

Lecture Notes in Computer Science: Authors' Instructions for the Preparation of Camera-Ready Contributions to LNCS/LNAI/LNBI Proceedings

Alfred Hofmann*, Ursula Barth, Ingrid Haas, Frank Holzwarth,
Anna Kramer, Leonie Kunz, Christine Reiß,
Nicole Sator, Erika Siebert-Cole, and Peter Straßer

Springer-Verlag, Computer Science Editorial,
Tiergartenstr. 17, 69121 Heidelberg, Germany
{alfred.hofmann,ursula.barth,ingrid.haas,frank.holzwarth,
anna.kramer,leonie.kunz,christine.reiss,nicole.sator,
erika.siebert-cole,peter.strasser,lncs}@springer.com
<http://www.springer.com/lncs>

Abstract. The abstract should summarize the contents of the paper and should contain at least 70 and at most 150 words. It should be written using the *abstract* environment.

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1 Introduction

Metagenomics is a direct sequencing of DNA from all organisms in an environment without culturing. It is a culture-independent tool for studying environmental microorganisms. In addition to the information about taxonomic diversity (who is there), metagenomics gives insight into the physiology of the organisms present in the environment (what are they doing), through studying their genes. Two main goals to be achieved with metagenomics are finding new genes with desired biological activity (bioprospecting) and studying environmental microbes without the need to culture them.

Metagenomic data are considerably more complex. The assembly of metagenomic data is complicated due to several reasons. Few of them are: (i) widely different levels of representation for different organisms in a community; (ii) genomic variation between closely related organisms; (iii) conserved genomic regions shared by distantly related organisms; and (iv) repetitive sequences within individual genomes. Genomic repeats are the major challenge when assembling

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isolated genomes and their effect is prominently seen in metagenomic datasets. It has been shown in (cite kingsford) that the number of reconstructions grow exponentially with the number of repeats. Therefore it is impossible to find one correct solution for assembly. There are several approaches such as (cite bambus2) to find repeats in metagenomic data. The main drawback of these methods is that they do not scale well as the number of nodes in the assembly graph increases and prove very inefficient as the number of nodes reaches to about a million. To tackle this problem, we explore some of the work in social network analysis, particularly in the area of node centrality. We make use of betweenness centrality to find out repeats in the assembly graph.

2 Related Work

In graph theory and network analysis, indicators of centrality identify the most important vertices within a graph. Several metrics to measure centrality have been proposed. We make use of betweenness centrality. For a particular node, betweenness centrality is equal to the number of shortest paths from all vertices to all others that pass through that node. Formally, for a node v , it is defined by the following expression:

$$g(v) = \sum_{s \neq t \neq v} \frac{\sigma_{st}(v)}{\sigma_{st}}$$

where σ_{st} is the total number of shortest paths from node s to node t and $\sigma_{st}(v)$ is the number of those paths passing through v .

Brandes (cite brandes) gives an exact algorithm for computing betweenness centrality of all the nodes that is based on solving a single source shortest path problem for each node. This algorithm takes time $\Theta(mn)$ for unit edge weight graphs and $\Theta(mn + n^2 \log(n))$ for weighted graphs. This algorithm does not scale well with large networks with millions of nodes and edges.

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Here are some examples of headings: “Criteria to Disprove Context-Freeness of Collage Language”, “On Correcting the Intrusion of Tracing Non-deterministic Programs by Software”, “A User-Friendly and Extendable Data Distribution System”, “Multi-flip Networks: Parallelizing GenSAT”, “Self-determinations of Man”.

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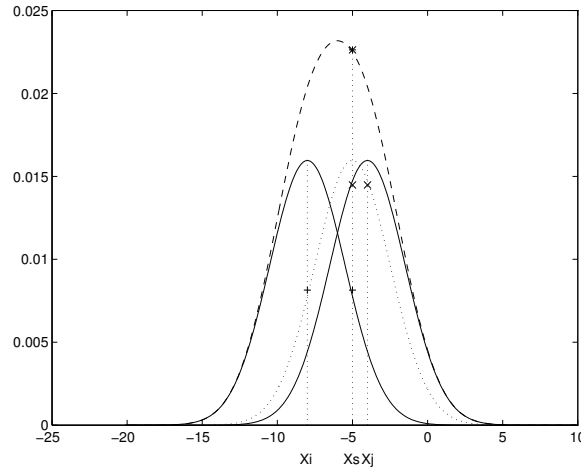


Fig. 1. One kernel at x_s (*dotted kernel*) or two kernels at x_i and x_j (*left and right*) lead to the same summed estimate at x_s . This shows a figure consisting of different types of lines. Elements of the figure described in the caption should be set in italics, in parentheses, as shown in this sample caption.

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Displayed equations or formulas are centered and set on a separate line (with an extra line or halfline space above and below). Displayed expressions should be numbered for reference. The numbers should be consecutive within each section or within the contribution, with numbers enclosed in parentheses and set on the right margin – which is the default if you use the *equation* environment, e.g.,

$$\psi(u) = \int_o^T \left[\frac{1}{2} (\Lambda_o^{-1} u, u) + N^*(-u) \right] dt. \quad (1)$$

Equations should be punctuated in the same way as ordinary text but with a small space before the end punctuation mark.

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The superscript numeral used to refer to a footnote appears in the text either directly after the word to be discussed or – in relation to a phrase or a sentence – following the punctuation sign (comma, semicolon, or period). Footnotes should appear at the bottom of the normal text area, with a line of about 2 cm set immediately above them.¹

2.4 Program Code

Program listings or program commands in the text are normally set in typewriter font, e.g., CMTT10 or Courier.

Example of a Computer Program

```
program Inflation (Output)
{Assuming annual inflation rates of 7%, 8%, and 10%,...
 years};
const
  MaxYears = 10;
var
  Year: 0..MaxYears;
  Factor1, Factor2, Factor3: Real;
begin
  Year := 0;
  Factor1 := 1.0; Factor2 := 1.0; Factor3 := 1.0;
  WriteLn('Year 7% 8% 10%'); WriteLn;
  repeat
    Year := Year + 1;
    Factor1 := Factor1 * 1.07;
    Factor2 := Factor2 * 1.08;
    Factor3 := Factor3 * 1.10;
    WriteLn(Year:5,Factor1:7:3,Factor2:7:3,Factor3:7:3)
  until Year = MaxYears
end.
```

(Example from Jensen K., Wirth N. (1991) Pascal user manual and report. Springer, New York)

2.5 Citations

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Acknowledgments. The heading should be treated as a subsection heading and should not be assigned a number.

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References

1. Smith, T.F., Waterman, M.S.: Identification of Common Molecular Subsequences. *J. Mol. Biol.* 147, 195–197 (1981)
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3. Foster, I., Kesselman, C.: *The Grid: Blueprint for a New Computing Infrastructure*. Morgan Kaufmann, San Francisco (1999)
4. Czajkowski, K., Fitzgerald, S., Foster, I., Kesselman, C.: Grid Information Services for Distributed Resource Sharing. In: *10th IEEE International Symposium on High Performance Distributed Computing*, pp. 181–184. IEEE Press, New York (2001)
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6. National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov>

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