

Maximal Unique Match as heuristic in Whole Genome Alignment parallelization

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Abstract—The abstract goes here.

I. INTRODUCTION

This demo file is intended to serve as a “starter file” for IEEE conference papers produced under L^AT_EX using IEEE-tran.cls version 1.7 and later. I wish you the best of success.

mds

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II. CONCLUSION

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The authors would like to thank...

REFERENCES

- [1] H. Kopka and P. W. Daly, *A Guide to L^AT_EX*, 3rd ed. Harlow, England: Addison-Wesley, 1999.