



**KTH Computer Science
and Communication**

EM algorithm for binning metagenomes based probabilistic composition and coverage models

Lots of Binning

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TRITA xxx yyyy-nn

Abstract

English abstract

Referat

Svensk titel ääö

Sammanfattning på svenska. ääö

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Chapter 1

Introduction

This is my introduction

1.1 Theory

my theory

Chapter 2

Results

my results

Chapter 3

Discussion

my discussion

Bibliography

[Hess et al., 2011] Hess, M., Sczyrba, A., Egan, R., Kim, T.-W., Chokhawala, H., Schroth, G., Luo, S., Clark, D. S., Chen, F., Zhang, T., Mackie, R. I., Pennacchio, L. a., Tringe, S. G., Visel, A., Woyke, T., Wang, Z., and Rubin, E. M. (2011). Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. *Science (New York, N.Y.)*, 331(6016):463–7.

Appendix A

RDF

And here is a figure

Figure A.1. Several statements describing the same resource.

[Hess et al., 2011] that we refer to here: A.1