Reviewing Manuscripts

Guest Lecturer:
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Why serve as a reviewer?

- Contribution to the scientific community
- Keep current with the literature
- Good experience for own manuscript submissions
- Improve your communication skills

Overview of the Scholarly Publishing Process

1. Author submits manuscript to academic journal editor
2. Editor determines whether manuscript has sufficient merit to be reviewed by editorial board or selected external reviewers
3. Manuscript sent back to the author with a rejection letter or on to reviewers

http://www.publishnotperish.org
Overview of the Scholarly Publishing Process

4. Reviewer contacted by editor (abstract & title) and either declines review or agrees to review and discusses possible conflicts of interest or if work is outside specialty
5. Reviewers return the manuscript to the editor with comments and recommendations (depending on peer review model)
6. Editor sends manuscript back to the author with either a rejection letter or a request for revisions

Roles in Scholarly Publishing

1. Scholars create the work that is published. What is most important to scholars is the prestige of the journal, the efficiency and fairness of the review process, the timeliness of publication, and their out-of-pocket publication costs.

Roles in Scholarly Publishing

2. Editors and peer reviewers provide quality control for the content, including screening submissions, reviewing manuscripts, suggesting revisions, corresponding with authors, and overseeing the final copy. Their main concern is advancing knowledge in their field, creating a prestigious journal, increasing the potential impact of the journal, and obtaining the support of the publisher.
Roles in Scholarly Publishing

3. **Publishers** (usually commercial publishers or professional societies) are responsible for getting the journal into the marketplace. What drives publishers is making a profit (or for professional societies, at least breaking even) on the publication. They are concerned about holding costs down and raising subscription rates to create a healthy profit margin.

4. **Subscribers** mostly institutions and libraries, purchase the journals and provide access to the scholars in their community. They are concerned about their budgets and deeply affected by increases in the price of journal subscriptions. They also want to provide access to the most prestigious journals for their faculty and students.

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Open Access

- Digital, online, free of charge & free of most copyright and licensing restrictions
- Authors retain copyright to their scholarly works but pay for dissemination costs ($500-$1500)
- Response to spiraling journal subscription costs & need for free and immediate access to research results
- Repositories such as BioMed Central

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Reviewing Process

- Be familiar with:
  - Journal guidelines
  - Journal audience
- Confidentiality
- Timing
  - Should take several hours (read at least twice)
  - Meet deadlines!
### What to look for when reading the manuscript

**Introduction**
- Significance and originality
- What is the question/problem?
- Why is this important?
- What ‘gap’ does this work fill?

**Literature Review**
- Insist on correct and thorough citations of existing work
- If necessary & time permits, check on reference(s) and provide citations that are helpful

**Methods**
- Enough details to reproduce results?
- Appropriate for answering question or problem?

**Results**
- Does the study address question or problem?
- Do the conclusions follow?
- Check figures/tables carefully

**Review Style**
- Put yourself in their shoes!
- Write to convince the author
- Be positive and kind (no sarcasm & hostility)
- Be tough and demanding (but not confrontational)
- Provide constructive criticisms
Review Style

• Use conditional wording (perhaps, but, etc.)
• Write clearly & use complete sentences
• If making a specific comment in the text, quote or state location in the manuscript (page number, paragraph, etc.)
• Organize comments in a numbered list

Review Content

• Summary of paper (short paragraph)
  • Encourages thorough reading of the manuscript
  • Shows authors that you read it
  • Helps the editor make decision
• Give overall reaction
• Pinpoint the good AND the bad
• List of suggestions/do-able tasks
  • Helps authors
  • Helps you judge revisions

Review Content

• Don’t spend too much time on grammar/style, but state if repeated errors or if the manuscript does not read well
• If recommending revision: Be specific and justify possible changes
• If recommending rejection: Address reasons and suggestions for future work

Other References

Example Review #1

Critique #1:
The EM algorithm proposed here is derived in a principled manner using Bayesian change point algorithm with either a double exponential distribution or a normal distribution for the priors. The authors likely didn’t know of a paper outside their field showing that the motif detection problem as a whole can be seen as a change point problem (Liu et al., http://lib.stat.cmu.edu/bayesworkshop/2001/invited.html). The proposed model fits this paradigm. This connection should be cited.

Closed form solutions for estimation on the M-step are derived, and a revised E-step with both the motif locations and the change points as missing data is also derived. The choice of a motif model with two change points, and thus three models, covers unimodal and bimodal distribution models for motifs. This seems the most complex model that current evidence from existing analyses of PWM based on experimentally reported transcription factor binding sites justifies.

Example Review #1

Example Review #1

With sequence data from one transcription factor, CRP, and a motif of 16 bp, they show that with values of the prior weights on the conservation penalty greater than the null of zero, they detect motifs in about 50% more sequence than under the null of lambda = 0 using the variable change point model. While this does provide some very preliminary evidence of improved performance using a model sensitive to information profiles, it is very limited. I recommend a broader analysis with several more transcription factors in any revision.

Example Review #1

Some other less central points are the following. E. coli intergenic sequences are rarely more than 500 bp long. The two part approaches of MEME and BIOPROSPECTOR, and the fragmentation algorithm of Liu et al. with some minor restrictions, provide alternate models for the one proposed here. A better review of these related methods should be presented. The paper is too long. The long length will yield lower readership. With careful choice of what to include and more concise writing it should be possible to trim the paper to half its current length.

I recommend that the authors be encouraged to resubmit a substantially shortened version that includes analyses for other transcription factors and other modifications mentioned above. This revision can and should be written as a stand-alone paper with the addition of a paragraph that covers the limited material in the companion paper.

Example Review #1

Example Review #2

Critique #2:
Referees are asked to ensure that the following questions are addressed in their reports:

1. Does the work include all necessary controls?
   YES

2. Are the conclusions drawn adequately supported by the data shown?
   YES/NO

The results of the evaluation on the Crp data set seem reasonable, but there are some artifacts in the results: for example, the failure to retrieve any motifs for L=700, lamda=30. Is it possible to include results for some similar systems as well to provide additional confirmation of these results?
Example Review #2

5. If you feel that the paper is of broad interest to others in the field, or of outstanding interest to a broad audience of biologists, please say so, with a brief explanation of why. YES/NO

Minor points:
• pp12-13 Clarify that the constants in (4) and (5) are to normalize the probability distributions. This would be more obvious if the probability functions were given as well as the log likelihoods.
• p23 typing error in the regime specification (I 3, 2 11, I 3) should be (I 3, II 11, I 3). Can regime specifications be expressed in a clearer form?
• p27 I am assuming that by "elongation" you mean that a random amount of flanking sequence was included on each side. Please clarify this, to confirm that it is real flanking sequence and not randomly-sampled synthetic sequence.