Discussions on the Growth and Future of Biostatistics and Statistics

Yi Li

Harvard University

SUMMARY

A panel discussion jointly sponsored by the Department of Biostatistics, Harvard School of Public Health (HSPH) and the Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute (DFCI), was held in Boston, Massachusetts on April 3, 2008. The panel included Colin Begg from Memorial Sloan Kettering/Cornell Medical School, Bradley Efron from Stanford University and David Harrington from Dana-Farber Cancer Institute/Harvard School of Public Health, and the meeting was organized and moderated by Yi Li from Dana-Farber Cancer Institute/Harvard School of Public Health. Discussions focused on the growth and future of Biostatistics and Statistics and their connections with the other fields, e.g. Probability, Biology, Bioinformatics and Computer Science.

Key Words: Biostatistics; Statistics; Growth and Future.

1 Topics and Questions for Discussion

Prior to the meeting, Yi Li polled HSPH and DFCI faculty and researchers. The following topics were deemed important for the discussion on the growth and future of the profession.

Q.1 Should Biostatistics continue to be a separate discipline from Statistics? Should Departments of Biostatistics and Statistics merge? In other words, are we seeing a convergence of biostatistics and statistics? Biostatisticians develop statistical methodology, statisticians

are getting involved in biological/clinical data. For example, at Harvard, we are debating over moving closer to Cambridge - some say that the move might lead to the eventual merge of the Biostatistics and Statistics departments. What are your thoughts on the division between the disciplines of statistics and biostatistics in general, whether it is widening or closing, and how it may affect our careers and career choices, especially for starting faculty, postdoctoral fellows and students?

Q.2 How should statistics/biostatistics as a field respond to the increasing development of statistical and related methods by non-statisticians, in particular computer scientists? It is striking to some extent that statisticians get involved in applied problems in a rather arbitrary fashion based on personal connections and whether the statistician's personal methodological research fits with the applied problem. Are statisticians sufficiently involved in the most important scientific problems in the world today (at least of those that could make use of statistical methods) and if not, is there some mechanism that could be developed by which we as a profession can make our expertise available to the scientists tackling those problems?

Q.3 How do we close the gap between the sophistication of methods developed in our field and the simplicity of methods actually used by many (if not most) practitioners? Some scientific communities use sophisticated statistical tools and are up to date with the newest developments. Examples are clinical trials, brain imaging, genomics, etc. Other communities routinely use the simplest statistical tools, such as single two-sample tests. Examples are experimental biology and chemistry, cancer imaging, and many other fields outside statistics. How do we explain this gap and what can we do to close it?

Q.4 What makes a statistical methodology successful? Some modern statistical methods have gotten to be very well known in the scientific world, even though they are not usually part of any basic statistics course for non-statisticians. The best examples might be the bootstrap, regression trees, wavelet thresholding. Even Kaplan-Meier and Cox model are not in elementary statistics books! But most statistical methods, even when they are good enough to be published in a statistical journal, might get referenced a few times within the statistics literature and then forgotten, never making it outside the statistics community. What makes a statistical methodology gain widespread popularity?

Q.5 Where should computational biology and bioinformatics sit in relation to biostatistics? Should these subjects be taught as part of cross-departmental programs of which biostatistics is a part or should they be housed within an expanded biostatistics department?

Q.6 Terry Speed (2007) stated "... the most prominent features of the data were systematic. Roughly speaking, we saw in the data very pronounced effects associated with almost every feature of the microarray assay, clear spatial, temporal, reagent and other effects, all dwarfing the random variation. These were what demanded our immediate attention, not the choice of two-sample test statistic or the multiple testing problem. What did we do? We simply did things that seemed sensible, to remove, or at least greatly reduce, the impact

of these systematic effects, and we devised methods for telling whether or not our actions helped, none of it based on probabilities. In the technology-driven world that I now inhabit, I have seen this pattern on many more occasions since then. Briefly stated, the exploratory phase here is far more important than the confirmatory... How do we develop the judgement, devise the procedures, and pass on this experience? I don't see answers in my books on probability-based statistics." Are or aren't we better off without probability?

2 Meeting Summary

Yi Li convened the session at 2:00pm on the 3rd of April, 2008, by welcoming the audience and introducing the panelists.

2.1 Opening Statements

Yi Li: Many in our profession feel swamped with an ever increasing demand for statistical and biostatistical support, and are often stressed by the need to engage in problems spanning diverse areas. It is helpful to step back and get some perspective on what is happening with our field and where it is likely to go in, say, the next 5 years. It's a privilege today to hear the personal views from the leaders like the panelists and many others in the audience on the growth and future of our profession and its connections with the other fields, including Probability, Biology, Bioinformatics and Computer Science. Let us start with Professor Harrington, followed by Professors Efron and Begg.

David Harrington: On the question of whether departments of Statistics and Biostatistics should merge, it is tempting to say something provocative, that perhaps it is time for departments of Biostatistics and Statistics to merge. Much of the methods development in Biostatistics involves difficult mathematics, and the faculty in Statistics Departments increasingly recognize the value of collaboration with scientists from other disciplines. But a moment's thought shows that answer to be glib and superficial. The rapid and remarkable growth of of Statistics and Biostatistics departments in the last 20 years shows how much work there is to do in each of these fields, and that growth is (thankfully) not reversible. Since I posed the question to Yi Li to begin with, I am free to say that the question as posed may be more than a little silly!

Why did I raise the question? The increasing gap between academic departments of Biostatistics and Statistics raises some important issues that need attention. At most universities, academic biostatisticians are too distant, both geographically and intellectually, from undergraduate populations. Undergraduates who have had an introduction to Statistics lack the opportunity to see the vitality of Biostatistics as a scientific discipline that

is deeply embedded in cancer, HIV or cardiovascular research. As a discipline, we lose the opportunity to recruit the best of these students into Biostatistics graduate programs. Statistics education for undergraduates in Statistics Departments tends to concentrate on the mathematics of statistics, and that is a narrow slice of the discipline in practice. I believe that is part of the reason we are increasingly unsuccessful at attracting talented U.S. citizens to pursue statistics in general, and biostatistics in particular

I think both types of departments have some strong tendencies that need to be mitigated. On the one hand, biostatisticians can sometimes latch onto solutions too quickly without carefully thinking about whether the solution is optimal. In some situations, such quick solution is not only suboptimal but also wrong! On the other hand, some statistics department faculty members tend to make the perfect be the enemy of the good. The tendency to focus too much on fine tuning a solution can sometimes slow down the research.

What steps can be taken to build stronger ties between Statistics and Biostatistics Departments? Some steps are obvious – jointly sponsored seminars and social activities. Biostatistics faculty should be come more involved in undergraduate education, including supervising advanced undergraduates in summer research or internship opportunities. University administrations should be convinced to fund intra-university sabbaticals that would allow Statistics faculty to spend significant amounts of time a Biostatistics environment, perhaps with a focus on collaborative research, and vice versa. Graduate students should be encouraged to cross-register for courses and to seek members of dissertation committees from both departments.

I view Q2 as a non-starter! It is terrific when other fields dabble in statistics. That 'dabbling' often leads to significant contribution to statistical methods. Imitation is a sure sign of flattery! It appears that data are driving research in almost all fields now, ranging from data intensive genomics to traditional Arts and Sciences disciplines, such as, history, archaeology and architecture. One of my undergraduate students in an introductory course in Statistics at Harvard College used the distribution of archeological findings of clay pot shards and spatial statistics to determine how villages were organized and distributed in ancient China. The problem was a very difficult one, both because of the uneven nature of the data and the difficulties of spatial inference, but the student had a wonderful intuition for empirical research.

With the merging of statistics with the other fields, we should take the opportunity to learn from other disciplines. Statisticians often overlook the chance to make substantial contributions to fields such as biology, artificial intelligence, or the social sciences. Fisher was known as a geneticist to the biologists; Fred Mosteller made important contributions to educational research. I hope to see a time when people from other fields ask why statisticians dabble so often in their domain! As scientists, statisticians should wander more into other fields where careful inference is essential to progress.

4

Q.5 is about biostatistics versus bioinformatics and their relationship. I think that biostatisticians should definitely play an extremely large role in the field. Technology development in the last 10 years has encouraged the rapid integration of molecular biology and biostatistical techniques. We simply cannot afford to walk away from the biological problems arising in this merger, since they are so important to science and contain so many unsolved statistical questions. We as a profession tend to be reluctant to touch problems until they are well-formulated mathematically, so that, for instance, we know how to calculate sampling distributions, based on finite-sample or asymptotic properties. Sometimes the epistemic variability (variability other than sampling variability) as mentioned in Speed (2007) scares us away from the difficult problems and slows down our engagement in this field.

Brad Efron: First consider Q.1. The training in the two departments is not very different, but the departments tend to attract different students with more mathematical students gravitating to statistics departments and biostatistics departments attracting more scientific students. It is very good for the field and for universities to have two strong departments that increase the visibility of statistics. We are likely to see even more growth in statistical departments including geostatistics and astrostatistics departments. I don't feel bad at all and actually think this is a healthy intellectual advancement.

What do we do about the computer scientists referred to in Q2? My experience is that scientists are good at developing probabilistic methods but are less good at analyzing them. Since other fields have the advantage of being closer to interesting datasets and problems, which will be brought to our attention. So this growth should be positive and will not put us out of business. As a matter of fact, I think this will only increase our business.

Q3 concerns sophistication versus simplicity, which is pretty much the opposite of Q2. I wouldn't feel bad if complicated methods such as neural networks took longer to be put to use, but the reverse seems to be the case. The more complicated a method is the harder it is to critique, but the more it may need criticism.

What makes methods successful (Q.4)? I wish I knew. For example, bootstrap standard errors caught on immediately, but bootstrap confidence intervals, which took a lot of my research time, were not interesting to most people. Another example is the Wilcoxon test. As one of the most cited statistical papers, it is only marginally better than the standard t-test. In contrast, James-Stein's Estimator, which offers dramatic increases in performance compared to the least-squares estimator, is largely ignored. I can never figure out what catches people's interest!

Let me deal with Q.5 and Q.6 altogether. I read Terry's article when it came out in the IMS bulletin, and in fact read all of "Terry's Stuff" in the IMS bulletin because they are so interesting. Terry must have had a lot of better microarrays than I have, because in his, everything is clear after a while, but mine are never so! The question is whether

5

we can have statistics without probability. My own preference is for Fisher's attitude toward statistical inference, which takes a midway point between theoretical models and informal numerical summaries. I understand, and sympathize with Terry's worry that fancy modelling calculations are taking the place of common-sense statistical inference, but Tukey (and Terry) go too far when they want to banish probability theory from our tool chest. There is a tradition of data driven statistics from a French school (correspondence analysis) and based on the "green book" (Mosteller and Tukey, 1977). All of that can be fun, but it does not get very far because real data analyses are dynamic, going back and forth between inference and descriptive statistics. If there were no probability theory, it would be the end of serious inference. So I am firmly against giving up on probability.

Colin Begg: Let me start with Q.1. I address my response from the perspective of a recruiter of graduate students, having been head of a biostatistics group for 20 years at a medical center. I am interested in students who show promise as independent investigators, have a genuine interest in collaborative work, demonstrate an aptitude to analyze and interpret data and know commonly used biostatistical methods (such as categorical data and survival analysis, longitudinal analysis and clinical trials). Biostatistics students tend to have taken more useful methods courses, but statistics students tend to have more of a focus on independent research. In general, I have not noticed a big difference in the credentials and quality of the graduates from each type of department.

For Q.2, as statisticians, we have all been exposed in our education to what might be called a "statistical tradition" that emphasizes scientific norms that characterize the best features of our work. These include the tradition of validating proposed new methods, a respect for the importance of data in scientific work, and a recognition of the importance of study design in the relevance/quality of the data. The work of methodologists not trained in statistics is much less likely to be characterized by these principles.

A short answer to Q.3 is to use simpler methods. Simplicity is a huge advantage in a method, for very good reasons. It is important to emphasize that simplicity is not equal to naïvete. Simpler methods enjoy the benefits of reducing the risk of gross interpretive errors, allowing for transparency of analysis and results and increasing interdisciplinary use. The additional complexity of a method needs to be balanced by the increased benefit due to the complexity.

With respect to Q.4, successful methods often address subject matters that people care about, are on a topic that is easy to explain and are often accompanied by conceptually simple statistics (not necessarily technically simple), plots, images and pivotal data summary that are easy to convey results. It would be interesting to conduct a study of the characteristics of methods that have been historically successful.

Q.5 is very interesting. Academic fields do evolve, so it is unclear what will happen in the future. Computational biology is distinctive from statistics and biostatistics

as it emphasizes, for example, sequence alignment algorithms, protein folding and knowl-edge of genomic databases, requires knowledge of biomathematics, and depends heavily on molecular biology knowledge. Given these differences, the two fields should have separate departments. I, however, do recognize the strong overlap in the interests of statisticians and computational biologists.

Finally turn to Terry's issue (Q.6), which is the most difficult one. Prior to most probabilistic analyses, any dataset requires cleaning, normalization and transformation, which is often done in an informal non-probabilistic manner. This is especially true for genomics, as Terry is trying to emphasize, where the data preparation process is even more intensive. However, does this invalidate the probabilistic principles? Analyses of genomic data should still adhere to the traditional statistical principles that I mentioned earlier and so probability theory is still relevant. In particular, validation of the predictions of data analyses is necessary and this is a key issue in genomics. In summary, the statistical tradition still has a lot to offer in this field and probability theory is essential in carrying out hypothesis testing and prediction validation.

2.2 More Discussion

Carl Morris: These aren't easy questions! At Harvard the statistics and biostatistics departments are physically far apart. We have been working to close that gap, and it will be good to find more ways to move toward a closer relationship. I have the following two comments.

Statistics is fundamentally interdisciplinary. Its core concerns the development of theory and methods for interdisciplinary use. It also fosters generalizing methods developed for one purpose and making them useable by researchers in other fields, often to be applied to quite different topics. Least-squares methods, Kaplan-Meier, and many other well-known procedures are examples of how a procedure developed for one purpose can have many other unsuspected applications.

Model building is an essential part of statistics. Doing that is fundamental to our future development, because good models correspond to advancing science and to understanding how the given data were generated. Methods arising from models built to fit a given data set stand in contrast to "off-the-shelf" methods. Even so, it is understandable that there is not always time for model-building with every data set, and that fields like law and medicine often require the tradition of "off-the-shelf" methods.

David Schoenfeld: I also like to add onto the issue of merger. Indeed, location does matter! If the Harvard School of Public Health were to move to Allston, which would be one and half mile away from the statistics department, it would be better for the statistics and biostatistics departments to combine because it would create a superpower

7

of a department. For example, Stanford medical school has a division of biostatistics which doesn't offer degrees, whose faculty have joint appointments and whose biostatistics students get degrees in statistics. The medical school is a short walk from the Statistics Department. The Department of Statistics at Stanford is a top school in Biostatistics with many recognized leaders in Biostatistics including Brad Efron who is here today. We compete with Stanford to attract students. They are strengthened by having a combined department.

L.J. Wei: I must confess that I have closely followed Brad Efron's work and I even know that when interviewed by Carl Morris (see Holmes et al., 2003), Brad Efron once said 'inference only exists in statistics departments!' I raise this issue because after having been working with bioinformatics people for 5 years as of now, I still find it rather difficult to convince bioinformaticians that inference is important. Here are my questions to Efron. Have we not sold probability and inference well or have we explained uncertainty satisfactorily? Or is the issue something else?

Brad Efron: Our profession has somewhat been bifurcated into two levels: methods development, which is the fun part, and inference. Inference concerns with what we actually learn, which can be less fun because it is sometimes discouraging and does not work well. But it is the crucial part that we provide to the other fields. If we do not, science suffers!

David Harrington: This pattern repeats itself whenever a discipline without statistical training starts relying on empirical methods. For example, statisticians had worked out most of the details of cancer clinical trials, but at the beginning of the HIV epidemic, statisticians had to start from scratch and re-explain clinical trial methodology to infectious disease researchers not used to large clinical trials with less than perfect adherence. As reproducibility becomes more important in bioinformatics, uncertainty and measuring uncertainty will become increasingly relevant and the issue will work itself out eventually.

Yi Li: I would like to elaborate on the lack of reproducibility of the statistical findings for modern microbiological experiments. This was actually an issue Marvin Zelen discussed with me prior to this meeting. For example, given a disease and millions of genes and through some magic of statistics, one will almost surely find several highly significant genes or find some highly significant pathways that are related to this disease. However, if these experiments were to be repeated, the significance would likely vaporize and some new "significant" genes and pathways would pop up! It seems that we just do not have adequate validation tools in this field. I worry that this will not be bona fide for our profession as we appear to lose credibility in the eyes of subject-matter scientists. Should we take one step back and try to conduct more "focussed" learning? Perhaps, it is more viable to link a particular gene to a variety of diseases than blindly finding a bunch of non-repeatable genes for a given disease.

Brad Efron: I've been worried about our credibility too. Part of the problem is power:

with 10,000 genes and 100 subjects, most of the "interesting" genes will be missed in any one analysis, just as you say. This is one of the concerns expressed in Efron (2008). But I've also been concerned about overly optimistic statistical methods that don't take into account all the things that can go wrong in massive data studies. Both of my talks at Harvard, titled by "Are a Set of Microarrays Independent of Each Other?" and "Simultaneous Inference: When Should Hypothesis Testing Problems Be Combined?", involved things that can go wrong.

James Ware: I have some comments on Colin Begg's response to Q.3 and Q.4. I would take the definition of a method being successful as its being well-known. Methods that are well-known, such as Kaplan-Meier and proportional hazards models, generally communicate results in a way that is apprehensible to colleagues in other disciplines. It is important that the results are less opaque so that our colleagues can understand them. This is also why some mathematically sophisticated methods do not fare very well.

Now let me raise the following issue to Efron, who is an institutional leader at Stanford. The DFCI has had more success at integrating computational biology and biostatistics because it is a research institute and so can be more aggressive. On the other hand, the HSPH, as an educational enterprise, has struggled because computational biology needs to be placed within a department but departments have professional boundaries, and it is unclear how far outside of a department's scope we can reach. So my question to Efron is this. What is the scope of computational biology that comfortably fits in the statistics?

Brad Efron: Stanford has a bioinformatics group in the medical school, which focuses on descriptive statistics, database management, and some sophisticated software development. The statistics department does not have man-power to do. The bioinformatics group is often a client for the statistics department, but their relationships, as Ware raises, are institution dependent. It often takes a leader or some key persons to bring groups together. For example, Lincoln Moses almost single-handedly put Stanford biostatistics together. However, when we once talked about the merger of the Bioinformatics department and the Health Research and Policy Department (our version of School of Public Health which contains Biostatistics) at Stanford, it was decided that the merger was of neither side's interest.

I'd like to address the issue of useful methods that Ware just raised. Simple and useful methods are good, but we are often the ones who tell scientists what is simple. If we stick to our guns we can convince them of the utility of a method. For example, ANOVA is in fact very complicated, but we have managed to sell it well to people who could find it useful.

Winston Hide: As a bioinformatician, I would like to make two comments. The first is that the statistical contributions to the algorithms and methodological developments, for example, the gene sequence searching algorithm, in bioinformatics have proved to be

very valuable. Secondly, Bioinformaticians recognize and appreciate the need for strong statistical knowledge for robust analyses and that they need to learn what they do not know about data from statisticians. The two groups should be brought close together. We did have some successful experience in my institute in South Africa.

David Harrington: It appears the solution to L.J. Wei's issue is on the way! Now I would like to ask my fellow panel members and Louise Ryan, the Chair of Harvard Biostatistics, the following questions. It is a question on whether our statistical methods developed are sometimes too opaque or at least too opaque to other fields. Do we train our students, the future statisticians, to be scientifically literate so that when they have a method they understand it will make a contribution to another field? Colin Begg, from the perspective of a recruiter who has done much hiring, do you find your recruits are scientifically literate so that they are good at picking out problems that are actually useful and important?

Colin Begg: There is wide variety in the breadth of scientific knowledge of statistics graduates. Some graduate are very knowledgeable about the scientific background of data, but it really depends on the candidate.

Brad Efron: These issues are time-dependent. When Carl Morris and I were graduate students, Stanford statistics was dominated by mathematics. Now statistics has moved closer to science. This movement is certainly positive since it broadens the base of the field.

Jun Liu: My comments are related to LJ Wei's question and Efron's answer. Under the current funding mechanisms there is a great emphasis on novel methods, for example, from non-statistical study sections. These methods appear attractive but are often inferior to existing methods. I am wondering how we can influence the funding mechanisms for promoting truly useful work.

We statisticians can of course do some clean-up work. For example, my recent two papers were pretty "bad" in the sense of criticizing two papers in *Cell* and *Science* for poor work in prediction and robustness of analysis. I do not know, however, whether such effort has any effect. If it does, we make enemies; otherwise we are wasting our breath. I am not sure what to do because based on my review experience simpler methods get shot down quickly. Simple methods appear successful or vice versa because we are looking at them retrospectively. Simpler and smarter methods are the hardest ones to find.

Colin Begg: As a field, which is not only limited to biostatistics/statistics, we are not self-critical enough of our methods, and would greatly benefit from more attention being paid in our journals to critical evaluation of complex new methods, as opposed to the overwhelming focus on novelty that seems to dominate our collective research output. That is, a more pro-active debate in the literature of the strengths and weaknesses of new

and existing methods would be beneficial.

Louise Ryan: The conversation has moved so quickly that I really do not know where to jump in! Returning though to David Harrington's question on producing scientifically literate student and on what methods actually are good or useful, I would like to say that methods do not need to be simple to be popular. Methods that fill a void or gap related to an interesting problem or question are often the best. The problem however lies in that methods developed for applied questions are sometimes not rewarded sufficiently because, for example, promotion committees tend to emphasize methodological journals too heavily. The issue is also tied to the funding mechanisms as Jun Liu mentioned. Sometime we are jealous of people from other fields, for example, computer scientists who take the "off-the-shelf" methods and come up with quick answers for compelling problems, because we often like to dig into the problems and find the optimal solutions. However, by the time we have found the optimal answers, the problem has been solved and the question of finding the optimal solution has become irrelevant. So our struggle lies in the fact that we are trained to establish the mathematical foundation of problems but our effort is often unappreciated by the academic reward systems. It appears that we do need to learn to how balance theory and application, especially under the tight funding situations that we currently face.

While I am here, I can't resist commenting on Q.6! I very much like what Speed (2007) says. In my own field of application, environmental health research and risk assessment, the variability and uncertainty arising from scientific mechanisms, bias attributable to data problems and so on, often completely swamp the variability we statisticians tend to focus on. My concern is that we as a profession take too narrow a view of inference and uncertainty. Probability is surely very important, but, as Terry argues, we do need to think about it in a much broader way. We need to look beyond the confines of traditional statistical analysis and think about the real underlying questions of interest. Sometimes there are exciting opportunities to use our tools of probability and inference to explore bias, to incorporate multiple sources of data and to think in terms of synthesizing information to aid in effective and appropriate decision-making.

David Harrington: I strongly believe that biostatistics is most successful when it is embedded in a field. For example, biostatisticians can avoid bias and reduce uncertainty in AIDS and cancer trials by good design. As I mentioned to our statisticians at the DFCI, a well designed clinical trial is one that can be explained to a high school student! Of course, outside the experimental world, like in the observational studies, it is much harder to do so.

In fact the integration of our field with the science has put us in the frontlines to handle the uncertainty arising from applied projects. A merger of biostatistics and statistics would probably not be beneficial as it would take biostatistics away from the front-lines and take biostatistics to a place where it is difficult to reward for interdisciplinary research.

Cheng Li: Going back to L.J. Wei's comments on the difficulty of convincing bioinformaticians to believe in statistical inference, I'd like to share some observations from my collaborative experience in genomics. At the initial stage, molecular biologists want to identify top genes from genomics studies and use these genes for further experimental validation or hypothesis generation. Complex inference methods tend to give similar conclusions as simpler and faster methods in these initial analyses. This may partially explain why inference is not widely appreciated by biologists in genomics analysis.

It is a rare chance that we are sitting in the same room with Brad Efron, Colin Begg and many other top statisticians! As a junior faculty member, I would like to ask the senior folks on what problems junior faculty should work on. What kind of work will likely attract funding or have long-term impact?

David Harrington: Ask biologists you work with for questions, because they know what is going on. You may need to translate those questions into those which can be posed as statistical inference problems. We hire junior faculty like those at this meeting because of their potential to both extend our discipline and to conduct significant joint research with other scientists as well.

Brad Efron: Work on what is interesting to you personally because good science cannot come out of rote work. Biological questions have opened up the statistical field, with massive inference being a typical example. Classical 20th Century statistics developed superb theories for estimation and testing in small problems, but not for the kind of massive inference situations we see for example in microarray situations. Notably missing are convincing theories of prediction and model selection, so these are promising open areas for 21st Century statisticians. Personally, I find it much easier to work on something when I have a compelling data example, so hanging around a good source of data is a useful tactic.

Armin Schwartzman: Are statisticians sufficiently involved in the most important scientific problems in the world today? For example, climate change is an important and emerging issue that intrinsically involves statistical questions which remain unaddressed. Where do we stand and where should we go?

Colin Begg: It is important to think big, but unfortunately most statisticians think small because it helps move our careers along more quickly. This question goes to the heart of the issue of what value statisticians add to scientific debates. We have value to add, but not everyone thinks statisticians are crucial to this area of research so we need to prove ourselves. Also, we cannot assume we are the best people to analyze the data simply because we are trained statistically. Some scientists do have a good sense of making right decisions for their data even without in-depth statistical training.

Chris Paciorek: As a junior statistician, I am asking whether the current incentive structure is appropriate in our field for faculty evaluation. Can we go beyond counting

the number of papers published and pay more attention to the work that generates more discussion and point-counterpoint debate?

Colin Begg: This is a very live issue in our field and beyond. Promotion committees struggle with the issue since we are increasingly involved in Team Science. In this situation everyone on a team needs recognition in a promotion system, but it is often hard to pick out individual contributions for evaluation. This is an issue because throughout science there is a deep seated tradition to give priority to leaders and to independent research.

David Harrington: Promotion evaluation involves so much uncertainty because we have to use 6-10 years of research as a surrogate for a lifetime of research. It is an imperfect surrogate, but we do need to make a decision somehow. In some cases at the Harvard medical school, the process can take as long as 15 years, but still I am not sure how well it works. The easy solutions can be extreme: tenure for everyone or tenure for no one. But when it may take 15 or even more years for work to flourish, I really do not see there is an easy fix!

Layla Parast (first year Harvard PhD student): I would like to go back to Q.1. Many students think hard about whether to apply to statistics or biostatistics departments and merging the departments would get rid of the differences and benefits that drove students' decisions. Most biostatistics students have math backgrounds so there is a lot they can learn from biologists. It is good that the departments are separate and allow for more freedom for biostatistics students to take classes and pursue interests in non-quantitative fields. It would be very nice if there was more collaboration between the Harvard biostatistics and statistics departments, for example, with inter-departmental talks.

David Harrington: I think this is a great idea.

3   Conclusion

Yi Li thanked the panel again and adjourned the meeting at 3:30pm.

Acknowledgements

http://www.stat.columbia.edu/∼cook/movabletype/archives/2008/03/some_thoughts_o_4.html

Reference

Efron, B. (2008) Microarrays, Empirical Bayes, and the Two-Groups Model. *Statistical Science*, in press.

Holmes, S., Morris, C. and Tibshirani, R. (2003) Bradley Efron: a conversation with good friends. *Statistical Science*, **18**, 268-281.

Speed, T. (2007) Statistics without Probability. *IMS Bulletin*, **36**, page 12.

Mosteller, F. and Tukey, J. (1977) *Data Analysis and Regression: A Second Course in Statistics* Addison-Wesley Series in Behavioral Science.