MASTER'S THESIS

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BIOINFORMATICS AND GENOMICS MASTER'S DEGREE

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VISUAL REPRESENTATION AND COMPARATIVE EVALUATION OF SCAFFOLDING TOOLS FOR CIRCULAR GENOMES

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Thanks

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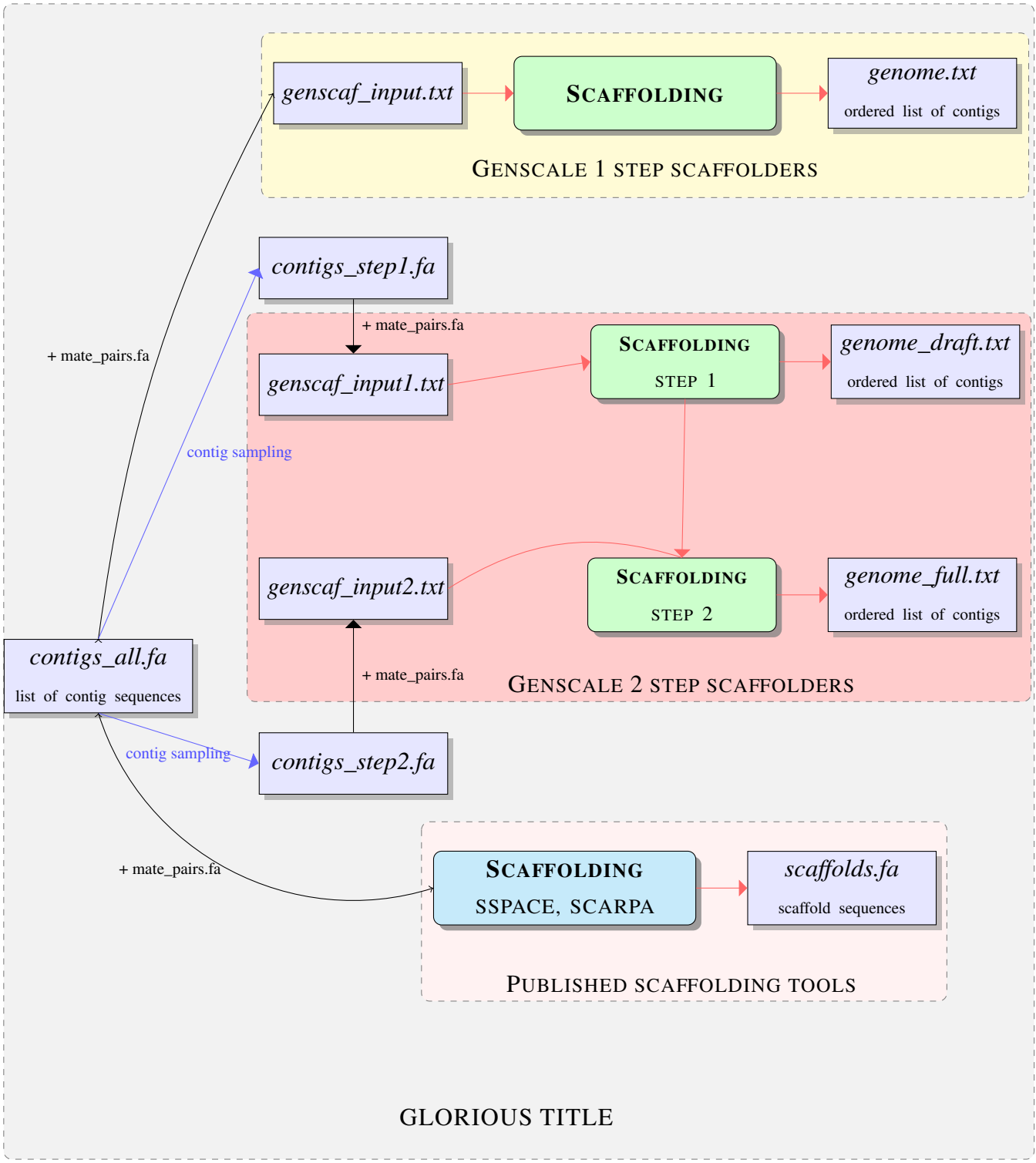
1 Introduction

1.1 Context

1.2 Scaffolding

1.3 Workflow


genscaf_input.txt
SCAFFOLDING
genome.txt
ordered list of contigs
GENSCALE 1 STEP SCAFFOLDERS
contigs_step1.fa
+ mate_pairs.fa
+ mate_pairs.fa
genscaf_input1.txt
SCAFFOLDING
STEP 1
genome_draft.txt
ordered list of contigs
contig sampling
genscaf_input2.txt
SCAFFOLDING
STEP 2
genome_full.txt
ordered list of contigs
contigs_all.fa
list of contig sequences
+ mate_pairs.fa
GENSCALE 2 STEP SCAFFOLDERS
contig sampling
contigs_step2.fa
+ mate_pairs.fa
SCAFFOLDING
SSPACE, SCARPA
scaffolds.fa
scaffold sequences
PUBLISHED SCAFFOLDING TOOLS
GLORIOUS TITLE

2 Challenges of the scaffolding problem

2.1 Definition

2.2 Proposed models

2.3 Distinctive features of circular genomes

3 Methods for benchmarking

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