Read construction

Read construction

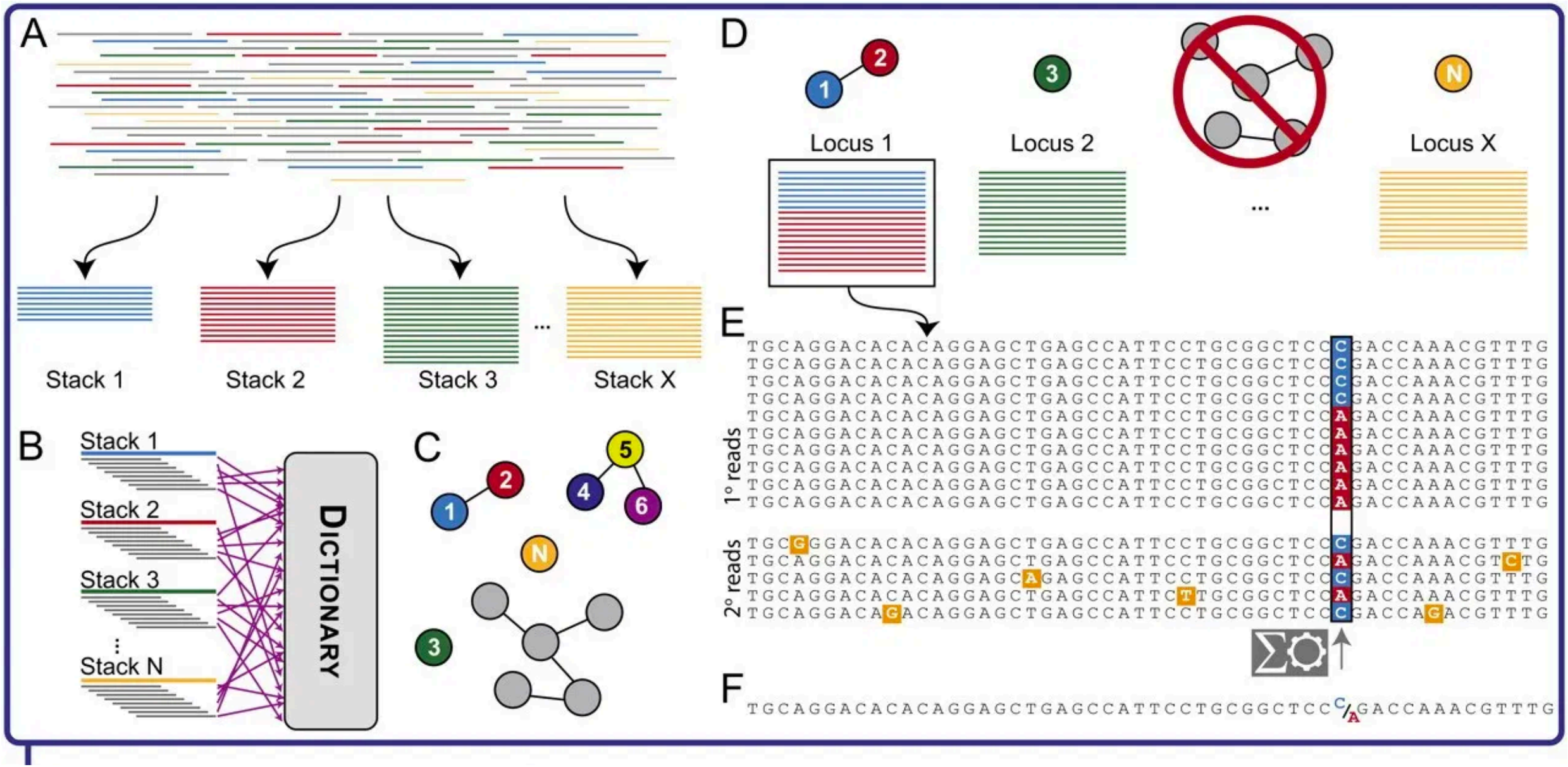
Denovo pipeline

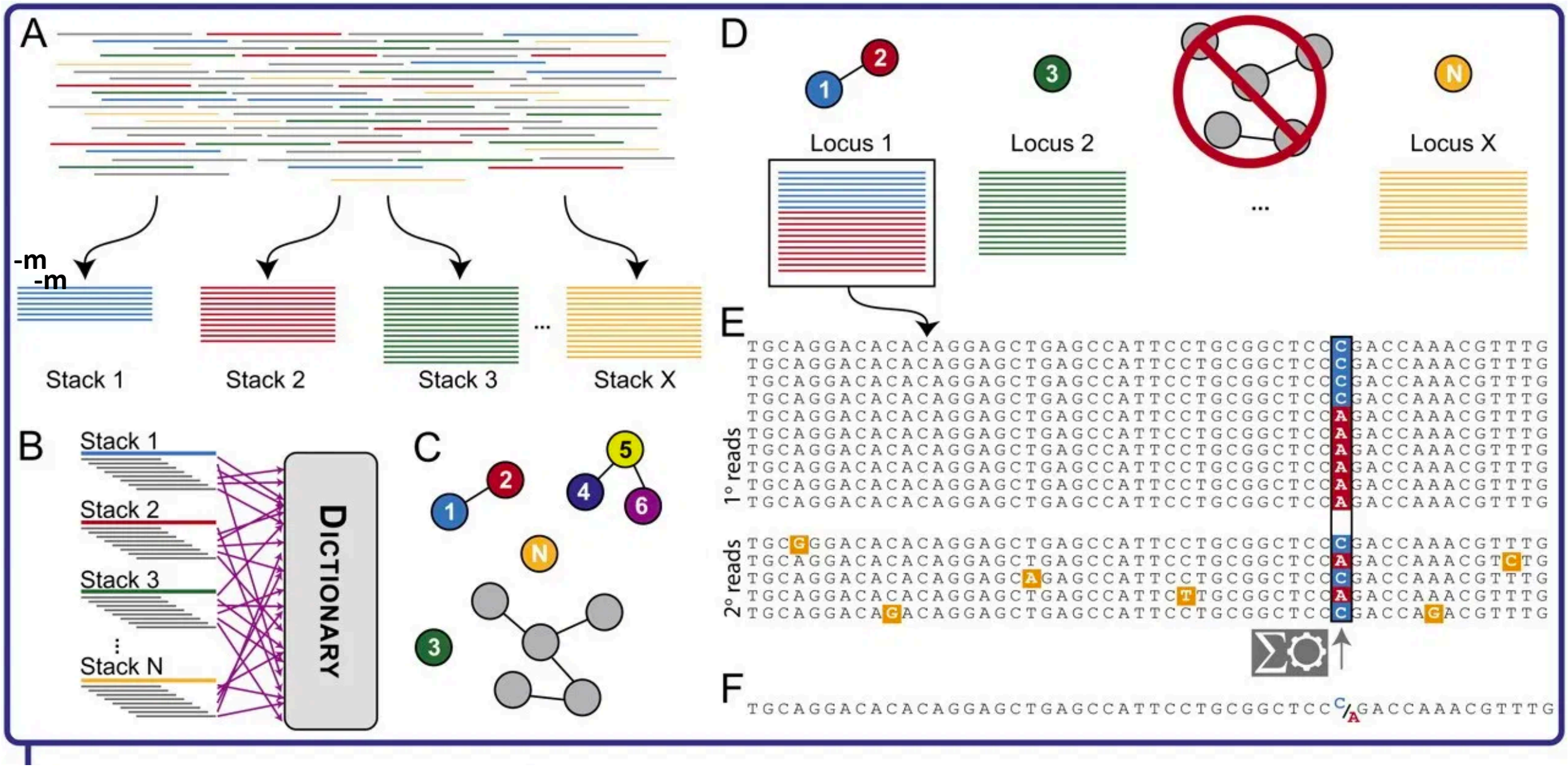
USTACKS Build loci de novo

CSTACKS Assemble catalog

SSTACKS Match to catalog

Populations Filter loci and compute Population statistics


A
Stack 1
Stack 2
Stack 3
...
Stack X
B
Stack 1
Stack 2
Stack 3
Stack N
DICTIONARY
C
1
2
3
4
5
6
N
D
1
2
3
N
Locus 1
Locus 2
...
Locus X
E
1° reads
2° reads
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
TGCGGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCAGACCAAACGTCTG
TGCAGGACACACAGGAGCAGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
TGCAGGACACACAGGAGCTGAGCCATTCTTGCGGCTCCAGACCAAACGTTTG
TGCAGGACAGACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAGACGTTTG
F
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCC/AGACCAAACGTTTG


A
-m
-m
Stack 1
Stack 2
Stack 3
...
Stack X
B
Stack 1
Stack 2
Stack 3
Stack N
DICTIONARY
C
1
2
3
4
5
6
N
D
1
2
3
N
Locus 1
Locus 2
...
Locus X
E
1° reads
2° reads
F

Denovo pipeline

USTACKS Build loci de novo

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Parameter Description	`denovo_map.pl` Parameter	Pipeline component	Component Parameter	Default Value
Minimum stack depth / minimum depth of coverage	`-m`	**`ustacks`**	`-m`	3
Distance allowed between stacks	`-M`	**`ustacks`**	`-M`	2
Distance allowed between catalog loci	`-n`	**`cstacks`**	`-n`	1

reference pipeline

~~**USTACKS**~~ Build loci de novo

~~**CSTACKS**~~ Assemble catalog

~~**SSTACKS**~~ Match to catalog

Populations Filter loci and compute Population statistics

Reference pipeline

Alignment to a reference genome

Populations

Filter loci and compute
Population statistics