NOTES ON THIS EXAMPLE: Four very well done and technically competent first reviews of a paper submitted to a top journal. All four reviewers recommend "REVISE AND RESUBMIT". However, you can easily see the breadth of their comments – while some are similar (the paper is too long and has too many figures), the technical reaction varies.

As an **author** of the submitted paper, you would have many useful suggestions to undertake additional work, consult new references in the literature and reorganize and condense the paper. You would also need to respond to numerous points adequately to have a chance of acceptance in the second round.

As a **reviewer**, you can see the amount of time and effort spent by each person below. A well done review represents a considerable amount of work done even if the reviewer is technically expert in that area and current with the literature.

As an **editor** or associate editor, the task here was to enlist the services of multiple technically expert reviewers for this paper (after first reviewing the paper quickly to make sure it is appropriate for the journal). The editor / associate editor must ensure the reviews are returned in a timely manner, summarize these results and make a recommendation to the editor in chief / authors.

These reviews are reported verbatim so you can see them as they would be returned to the authors. As with most technical areas today, the scholarly community is global (in this case, the four reviews come from four different countries, while the paper itself is submitted from a fifth country, the editor in chief is in a sixth country and the associate editor in a seventh country!)

REVIEW 1

CONFIDENTIAL COMMENTS TO EDITORS

I like the research, solid and publishable, but the exposition is lackluster.

COMMENTS TO AUTHOR(S)

Overview:

This paper tests the impact of a collection of spatial structures (networks) on an MOEA and finds that network topology has a significant impact on performance for problems with more than two objectives. The paper is somewhat innovative, taking ideas from different lines of research and connecting them. The strongest points of the paper are its careful experimental design and statistical rigor. The experiments are reproducible and the conclusions are well supported. I also like the variety of different analyses performed; the number of non-dominated individuals plots gives a nice perspective on the evolutionary dynamics. The weakest part of this paper is its organization and clarity. I think the authors need to review the organization of the paper. Too much of the core of the paper appears only by reference. Succinct summaries of referenced material should be included. Likewise I did an inordinate amount of flipping back and forth to find things. I think a better organization of the material is possible (and apologize for not supplying a suggested one). Finally the paper needed one more proof reading pass, see comments.

Overall I think there is publishable work here but it needs a somewhat improved exposition. An interesting paper that triggered several ideas as I read it.

A Few Comments:

So far, equation 3 makes no sense? Is epsilon-dot-g-sub-i supposed to be epsilon-plus-g-sub-i? The inequality also seems to be backwards for maximization (unless that was a minus, not a plus). I looked up epsilon dominance in the references and it seems to consist of partitioning space into epsilon-boxes and permitting only one non-dominated solution per box. The current equation three seems to suggest an unproductive crushing of space? Unless we have an Adobe character set problem that replaced your plus or minus with a dot?

The example scale-free network in figure 4 is a tree. Is this an accident? If so a non-tree might be better because it seems more representative.

The details of the re-wiring used to create small-world networks in Section V, part A needs to be explained in a good deal more detail. How are the links chosen and are they reassigned completely at random?

The paper relies too much on description by reference, both to external references and internally where material seems to be presented out of sequence and then referenced from where it is needed in sequence. There is a need to reorganize the paper so that the reader need no flip back and forth so much and a greater need to incorporate succinct summaries of references so that the reader need not flip to the web over and over.

The specific networks you used should be placed in a web archive. Some of my own research, not yet published, demonstrates that different random network selected by the same method are pretty much equivalent for most problems but, occasionally, the details of the random network matters; so far always on a difficult problem. Archiving the networks you use should nail down replicability.

REVIEW 2

CONFIDENTIAL COMMENTS TO EDITORS

none

COMMENTS TO AUTHOR(S)

Review

Multiobjective optimisation using a complex network-based evolutionary algorithm

General impression:

Text is generally too long. The content could be more compact. The text seems to be a slightly abridged version of a complete very good Master thesis. The text is very elaborate, too detailed and also often too specific to be applicable in general. A real interpretation of the empirically found results is missing.

The reader is left with a lot of details and many graphs on specific examples. The details are very interesting but are not too helpful for the general understanding of the complex behaviour of multi-objective evolutionary algorithms with structured populations. The core findings are certainly worth publishing but can be summarised on much less pages than 40.

Hints for improvements:

- Title is irritating: What do you mean by 'complex'? A title should guide a reader. Suggestion: "An empirical study of multi-objective evolutionary algorithms with network-based population structures" or something similar that reflects the content of the article.

- Abstract too long: 220 words (should be 100 to 200)

- Abstract is quite general. It should contain the core topics of the paper and mention them by name: "A variety of techniques ..." was Krusak-Wallis test or Epsilon-MOEA and NSGA-II with archive served as basis structure. , L, C and I indicators was used.

- Please use passive voice throughout the text, i.e. avoid 'we' etc. where possible.

- Hardware used not mentioned (parallel computer?). Speed-up recognised?

- Some pages are nearly empty due to page breaks (e.g. page 7, page 11, 33).

- Text in the graphics sometimes very hard to read (too tiny), see pages 2, 16, 17, 24, 28, 31, 32, 34-37

- Fig 1. poor picture quality (jpg shadows). Reference is missing in caption.

- Lines sometimes hard to distinguish or quite thin (e.g. pages 15, 25, 26).

- Convergence plots may improve with log scaling in the y-axis (fig 6, 7)?

- A clue to interpret the effect of the network structure may be selection pressure.

- Figures 8 to 10 could be described in short highlighting the most relevant observations. Perhaps two most relevant figures should be shown for illustration purposes only.

- Table IV, V, VI, VII are too detailed. I think the most relevant statements of the tables should be extracted and interpreted. If the tables are really relevant in detail, they may be added as an appendix.

- In the paragraph about the scalable problems (pp 20) NSGA-II was not used for comparison. This could be interesting because the behaviour of NSGA-II is known.

- The term 'evolutionary trajectory' on page 24 does not become clear and is used – I think – in a more colloquial way.

- Figure 19 to 20 seem not really relevant. The figures are described with just one sentence only.

- Stating questions directly is not a good writing style (page 30). Better set up a hypotheses and proof or disproof it.

- Figures 21 to 24 are very problem specific and may be omitted. A reader would be interested in the interpretation of the distribution rather than in the pictures of the concrete distributions.

- Page 38: A Pareto-optimal front is in general not necessarily a high-dimensional surface.

- Page 38: Idea of may be mentioned briefly again because some busy reader just looks at the conclusions.

Questions:

- Is it possible that parts of the populations in a random network may be completely disconnected? This implies a parallel evolution of separated populations without genetic exchange. In some cases the random networks performed quite well. This behaviour is known for single objective algorithms (see e.g. nested ES by Herdy and Rechenberg 1994) but has not been shown – as far as I know – for multi-objective algorithms which share a common archive. How many disconnected populations appeared and what was their average size?

- The e-dominance was introduced but never used for interpretation purposes.

- Is it possible to suggest some harder general rules which can be draw from this empirical study? This will help other researchers in related areas.

Additional literature on dynamic population structures:

"Evolutionary Algorithms on a Self-Organized, Dynamic Lattice," P. Halpern, in Unifying Themes in Complex Systems, Vol. 2, Proceedings of the Second International Conference on Complex Systems, edited by Yaneer Bar-Yam and Ali Minai, (Boulder, CO: Westview Press, 2003).

REVIEW 3

CONFIDENTIAL COMMENTS TO EDITORS

I belive that the topic and the investigation proposed by the authors is interesting and absolutely relevant for the field of Evolutionary Computation, and in particular to those interested in multiobjective optimization.

However, I think that the article cannot be accepted for publication in its present status, the main reasons for this being:

(1) The article is too long and contains too many figures.

(2) Probably a more important reason than the one in the previous point. I don't agree with the authors' research line: the comparison the authors make between different structures is in most cases meaningless.

The two issues raised above must be, to my opinion, answered by the authors in a satisfactory way before the article is published on this journal. In particular, if the authors agree on point (2), then it will probably be necessary to reorganise and somehow rewrite the article.

COMMENTS TO AUTHOR(S)

I belive that the topic and the investigation proposed by the authors is interesting and absolutely relevant for the field of Evolutionary Computation, and in particular to those interested in multiobjective optimization.

However, I think that the article cannot be accepted for publication in its present status, the main reasons for this being:

(1) The article is too long and contains too many figures. If it is true that the authors have performed many experiments to support their conclusion, I believe that an effort could be done in eliminating many figures (I'm mostly talking of figures 6,7,12,13,14,15,18,19,20). It is clearly up to the authors to decide what to do, but I suggest to state in some sentences the observation and the conclusions that can be derived by the results shown in those figures, showing only few significant figures. Moreover, those figures and very difficult (if not impossible) to read: the superposition of so many curves derives in a hard job in discriminating the different lines. Finally, those average lines without a discussion on the standard deviation or the confidence intervals of the results is almost useless to draw meaningfull conclusions.

Also some of the figures on clustering could be eliminated without reducing the scientific quality of the paper, resulting in a more enjoyable reading for the reader.

(2) Probably a more important reason than the one in the previous point. I don't agree with the authors' research line (not the direction that I absolutely encourage the authors to pursue). The comparison the authors make between different structures is in most cases meaningless.

When proposing the 9 different graphs, an important caracteristic is uderestimated: different s in the networks implies a different total number of edges in the graphs. Having a different density of edges in a graphs means different caracteristics in the propagation of information, thus different optimization behaviors that are observed in two structures can be due to this difference instead of the different family (scale-free, regular, random, or small world). The 9 graphs used have a total number of edges (according to the order in table I) of 4096, 2048, 4045, 6093, 8090, 4096, 12288, 24576, 25959.

The general conclusion that the fact that the population has a structure makes a difference in the optimization process can be surely drawn (but there is only a small novelty, since it has already been said in classical cellular EAs, see remarks on missing biblio below). However, the only fair comparisons that can be done to examine the influence of the family of graphs on the dynamics are those between graphs M, SFB, and SWA (that have a comparable number of edges around 4096).

Some other comments on the used structures:

- The scale-free are generated only with the Albert-Barabasi algorithm, thus all have a gamma around 3. It would be interesting to investigate the dynamics of other scale free structures with different gammas (but with a common total number of edges).

- The small-world graphs are all generated with the same rewiring probability. It would be preferable to investigate small-world obtained with different rewiring probabilities (of course with the same total number of edges).

- The random graph is absolutely too dense (as the SWC), an average degree of 50 makes it almost equivalent to a panmictic population from an EA point of view.

The two issues raised above must be, to my opinion, answered by the authors in a satisfactory way before the article is published on this journal In particular, if the authors agree on point (2), then it will probably be necessary to reorganise and somehow rewrite the article.

Some other remarks/commets/suggestions:

(i) From the title to the rest of the article the authors talk of complex networks. If I can agree that scalefrre and small-world graphs can be considered as complex structures, I doubt it for random graphs (that are also analised), and I surely not agree for regular lattices (also employed in the study). I would suggest to avoid to use this term for all networks as in the title.

(ii) Page 2, important bibliography missing. Cellular EAs have been used not only for theoretical studies (as stated in the introduction). The influence of the topology of the population on the serach dynamics has been studied by Dorronsoro et al. @ CEC2004, Preuss and Lasarczyk @ PPSN2004, and Giacobini et al. @ EVOCOP 2005. The authors should cite these works.

(iii) Page 6: the authors should say something on the fact that also asynchronous update policies have been proposed.

(iv) Page 6, line 9: "Proportional or linear ranking" -> I would at least add tournament, and i would even discuss proportional since it is not widely accepted as a good selection mechanism in cellular EAs.

(v) Page 9, subsection B, line 1: "cellular genetic algorithms" -> "cellular evolutionary algorithms".

(vi) Page 9, subsection B, line 1: only one is the authors' "personal extension", the added archive.

(vii) Figs 8-9-10: since a fair comparison can only be done between structures M, SFB, SWA, the only statistically relevant differences are: M-SFB in Fig. 8-a, 9-a and 9-b, M-SFB and SFB-SWA in Fig. 8-b, 10-a, 10-b, 10-e and 10-f. In general, there is more problem dependance than structure dependance in the results shown in these figures.

(viii) Table VIII: always comparing only the 3 fairly comparable, SFB performes worst than M and SWA, and those 2 performs equivalently ... it sounds as in classical cellular EAs for problems that need slow selection pressure.

(ix) Table IX: always comparing only the 3 fairly comparable, M-SFB-SWA performs equivalently (problem hardness dependance, probably no influence by the structure).

(x) Page 24, line 13-14: similar s imply similar behaviors, that is not surprising (see point (2)).

(xi) Page 24, line 17->20: he behavior is probably not due to L but to the increasing number of edges.

REVIEW 4

CONFIDENTIAL COMMENTS TO EDITORS

none

COMMENTS TO AUTHOR(S)

This is a well presented work dealing with using complex networks to MO. The ideas of decentralized search are nice and similar to that of cellular algorithms, which are conveniently cited in the paper. In this sense, there is not a high contribution to the field from a general point of view. However, the work could be interesting if authors succeed in including the following advices in the next version:

1. Include examples of the resulting Pareto fronts for all the algorithms evaluated.

2. Remove the large amount of figures in 12/13 and 14/15 and just keep some of them as examples. There are too many graphs in the paper and too few tables with concrete values that are more important for future comparisons.

3. Some benchmarks are coming from PISA. Authors don't clarify if the NSGA II implementation is coming also from PISA... If so, this is the reason to be able of beating it with their algorithms, since the PISA implementation is known to have a non orthodox implementation of NSGA II. In fact, once the Pareto fronts are in the paper I'm not sure if the new proposals will be able of improving it.

4. Since the contribution on the technique is low (it works like a kind of cellular EA) authors are requested to include existing results on MO benchmarks with cellular EAs and show that they can improve on them. This is is must, since otherwise there is no contribution at all in the article.

5. Citing technical reports in a journal paper is usually not a good idea and out of standards (hypergraph inspired algorithms, for example).

6. Including an archive in the algorithm and not using it to feedback solutions is not a "future work" but a MUST: we all know that this is important; the idea belong to the state of the art in MO algorithms, so authors should include it in this paper (this journal is an important one in the field!). 7. The selection of DTLZ 4 and 5 and not all of them is suspicious. All the benchmark should be included in the next version to see the results of the proposed algorithms (by the way, not clear that number 6 is the hardest...).

8. Hypervolume CAN be used with 3 objectives, no problem in this relating computational times(!).

9. 200 time steps means probably more than 200.000 evaluations. In a world in which we all are going for 25.000 or similar figures it seems too much effort to solve these problems. Plot results with a fewer evaluations. Also, using an archive of 100 solutions could be fairer in the experiments with respect NSGA II.

I think that all this is needed, since the article right now is focused too much on minor details. First, present your contribution (not in the idea, since cellular EAs are almost the same, but on the results), plot Pareto fronts, use the appropriate algorithms to compare with, and show better accuracy and performance. What you have is visually attractive and with a couple of interesting data, but not really meriting a publication in TEC.