data problems occur when a clinical trial fails to collect all relevant failure time information. One nonparametric approach I have studied for this problem incorporates auxiliary longitudinal covariate information in estimation and testing in the survival setting. This allows for weaker assumptions on the censoring mechanism than the standard assumption of non-informative censoring used in nonparametric survival methods. Methodology for sequential monitoring of clinical trials with the modified statistics has also been developed.

I am also engaged in research on correlated survival endpoints. The problem first came to my attention in the context of quality-of-life research through a popular quality-of-life analysis tool called Q-TWiST. This statistic simultaneously analyzes length of time experiencing toxicity, time without symptoms or toxicity, and time in relapse in order to assess the tradeoffs between quality of life and length of life. In determining the variability of this statistic, I came to understand variability structures that I’ve since extended for use in other situations. My recent work makes available new methodology for nonparametrically analyzing censored survival data at a single analysis time or as part of a group sequential monitoring procedure in clinical trials.

I collaborate with pulmonary researchers in the UM Medical School and have been expanding my activities in collaborations and professional service in areas intersecting my new pulmonary research interests. For instance, I have become a member of the Clinical Research Committee for the Cystic Fibrosis Foundation Therapeutics, Inc., and a member of the Cystic Fibrosis Foundation Data Safety Monitoring Board. In addition to these activities, I am a senior biostatistician in heart and lung transplantation research who participates in the Scientific Registry of Transplant Recipients (SRTR), centered in Ann Arbor. This collaboration has great potential to impact the practice of heart and lung transplantation around the country and has inspired further methodologic work in survival analysis.
### Murray S

**Assistant Professor.** *Semiparametric models; survival analysis; missing data problems.*

MS and BS in aerospace engineering, Beijing University of Aeronautics and Astronautics, 1987 and 1984

MS in statistics, Virginia Commonwealth University, 1997

PhD in biostatistics, University of Washington, 2001

My research interests include topics in semiparametric models, survival analysis, and missing data problems. I am currently focusing on marker evaluation in the context of survival analysis, alternative models with censored data, and statistical issues in case-cohort and case-control studies as well as other missing data problems. I am also interested in developing methods in survival analysis with high dimensional covariates, which can be used for microarray data analysis.

**Selected Publications**


### Bin Nan

**Assistant Professor.** *Semiparametric models; survival analysis; missing data problems.*

MS and BS in aerospace engineering, Beijing University of Aeronautics and Astronautics, 1987 and 1984

MS in statistics, Virginia Commonwealth University, 1997

PhD in biostatistics, University of Washington, 2001

My research interests include topics in semiparametric models, survival analysis, and missing data problems. I am currently focusing on marker evaluation in the context of survival analysis, alternative models with censored data, and statistical issues in case-cohort and case-control studies as well as other missing data problems. I am also interested in developing methods in survival analysis with high dimensional covariates, which can be used for microarray data analysis.

**Selected Publications**


### Thomas E. Nichols

**Assistant Professor.** *Functional brain imaging.*

BS in mathematics and statistics, Carnegie Mellon University, 1992

MS in statistics, Carnegie Mellon University, 1997

PhD in statistics Carnegie Mellon University, 2000

I am interested in the statistical issues of functional brain imaging. In my work I try to get as close as possible to the machines that create the data and the users that are trying to understand the brain. With one method, Positron Emission Tomography (PET), I used the rawest form of the data ("List Mode") to create continuous movies of brain activity; this work was motivated by a user's frustration with existing methods which lacked temporal resolution. Another method, Functional Magnetic Resonance Imaging (fMRI), creates enormous datasets with complicated spatiotemporal covariance structure. Because of their large size, traditionally only very basic methods have been applied to this data (e.g. linear regression at every point in the brain). My current work involves working closely with cognitive neuroscientists and MR physicists to develop models for fMRI data; these models will accurately capture the features of interest, as guided by the neuroscientists, while accounting for the spatiotemporal noise structure, which requires an understanding of the physics.

**Selected Publications**


### Zhaohui (Steve) Qin

**Assistant Professor.** *Statistical genetics; computational biology; statistical computing.*

BS in probability and statistics, Peking University, 1994

PhD in statistics, University of Michigan, 2000

My research interests include topics in statistical genetics, computational biology, and statistical computing. I am currently focusing on developing methods for analyzing large-scale genomic data, with an emphasis on integrative analysis of next-generation sequencing data. I am also interested in developing statistical methods for functional data analysis and high-dimensional data analysis.
My long-term research goal is to develop sound statistical models and efficient computational algorithms to extract useful information from complex datasets. I am currently involved in projects analyzing data from the genetics and genomics fronts. Recently, my collaborators and I have developed new algorithms for reconstructing haplotypes from genotype data. We are investigating how these tools will aid scientists to locate genetic variants linked to complex diseases. I am also interested in biological sequence analysis, searching for statistically significant features and using them to infer biological functions. In terms of statistical methodology, I am interested in Markov chain Monte Carlo–based computation techniques.

Selected Publications


Trivellore E. Raghunathan

Professor. Analysis of incomplete data; sample surveys; Bayesian and empirical Bayesian methods; epidemiology.

BSc Nagpur University, 1977

MSc in statistics, Nagpur University, 1979

MS in statistics, Miami University, 1983

PhD in statistics, Harvard University 1987

My primary research interest is in developing methods for dealing with missing data in sample surveys and in epidemiological studies. The methods are motivated from a Bayesian perspective but do have desirable frequency or repeated sampling properties. The analysis of incomplete data from practical sample surveys poses additional problems due to extensive stratification, clustering of units and unequal probabilities of selection. The model-based approach provides a framework to incorporate all the relevant sampling design features in dealing with unit and item nonresponse in sample surveys. There are important computational challenges in implementing these methods in practical surveys.

My other research interests include Bayesian methods, methods for small area estimation, combining information from multiple surveys measurement error models, longitudinal data analysis, privacy, confidentiality and disclosure limitations, and statistical methods for epidemiological studies. My applied interests include cardiovascular epidemiology, social epidemiology, health care utilization, and social and economic sciences.

Multiple imputation and complex survey data analysis (IVEWARE). I also have an appointment in the Survey Methodology Program at the Institute for Social Research. The program, a multidisciplinary team of sociologists, statisticians, and psychologists, provides an opportunity to address methodological issues in: nonresponse, interviewer behavior and its impact on the results, response or measurement bias and errors, noncoverage, respondent cognition, privacy and confidentiality issues, and data archiving. I have developed SAS-based software, IVEWARE, for performing multiple imputation analysis and the analysis of complex survey data.

Selected Publications


Noah Rosenberg

Assistant Professor. Statistical methods for analysis of data on genetic variation, mathematical modeling, computer simulations, and statistical inference.

BA in mathematics, Rice University, 1997

MS in mathematics, Stanford University, 1999

PhD in biological sciences, Stanford University, 2001
The genotypes of individuals in a population arise from a complex genealogical history. Therefore, because of this shared history, data on genotypes can exhibit an intricate correlation structure. I am interested in statistical methods for the analysis of data on genetic variation, accounting for evolutionary processes that have given rise to the data. Currently, I am developing and applying statistical approaches for the study of human genetic history and its relationship to identification of disease genes, for inference of species relationships, and for inference about epidemics from genotypes in pathogens. Another focus of my research is the use of mathematical models and computer simulation to investigate various phenomena in evolutionary biology and human genetics.

Selected Publications

**Brisa Sánchez**

*Assistant Research Professor*. Structural equations and latent variable models; longitudinal data; study design; spatial statistics; interdisciplinary, environmental, and social epidemiology.

BS in mathematics, minor in physics, University of Texas, 2000
MS in statistics, University of Texas, 2001
MSc in biostatistics, minor in environmental health, Harvard, 2003
PhD in biostatistics, Harvard, 2006

One of my research interests is in statistical methodology applicable to environmental and social epidemiology. My current work involves developing robust fitting procedures and diagnostics for Structural Equation Models, and using these methods in applications to environmental health problems such as in-utero lead exposure and its effect on child development. I am also interested in spatial statistical methodology and its applications to social determinants of health and behaviors research.

Selected Publications

**Douglas Schaubel**

*Assistant Professor*. Multivariate survival analysis; recurrent event data; dependent censoring.

BMath in actuarial science and statistics, University of Waterloo, 1992
MSc in biostatistics, McGill University, 1996
PhD in biostatistics, University of North Carolina at Chapel Hill, 2002

With respect to statistical methodology, my areas of interest include survival analysis, recurrent event data, and epidemiologic methods. I collaborate with members of the Kidney Epidemiology and Cost Center (KECC) and the University Renal Research and Education Association (URREA). My work at KECC and URREA is mostly directed towards organ failure and transplantation, which feature complex data structures and censoring patterns not amenable to traditional survival analysis methods. Currently, I am conducting analyses geared towards rank-ordering liver transplant candidates with respect to expected transplant survival benefit. I have also begun to quantify the benefit of kidney transplantation with respect to hospitalization rates.
Selected Publications


Laura Scott
Assistant Research Scientist. Design and analysis of genetic studies of complex human diseases; integration of biological information in the evaluation of genetic associations; applied work focused on identifying genetic variants that increase risk of Type 2 diabetes and bipolar disease.

BA in chemistry with concentration in French, Albion College, 1985
PhD in biochemistry, cell and molecular biology, Johns Hopkins, 1993
MPH in epidemiology, University of Michigan, 1995

My primary research interest is the identification of genetic variants that increase the risks of common diseases. For Type 2 diabetes, as part of the Finland–United States Investigation of NIDDM Genetics (FUSION) study, and for bipolar disease, as part of the Pritzker Neuropsychiatric Disorders Research Consortium, I am involved in genome-wide association studies of e300K SNP variants. Analysis of the SNP variants in the context of their biological function(s) will provide information on the spectrum of disease causing variants for common diseases.

Efficient design of two-stage studies for genome-wide association studies can be prohibitively expensive because of the need to genotype large numbers case/control samples on large numbers, e300K, SNP markers. In collaboration with Andrew Skol, Goncalo Abecasis, and Michael Boehnke, I am investigating the optimal design of two-stage studies in which a subset of the cases and controls are genotyped on all the markers in the first stage and the remaining cases and controls are genotyped on a subset of the original markers. Optimal two-stage designs can reduce the genotyping costs by >50% while retaining almost all of the power of the one-stage design.

Design and analysis of experimental studies of animal and cell culture I am working with basic scientists on the design of experimental studies that aim to discover the underlying biological mechanisms for disease. My current focus is on the effect of fatty acid feeding/supplementation on the development of diabetic retinopathy in rats and the signaling pathways in cultured cells from human eyes.

Selected Publications


Kerby Shedden
Associate Professor. Statistical modeling in the natural sciences; high dimensional and massive data sets; statistical computing.

BS in mathematics, University of Michigan, 1994
PhD in statistics, UCLA, 1999

One of my major interests is in statistical analysis of molecular assay data for cancer studies, such as gene expression microarray data and proteomics data from mass mapping and UV mapping. I have worked on low-level data processing such as how to convert raw fluorescence intensities into quantitative expression measurements. I have also worked on high level modeling and inference problems such as how to account for intergene correlations when doing statistical inference with microarray data, and how to detect complex interactions between gene expression levels that are associated with clinical outcomes.
I am also very interested in data analysis and modeling in pharmaceutical science. This includes predictive modeling of drug activity in cells based on structures and properties of the drugs and biological properties of the target cells. This collaborative work also involves statistical analysis of fluorescent cell images to assess subcellular transport and compartmentalization of small molecules.

Some of my other work includes mathematical modeling and analysis of gene and protein expression during the cell cycle, and longitudinal analysis of behavioral and psychiatric measures.

Selected Publications

Jeremy M.G. Taylor
Professor. Modeling; survival analysis; and longitudinal data.
BA in mathematics, Cambridge University, 1978
Dip. Stat. in statistics, Cambridge University, 1979
PhD in statistics, University of California, Berkeley, 1983

My interests are the theory and application of statistics to biomedical problems. I believe that data-driven, robust, flexible statistical methods should be used, incorporating scientific knowledge from the substantive area of investigation. A good statistician has to be heavily involved in the underlying science of the data he/she is investigating.

My theoretical statistical interests are in Box-Cox power transformations, robust methods, nonparametrics, longitudinal models, and smoothing techniques.

My research has focused on the application of statistics to cancer, especially to radiation oncology, to biomarker evaluation, and to genomics. The specific areas are modeling, survival analysis, and longitudinal data. This has led to developing methods involving the use of mixture models, stochastic processes, and multiple imputation.

My work in cancer research has focused on modeling and evaluating biomarkers, particularly PSA in prostate cancer. We have developed joint longitudinal-survival models and cure models for these applications. More recent applied work has been concerned with methods for combining multiple biomarkers and methods for analyzing data from gene expression arrays.

Selected Publications

Alexander Tsodikov
Professor. Multivariate semiparametric survival models, applications in cancer.
MSc in applied mathematics, St. Petersburg State Technical University, 1988
PhD in mathematics/application of computing, mathematical models and methods in natural sciences, St. Petersburg State Technical University, 1991
My research interests have mainly been evolving around cancer research. My recent methodological interest has centered on the idea of fake-mixture or frailty models and their generalization as a tool to derive computationally efficient inference procedures for a wide variety of statistical models.

Much of this methodology was initially developed for so-called semiparametric cure models that incorporate improper distributions showing a tail defect. I am working on a project funded by the National Cancer Institute applying these methods to build a comprehensive model of the dynamics of the national incidence and mortality trends in prostate cancer in the presence of variable utilization of screening. I am also interested in multivariate semiparametric survival models, age-period-cohort models, categorical data analysis, and computational approaches to statistical inference such as EM and MM algorithms. I also have a broad ongoing statistical consulting experience in basic and clinical research as well as epidemiology and population sciences.

Selected Publications


Robert Wolfe

*Professor Emeritus. Survival and longitudinal data analysis.*

BA in mathematics, Oberlin College, 1968

MS in mathematics, Stanford University, 1973

PhD in statistics, Stanford University, 1978

My research interests are focused on methods to study the mechanisms and associations that underlie processes which unfold through time. Such methods include both aspects of the design of experiments and of the analysis of data from experiments and surveys. I am particularly interested in methods that help to disentangle complex sequences of information related to the natural history of specific disease processes and their treatment. My recent collaborative work includes: 1) comparison of treatment modalities for patients with end stage renal disease and 2) evaluation of variability in hospital admission rates among communities.

Selected Publications


Sebastian Zöllner

*Assistant Professor. Genetic modeling, particularly the inheritance process; gene mapping.*

MS in mathematics, University of Munich, 1997

PhD in biology, University of Munich, 2001

As genetic information is inherited between generations, different segments of DNA are transmitted to different descendants, creating a complex structure of dependencies between sequences in present-day individuals. The results of this transmission process are utilized in modern gene-mapping designs, notably association mapping. The major aim of my research is to model this inheritance process, to use the resulting models for improving gene-mapping algorithms and for making inferences about events in the history of a population. Presently I am working on the following ongoing projects:

1. Genome-wide association mapping in Arabidopsis thaliana with tiling arrays. Oligonucleotide tiling arrays are a novel sequencing method that is employed in Arabidopsis thaliana, covering nearly every base of its genome. A single array contains 6.3 million different 25bp oligonucleotides and can be used for detecting polymorphism or small deletion and
studying gene expression. My work aims to evaluate the data from the arrays to identify haplotypes that span multiple oligonucleotides and to identify typing errors. A further goal is then to use the identified haplotypes for identifying variants that underlie quantitative traits like flowering time and seedling elongation.

2. Association mapping of alleles with complex penetrance. Most algorithms that are used for fine-mapping of complex traits assume a simple penetrance model for the causative allele. Furthermore, they are generally not designed to allow for environmental heterozygosity. I am extending the models developed for TreeLD to allow for penetrance models like overdominance and to include environmental heterozygosity in the sample in the analysis.

3. Estimating genetic effects and models from genome wide association scan data. After a successful scan for association it is of great interest to estimate the impact of a detected variant on the phenotype of a carrier (penetrance) and on the population as a whole (frequency). These estimates allow assessing the importance of a mutation; they may provide information about its biological effect and facilitate planning replication studies. I am developing an algorithm for estimating these parameters and the interaction of multiple loci while allowing for ascertainment effects.

Selected Publications


A Letter from the President

Welcome to the University of Michigan, one of our country’s great public universities. One of the many reasons I am thrilled to be part of this university community is because of its long-standing commitment to diversity. I firmly believe that we can learn some of life’s most important lessons from each other. The more varied the perspectives represented, the richer our education. Our differences—whether they be the academic questions that engage us, age, economic background, gender, or race, to name just a few—bring a buoyancy to our campus community and help create the intellectual vitality that makes Michigan internationally renowned.

Since its founding more than 180 years ago, the university has aspired to provide an outstanding education to a diverse student population. Former President James B. Angell, in his 1879 commencement address, said, “Good learning is always catholic and generous... It frowns on caste and bigotry. It spurns the artificial distinctions of conventional society. It greets all comers whose intellectual gifts entitle them to admission to the goodly fellowship of cultivated minds. It is essentially democratic in the best sense of that term.”

Several years ago, Michigan’s faculty, through the university senate, reaffirmed its commitment “to recruiting and maintaining a culturally and racially diverse student body and faculty that are representative of contemporary society, and to assuring that these diverse influences are respected and incorporated into the structure of the university.”

I am proud to belong to an academic community that historically has embraced diversity and is as committed today to this ideal as it was during the days of President Angell. I invite you to join me in supporting Michigan’s ongoing efforts to promote an appreciation of and openness to the viewpoints and contributions of others.

Sincerely,

Mary Sue Coleman
President

Key Contacts

School of Public Health Website
www.sph.umich.edu

U-M Website
www.umich.edu

Admissions
734.764.5425
734.763.5455 fax
sph.inquiries@umich.edu
www.sph.umich.edu/admissions/

Departments
Biostatistics
734.764.5450
734.763.2215 fax
sph.bio.inquiries@umich.edu
www.sph.umich.edu/biostat/

Environmental Health Sciences
734.764.3018
734.764.9424 fax
sph.ehs.inquiries@umich.edu
www.sph.umich.edu/ehs/

Epidemiology
734.764.0274
734.764.3192 fax
sph.epid.inquiries@umich.edu
www.sph.umich.edu/epid/

Health Behavior and Health Education
734.763.9938
734.763.7379 fax
sph.hbhe.inquiries@umich.edu
www.sph.umich.edu/hbhe/

Health Management and Policy
734.763.9900
734.764.4338 fax
sph.hmp.inquiries@umich.edu
www.sph.umich.edu/hmp/

On Job/On Campus Web Page
www.sph.umich.edu/exec_ed/ojoc/

Financial Aid
734.763.6600
734.647.3081 fax
financial.aid@umich.edu
www.finaid.umich.edu/

University Housing
734.763.3164
734.763.2313 fax
www.housing.umich.edu/

U-M Residency Office
734.764.1400
www.umich.edu/~regoff/resreg.html
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