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Alignment

AACCGCTAACGGTAA AACCGCGAACTAA

Alignment

AACCGCTAACGGTAA AACCGCGAACTAA



AACCGCGAAC - TAA

Find the read in the genome

• Challenges?

Challenges

- Small length
- Gigabytes of data
- Different sequencing errors
- SNPs
- Genomic repeats

Tools

- Bowtie2, BWA MEM, minimap2 (Genomic)
- HiSat2, STAR (RNA-Seq)
- and many more

Bowtie

Mapping Illumina reads

acaacg

acaacg\$

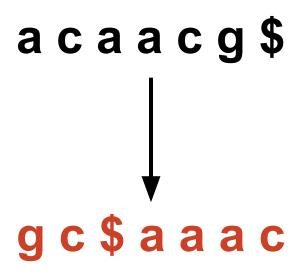
acaacg\$ \$acaacg

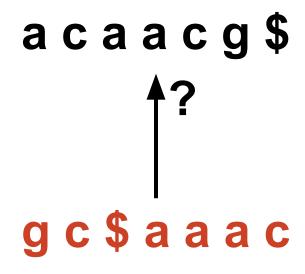
```
acaacg$
$acaacg
$acaacg
```

```
acaacg$
$acaacg
g $ a c a a c
cg$acaa
acg$aca
aacg$ac
caacg$a
```

```
$acaacg
aacg$ac
acaacg$
acg$aca
caacg$a
cg$acaa
g $ a c a a c
```

```
$acaacg
aacg$ac
acaacg$
acg$aca
caacg$a
cg$acaa
g $ a c a a c
```





```
$acaacg
aacg$ac
acaacg$
acg$aca
caacg$a
cg$acaa
g $ a c a a c
```

```
g $ a c a a c
caacg$a
$ a c a a c g
aacg$ac
acaacg$
acg$aca
cg$acaa
```

```
$acaacg
aacg$ac
acaacg$
acg$aca
caacg$a
cg$acaa
g $ a c a a c
```

g	\$acaacg
C	aacg\$ac
\$	acaacg\$
a	acg\$aca
a	caacg\$a
a	cg\$acaa
C	g\$acaac

\$	\$acaacg
a	aacg\$ac
a	acaacg\$
a	acg\$aca
C	caacg\$a
C	cg\$acaa
g	g\$acaac

C

\$ a c a a c g aacg\$ac acaacg\$ acg\$aca caacg\$a cg\$acaa g \$ a c a a c

g \$

ca

\$ a

a a

ac

ac

c g

\$acaacg

aacg\$ac

acaacg\$

acg\$aca

caacg\$a

cg\$acaa

\$ a

aa

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ac

c a

c g

g \$

\$acaacg

aacg\$ac

acaacg\$

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caacg\$a

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a a

a c

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ca

c g

g \$

\$acaacg

aacg\$ac

acaacg\$

acg\$aca

caacg\$a

cg \$acaa

g \$ a

caa

\$ a c

a a c

aca

acg

c g \$

\$acaacg

aacg\$ac

acaacg\$

acg\$aca

caacg\$a

cg\$acaa

\$ a c

a a c

aca

a c g

caa

c g \$

g \$ a

\$acaacg

aacg\$ac

acaacg\$

acg\$aca

caacg\$a

cg\$acaa

\$ac a a c aca acg caa cg\$ g\$a

\$acaacg aacg\$ac acaacg\$ acg\$aca caacg\$a cg\$acaa g \$ a c a a c

g \$ a c

caac

\$ a c a

a a c g

acaa

acg\$

cg\$a

\$acaacg

aacg\$ac

acaacg\$

acg\$aca

caacg\$a

cg\$acaa

\$aca aacg acaa acg\$ caac cg\$a g \$ a c \$acaacg aacg\$ac acaacg\$ acg\$aca caacg\$a cg\$acaa g \$ a c a a c

g	\$ a	C	a

\$acaa aacg\$ acaac acg\$a caacg cg\$ac g\$aca

\$acaacg aacg\$ac acaacg\$ acg\$aca caacg \$ a cg\$acaa g \$ a c a a c

g \$ a c a a
caacg\$
<pre>\$ a c a a c</pre>
aacg\$a
acaacg
acg\$ac
cg\$aca

\$acaac aacg\$a acaacg acg\$ac caacg\$ cg\$aca g \$ a c a a

\$acaac<mark>g</mark> aacg\$ac acaacg\$ acg\$aca caacg\$a cg\$acaa g \$ a c a a c

g \$ a c a a c	\$acaacg
caacg\$a	aacg\$ac
\$acaacg	acaacg\$
aacg\$ac	acg\$aca
acaacg\$	caacg\$a
acg\$aca	cg\$acaa
cg\$acaa	g\$acaac

Burrows-Wheeler transform

\$acaacg	\$acaacg
aacg\$ac	aacg\$ac
acaacg\$	acaacg\$
acg\$aca	acg\$aca
caacg\$a	caacg\$a
cg\$acaa	cg\$acaa
g \$ a c a a c	g\$acaac

$$a_k c_i a_m a_n c_j g_x$$
\$

$$\mathbf{S}_{1}$$
 a c a a c \mathbf{G}_{1} \mathbf{a}_{1} a c g \mathbf{S} a c \mathbf{a}_{2} c a a c g \mathbf{S}_{1} \mathbf{a}_{3} c g \mathbf{S} a c a c \mathbf{G}_{1} a a c g \mathbf{S}_{2} a c a a c \mathbf{G}_{2} g \mathbf{S}_{3} a c a a c \mathbf{G}_{1}

```
$<sub>1</sub> a c a a c g<sub>1</sub>
a<sub>1</sub> a c g $ a c
a, caacg $
a<sub>3</sub> c g $ a c a
c<sub>1</sub> a a c g $ a
c<sub>2</sub>g$acaa
 g<sub>1</sub> $ a c a a c
```

```
$<sub>1</sub> a c a a c g<sub>1</sub>
a<sub>1</sub> a c g $ a c
a, caacg $<sub>1</sub>
a<sub>3</sub>cg$aca
c<sub>1</sub> a a c g $ a
c<sub>2</sub> g $ a c a a
g<sub>1</sub> $ a c a a c
```

$$a a_3 c g $ a c$$
 $a c_1 a a c g $$
 $a c_2 g $ a c a$

```
$<sub>1</sub> a c a a c g<sub>1</sub>
a<sub>1</sub> a c g $ a c
a, caacg $<sub>1</sub>
a<sub>3</sub>cg$aca
c<sub>1</sub> a a c g $ a
c<sub>2</sub> g $ a c a a
g<sub>1</sub> $ a c a a c
```

 $a a_3 c g $ a c$ $a c_1 a a c g $$ $a c_2 g $ a c a$

\$₁ a c a a c g₁ a₁ a c g \$ a c a, caacg\$₁ a₃cg\$aca c₁ a a c g \$ a c, g \$ a c a a g_1 \$ a c a a c

 $a_{1} a_{3} c g $ a c$ $a_{2} c_{1} a a c g $$ $a_{3} c_{2} g $ a c a$

\$, acaacg, a₁ a c g \$ a c a, caacg\$₁ a₃ cg \$ a c a c₁ a a c g \$ a c, g \$ a c a a g_1 \$ a c a a c

 $a_{3} c g $ a c a_{1}$ $c_{1} a a c g $ a_{2}$ $c_{2} g $ a c a a_{3}$

\$, a c a a c g, a₁ a c g \$ a c a, caacg \$ a₃ cg \$ a ca c₁ a a c g \$ a c, g \$ a c a a g_1 \$ a c a a c

$$a_{3} c g $ a c a_{1}$$
 $c_{1} a a c g $ a_{2}$
 $c_{2} g $ a c a a_{3}$

```
$<sub>1</sub> a c a a c g<sub>1</sub>
a<sub>1</sub> a c g $ a c
a, caacg $
a<sub>3</sub> cg $ a c a
c<sub>1</sub> a a c g $ a
c, g $ a c a a
g<sub>1</sub> $ a c a a c
```

$$a_{3} c g $ a c a_{1}$$
 $c_{1} a a c g $ a_{2}$
 $c_{2} g $ a c a a_{3}$

```
$<sub>1</sub> a c a a c g<sub>1</sub>
a<sub>1</sub> a c g $ a c
a, caacg $
a<sub>3</sub> cg $ a ca<sub>1</sub>
c<sub>1</sub> a a c g $ a<sub>2</sub>
c<sub>2</sub> g $ a c a a<sub>2</sub>
 g<sub>1</sub> $ a c a a c
```

$$a_{2} c_{1} a_{1} a_{3} c_{2} g_{1}$$

acaacg\$

- 0. a c a a c g \$
- 1. c a a c g \$
- 2. a a c g \$
- 3. a c g \$
- 4. c g \$
- 5. g \$
- 6. \$

- **6.** \$
- 2. a a c g \$
- 0. a c a a c g \$
- 3. a c g \$
- 1. caacg\$
- 4. c g \$
- 5. g \$

- 6. \$ a c a a c g2. a a c g \$ a c
- 0. acaacg\$
- 3. a c g \$ a c a
- 1. caacg\$a
- 4. c g \$ a c a a
- 5. g \$ a c a a c

Suffix array and BWT

- 6. \$ a c a a c g
- 2. a a c g \$ a c
- O. acaacg\$
- 3. a c g \$ a c a
- 1. caacg\$a
- 4. c g \$ a c a a
- 5. g \$ a c a a c

- \$acaacg
- aacg\$ac
- acaacg\$
- acg\$aca
- caacg\$a
- cg\$acaa
- g \$ a c a a c

Suffix array and BWT

$$B[i] = $$$

if
$$S[i] = 0$$

$$B[i] = X[S[i] - 1]$$

otherwise

BLASR

k = 4
<u>AGGCAGGGCAGGTCGCCACCGACCTCT</u>

CCAGGCTGGGGAGGTGGCACCGTTTCCTCT

```
R_L(W) = min \{k: W \text{ is prefix of } X_{S[k]} \}
```

$$R_H(W) = \max \{k: W \text{ is prefix of } X_{S[k]} \}$$

$$C(x) = |\{0 \le j \le n-2 : X[j] < x\}|$$

acaacg\$

$$C(a) = 0$$
, $C(c) = 3$, $C(g) = 5$, ...

```
6. $
 2. a a c g $
 0. a c a a c g $
3. a c g $
 1.caacg$
 4. c g $
5. g $
```

$$O(x, i) = |\{0 \le j \le i : B[j] = x\}|$$

gc\$aaac

$$O(a, 0) = 0$$
, $O(a, 1) = 0$, $O(a, 2) = 0$, $O(a, 3) = 1$, $O(a, 4) = 2$, ...

$$1_1 a c a a c $1_1 0 a_1 a c g 1_2 a c a a c $1_1 0 a_2 c a a c g 1_1 0 a_3 c g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a $1_2 c_2 g 1_2 a c a a $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c $1_2 c_2 g 1_2 a c a a c a c $1_2 c_2 g 1_2 a c a a c c $1_2 c_2 g 1_2 a c a a c c a a c c_2 a c a c a c a c c_2 a c a c a a c c_2 a c a c a a c c_2 a c a a c c_2 a c a a c c_2 a c a a c c_2 a c a c a a c c_2 a c a a c a c a a c c_2 a c a a c a c a a c c_2 a c a a c a c a a c c_2 a c a a c a a c c_2 a c a a c a a c c_2 a c a a c a a c c_2 a c a a c a a c a a c a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a c a a a c a a a c a a c a a a c a a a c a a a c a a a c a a a c a a a c a a a c a a a$$$$$$$$$$$$$$$$$$$$$$$

$$\begin{array}{c} \$_1 \ a \ c \ a \ a \ c \ g_1 \ 0 \ a_1 \ a \ c \ g \ \$ \ a \ c \ g \ \$ \ a \ c \ g \ \$ \ a \ c \ a_1 \ 1 \ c_1 \ a \ a \ c \ g \ \$ \ a \ c \ a \ a_2 \ c_2 \ g \ \$ \ a \ c \ a \ a_3 \ g_1 \ \$ \ a \ c \ a \ a \ c_2 \ \end{array}$$

$$\$_{1}$$
 a c a a c $\$_{1}$ 0 a c a a c $\$_{1}$ 1 c a a c $\$_{1}$ 2 c a a c a a c $\$_{2}$ 2 c a c a a c $\$_{1}$ 3 a c a a c $\$_{2}$ 2

$$\mathbf{a}_{1}$$
 a c a a c \mathbf{g}_{1} 0
 \mathbf{a}_{1} a c \mathbf{g} \$ a c \mathbf{c}_{1} 0 O(a, 1) = 0
 \mathbf{a}_{2} c a a c \mathbf{g} \$ 1
 \mathbf{a}_{3} c \mathbf{g} \$ a c \mathbf{a}_{1} 1
 \mathbf{c}_{1} a a c \mathbf{g} \$ \mathbf{a}_{2} 2 O(a, 4) = 2
 \mathbf{c}_{2} g \$ a c a a \mathbf{c}_{3} 3
 \mathbf{g}_{1} \$ a c a a c \mathbf{c}_{2} 3

$$\mathbf{a}$$
 \mathbf{a}
 \mathbf{a}

```
acgt
\mathbf{S}_{1} a c a a c \mathbf{G}_{1} 0 0 1 0
a<sub>1</sub> a c g $ a c<sub>1</sub> 0 1 1 0
a, caacg $, 0110
a<sub>3</sub> c g $ a c a<sub>1</sub> 1 1 1 0
c<sub>1</sub> a a c g $ a<sub>2</sub> 2 1 1 0
c, g $ a c a a, 3 1 1 0
g, $ a c a a c, 3 2 1 0
```

First-last property

$$R_{L}(xW) = C(x) + O(x, R_{L}(W) - 1)$$

$$R_{H}(xW) = C(x) + O(x, R_{H}(W)) - 1$$

$$R_{L}("") = 0$$

$$R_{H}("") = Ien(X) - 1$$

a

acaacg\$

a

acaacg\$

ca

<u>a c a</u> a c g \$ ca \$₁ a c a a c g₁ a₁ a c g \$ a c₁ a, caacg \$ a₃ cg \$ a ca₄ c₁ a a c g \$ a₂ c, g \$ a c a a, g_1 \$ a c a a c_2

ca

$$\begin{array}{c} a & c & a & a & c & g \\ \$ & \$_1 & a & c & a & a & c & g_1 \\ \hline a_1 & a & c & g & \$ & a & c_1 \\ a_2 & c & a & a & c & g & \$_1 \\ a_3 & c & g & \$ & a & c & a_1 \\ \hline c_1 & a & a & c & g & \$ & a_2 \\ c_2 & g & \$ & a & c & a & a_3 \\ g_1 & \$ & a & c & a & a & c_2 \\ \end{array}$$

ca
$$a c a a c g$$

$$a_1 a c a a c g$$

$$a_1 a c g a c_1$$

$$a_2 c a a c g$$

$$a_3 c g a c a_1$$

$$c_1 a a c g a_2$$

$$c_2 g a c a a_3$$

$$g_1 a c a a c_2$$

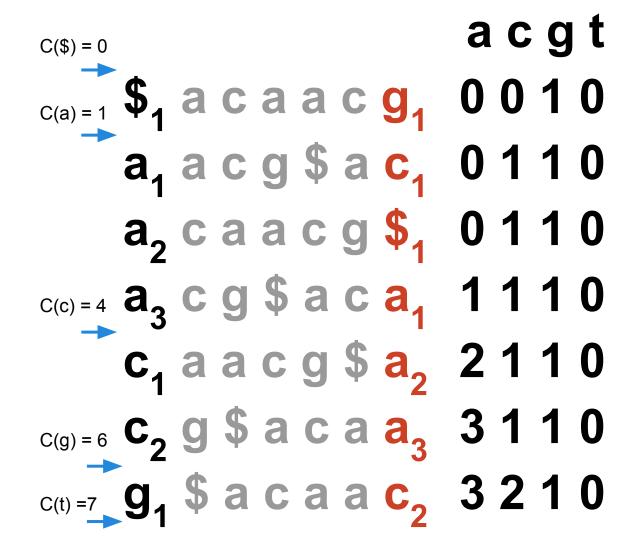
<u>a c a</u> a c g \$ ca \$, acaacg, a₁ a c g \$ a c₁ a₃/c g \$ a c a₁ c₁ a a c g \$ a₂ c, g \$ a c a a, g_1 \$ a c a a c_2

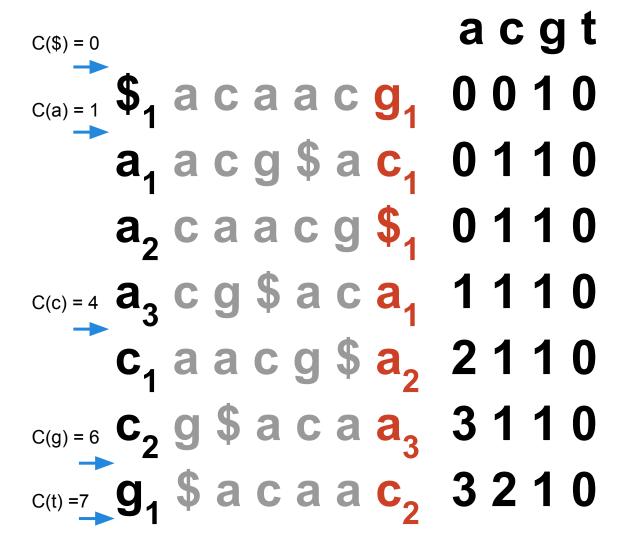
$$R_{L}(xW) = C(x) + O(x, R_{L}(W) - 1)$$

$$R_{H}(xW) = C(x) + O(x, R_{H}(W)) - 1$$

$$R_{L}("") = 0$$

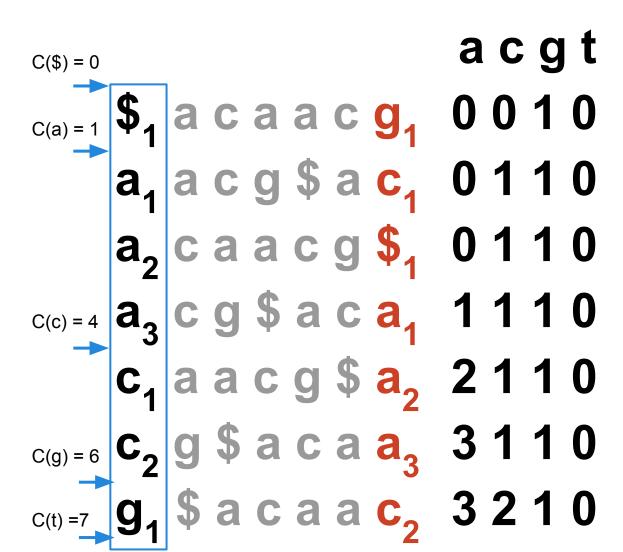
$$R_{H}("") = Ien(X) - 1$$

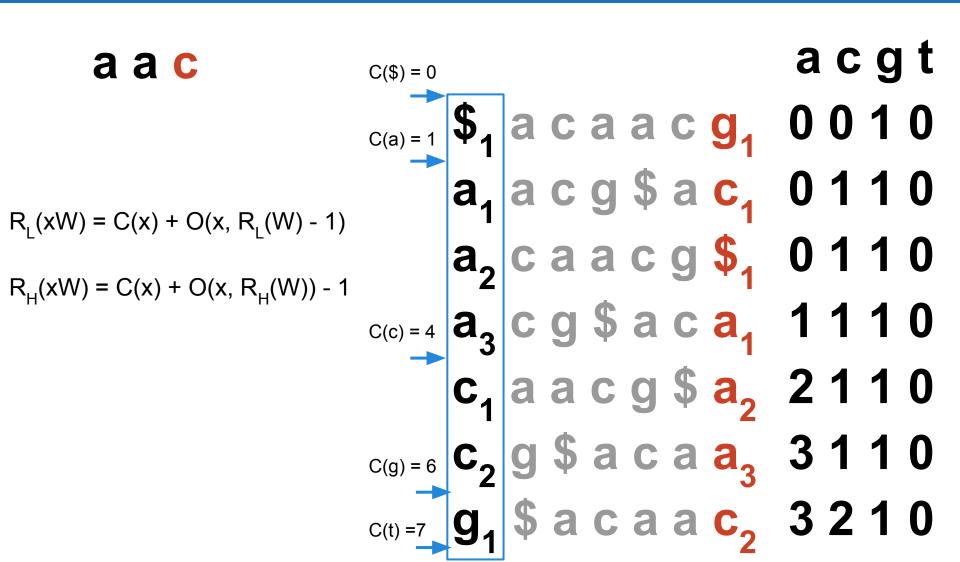




$$R_{I}("") = 0$$

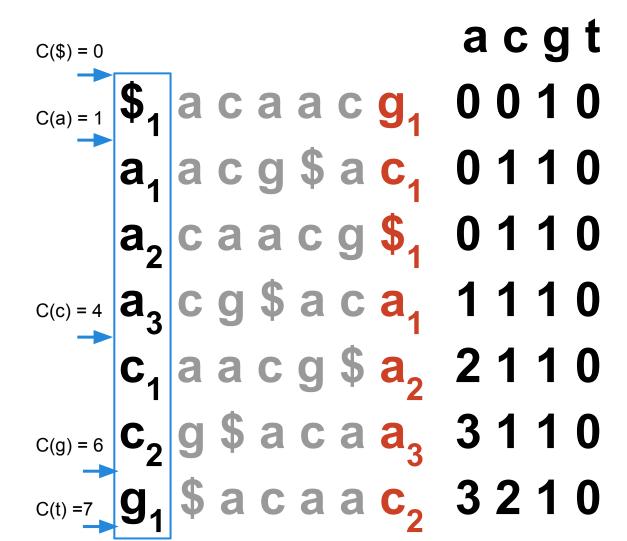
$$R_{H}("") = 6$$





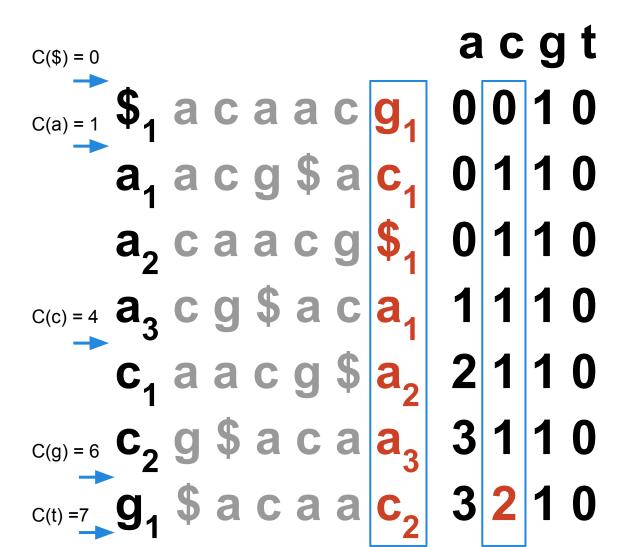
$$R_{l}(c) = C(c) + O(c, R_{l}("") - 1)$$

$$R_{H}(c) = C(c) + O(c, R_{H}("")) - 1$$



$$R_{l}(c) = C(c) + O(c, -1)$$

$$R_{H}(c) = C(c) + O(c, 6) - 1$$



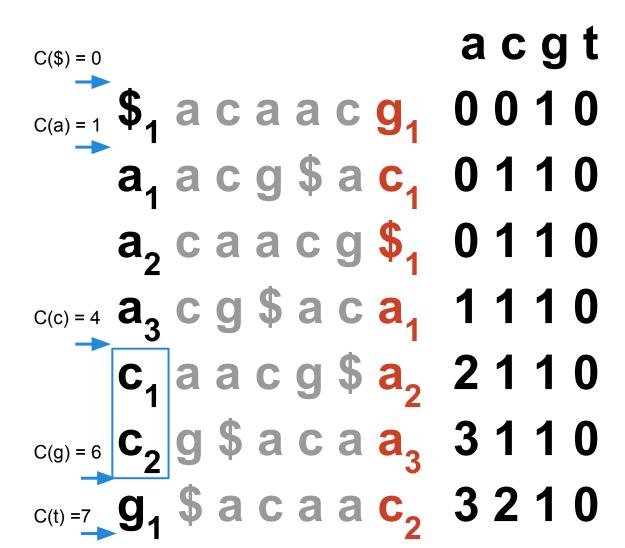
$$R_{l}(c) = C(c) + 0$$

$$R_{H}(c) = C(c) + 2 - 1$$



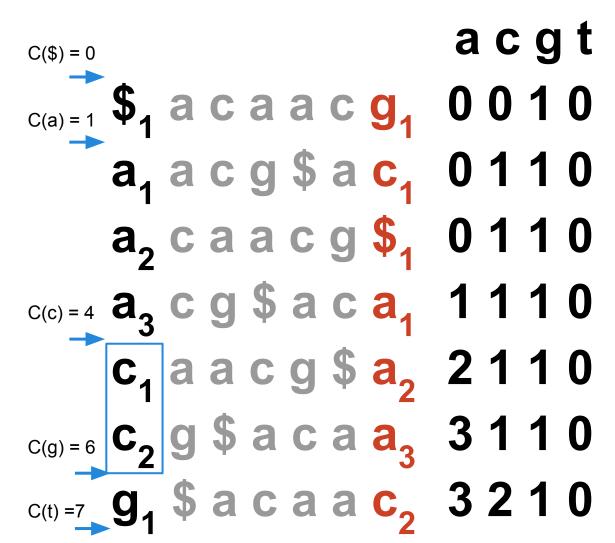
$$R_{i}(c) = 4 + 0 = 4$$

$$R_{H}(c) = 4 + 2 - 1 = 5$$



$$R_{L}(ac) = C(a) + O(a, R_{L}(c) - 1)$$

$$R_{H}(ac) = C(a) + O(a, R_{H}(c)) - 1$$



$$R_{I}(ac) = C(a) + O(a, 3)$$

$$R_{H}(ac) = C(a) + O(a, 5) - 1$$



$$R_{I}(ac) = C(a) + O(a, 3)$$

$$R_{H}(ac) = C(a) + O(a, 5) - 1$$



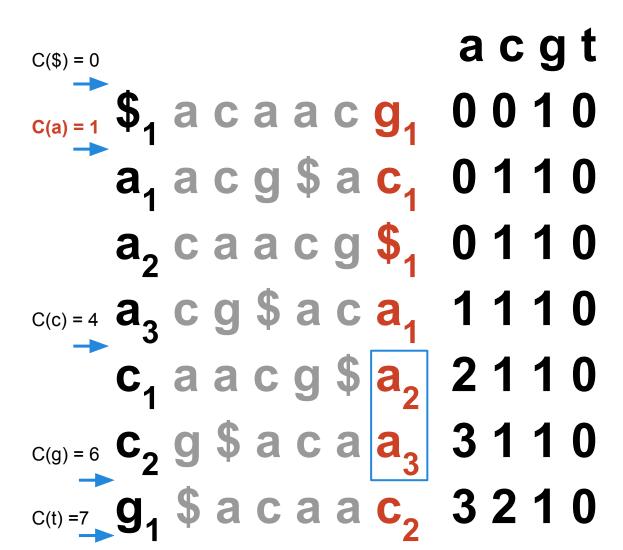
$$R_{l}(ac) = C(a) + 1$$

$$R_{H}(ac) = C(a) + 3 - 1$$



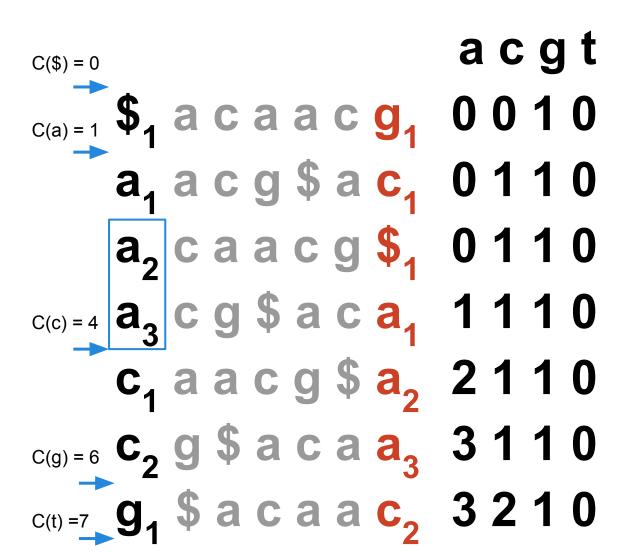
$$R_{i}(ac) = C(a) + 1$$

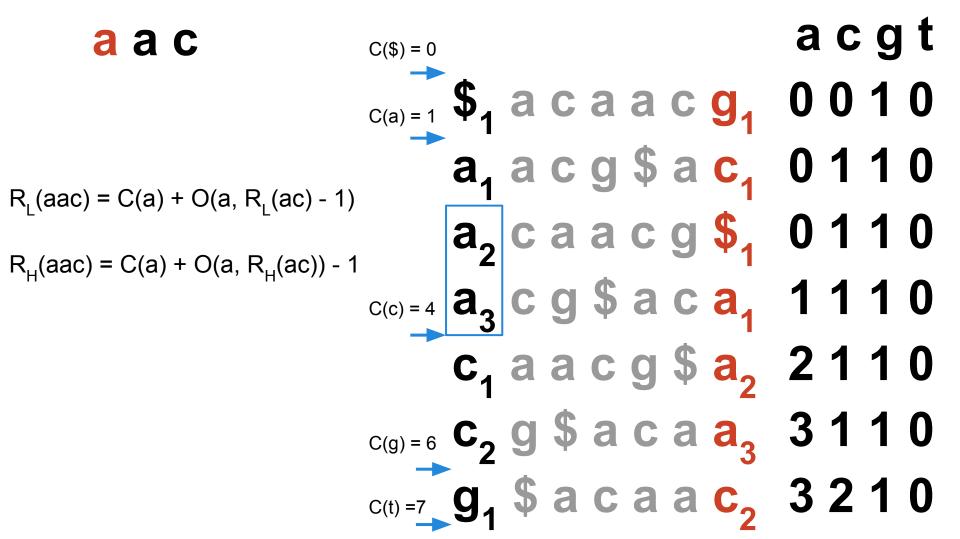
$$R_{H}(ac) = C(a) + 3 - 1$$



$$R_{l}(ac) = 1 + 1 = 2$$

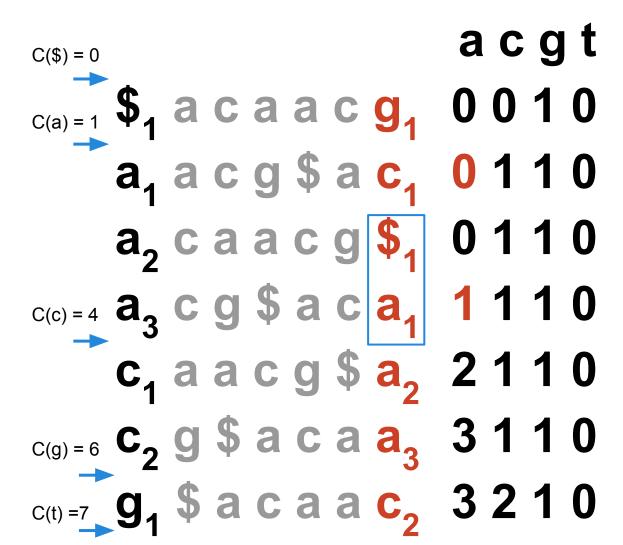
$$R_{H}(ac) = 1 + 3 - 1 = 3$$





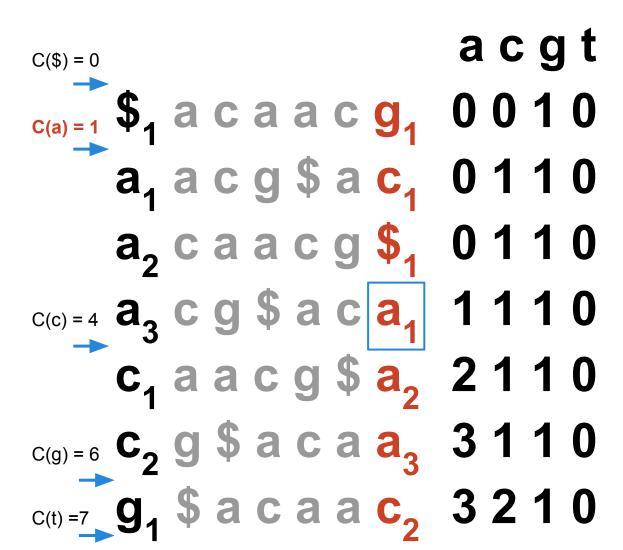
$$R_{1}(aac) = C(a) + O(a, 2 - 1)$$

$$R_{H}(aac) = C(a) + O(a, 3) - 1$$



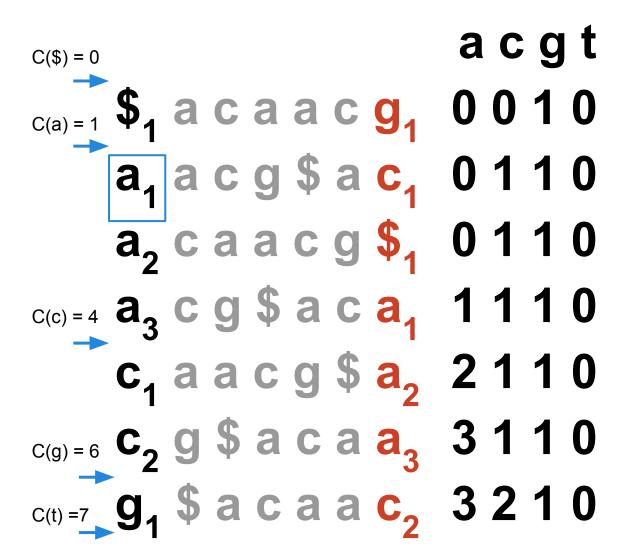
$$R_{l}(aac) = C(a) + 0$$

$$R_{H}(aac) = C(a) + 1 - 1$$



$$R_{l}(aac) = 1 + 0 = 1$$

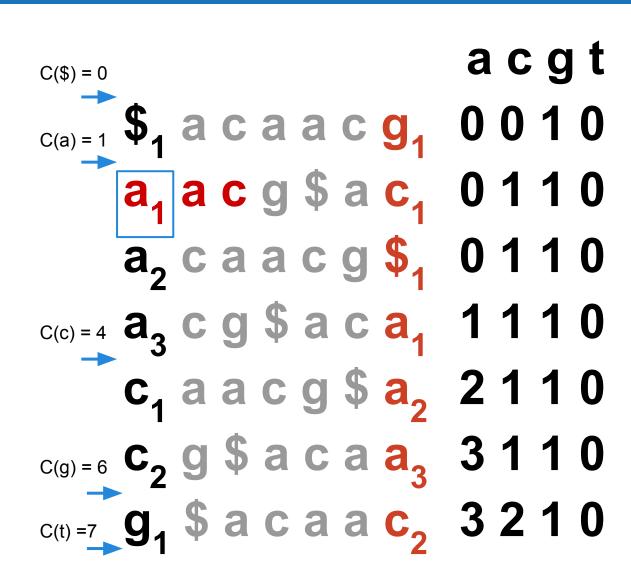
$$R_{H}(aac) = 1 + 1 - 1 = 1$$



$$R_{l}(aac) = 1$$

$$R_{H}(aac) = 1$$





For how long does it work?

For how long does it work? O(m)

gca

 $\mathbf{\$}_{1}$ a c a a c \mathbf{g}_{1} \mathbf{a}_{1} a c g $\mathbf{\$}$ a \mathbf{c}_{1} \mathbf{a}_{2} c a a c g $\mathbf{\$}_{1}$ $\begin{bmatrix} \mathbf{a}_3 \\ \mathbf{c}_1 \end{bmatrix}$ c g \$ a c \mathbf{a}_1 c₁ a a c g \$ \mathbf{a}_2 c_2 g \$ a c a a_3 g₁ \$ a c a a c_2

```
$1 a c a a c g1
a1 a c g $ a c1
a2 c a a c g $1
a3 c g $ a c g $1
a3 c g $ a c a1
c1 a a c g $ a c a1
c2 g $ a c a a2
g1
$2 a c a a c g $2
a2
g2 $ a c a a c2
```

$$s_1$$
 a c a a c g_1
 s_1 a c a a c g_1
 s_2 a c g s a g_1
 s_2 c a a c g s a c g
 s_1
 s_2 c g s a c g
 s_2
 s_3
 s_4
 s_4
 s_2
 s_4
 s_4
 s_5
 s_1
 s_2
 s_4
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 s_4
 s_5
 s_4
 s_5
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 s_5
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 s_4
 s_5
 s_5

$$$^{1}_{1}$ a c a a c g_{1}
 a_{1} a c g $$^{1}_{1}$
 a_{2} c a a c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{1}
 a_{2} c a a c g $$^{1}_{1}$
 a_{2}
 a_{3}
 a_{4}
 a_{5}
 a_{1}
 a_{1}
 a_{2}
 a_{2}
 a_{2}
 a_{3}
 a_{4}
 a_{5}
 $a_$$$

$$$^{1}_{1}$ a c a a c g_{1}
 a_{1} a c g $$^{1}_{1}$
 a_{2} c a a c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{1}
 a_{2}
 a_{3}
 a_{3}
 a_{4}
 a_{5}
 $a_{5$$$

gca

gca



$$$^{1}_{1}$ a c a a c g_{1}
 a_{1} a c g $$^{1}_{1}$
 a_{2} c a a c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{1}
 a_{2}
 a_{3}
 a_{3}
 a_{4}
 a_{5}
 $a_{5$$$

gca

$$$^{1}_{1}$ a c a a c g_{1}
 a_{1} a c g $$^{1}_{1}$
 a_{2} c a a c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{3} c g $$^{1}_{1}$
 a_{1}
 a_{2}
 a_{3}
 a_{3}
 a_{4}
 a_{5}
 a_{1}
 a_{2}
 a_{2}
 a_{3}
 a_{4}
 a_{5}
 $a_{5$$$

c c a

$$\$_{1}$$
 a c a a c $\$_{1}$ a $*_{1}$ a c $*_{2}$ a $*_{1}$ a $*_{2}$ c a a c $\$_{1}$ a $*_{3}$ c $\$_{1}$ a $*_{2}$ c $*_{3}$ a c $*_{1}$ a $*_{2}$ c $*_{2}$ $\$_{1}$ a c $*_{2}$ a c $*_{3}$ a c $*_{3}$ a c $*_{2}$ a c $*_{3}$ a c $*_{2}$

c c a



a c a

$$1_1 a c a a c g_1
 a_1 a c g $ a c_1
 a_2 c a a c g $_1
 a_3 c g $ a c a_1
 c_1 a a c g $ a_2
 c_2 g $ a c a a_3
 g_1 $ a c a a $c_2$$$

a c a

a c a

aca



Backtracking

Backtracking

- Quality-aware
- Limit total number of backtracks
- Limit quality distance

Backtracking

- Quality-aware
- Limit total number of backtracks
- Limit quality distance

- Selected at high-quality end
- Used to prevent excessive backtracking

acaacg\$ aac

\$gcaaca aac

\$gcaaca caa





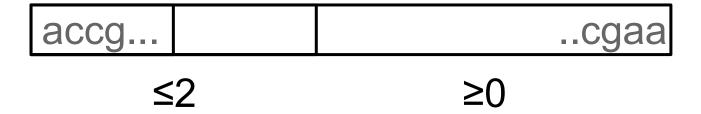
Backtracking

- Quality-aware
- Limit total number of backtracks
- Limit quality distance

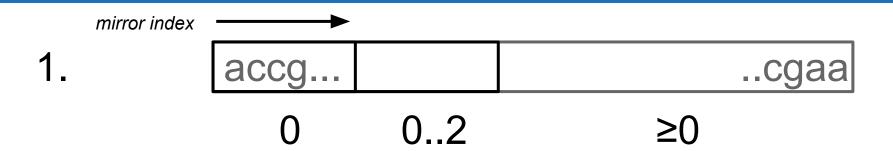
- Selected at high-quality end
- Used to prevent excessive backtracking

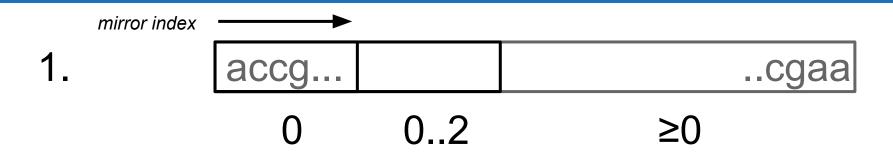
accg... ..cgaa

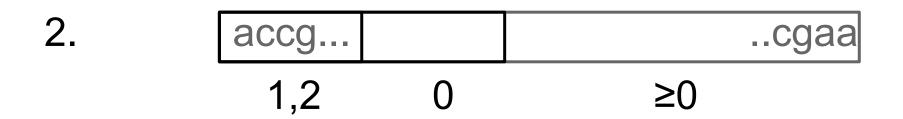
accg... ..cgaa ≤2 ≥0

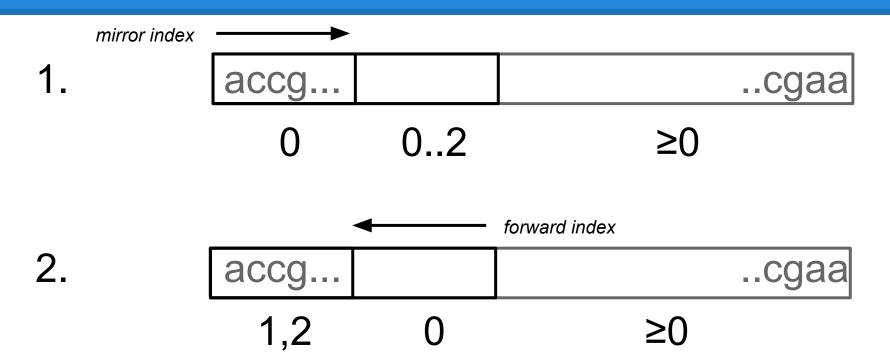


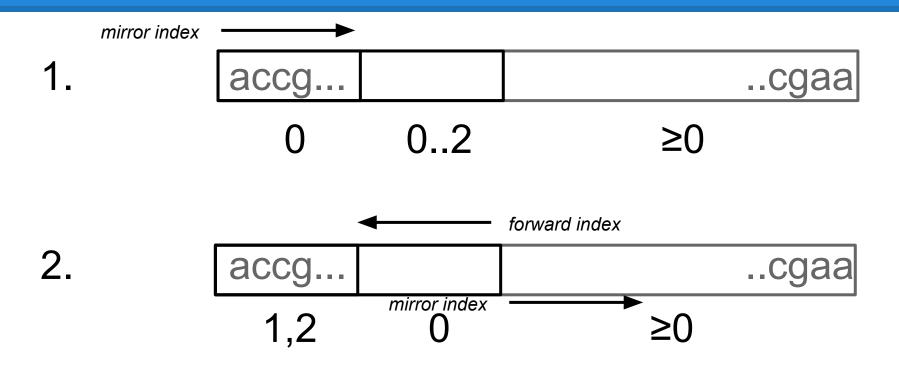




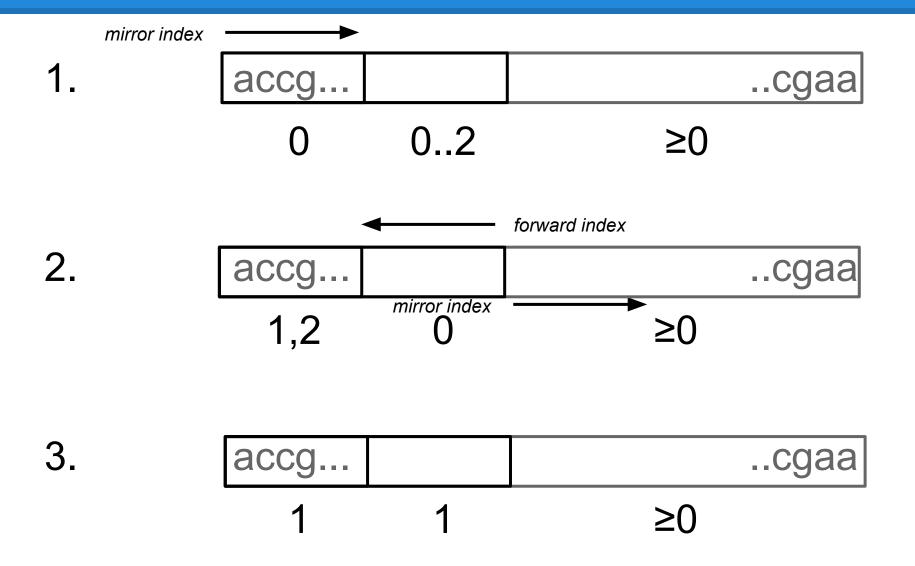




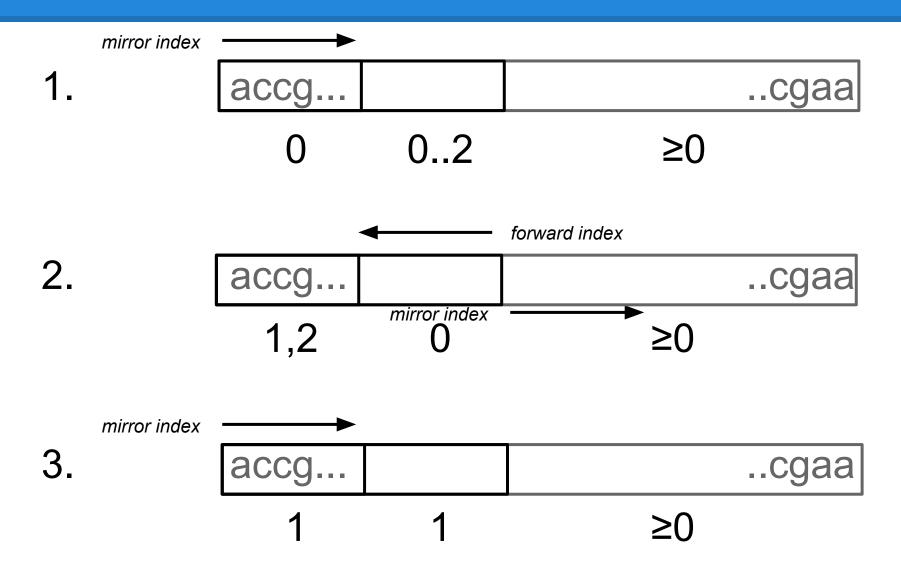




Seeds



Seeds



Working with alignments

Bowtie steps

Build index from the genome

bowtie2-build <genome.fasta> <index>

Map reads using index

bowtie2 -x <index>

- -1 <left.fastq> -2 <right.fastq>
- -S <output.sam>

BWA tool

- bwa index index construction
- bwa aln short read aligner
- bwa mem new long read and long sequence local aligner

Alignment applications

Alignment applications

- Quality assessment
 - Error rate
 - Insert size distribution
 - Chimeric read/read-pairs
 - Genome fraction
- SNP calling
- Comparative analysis
 - o CNVs
- Transciptomics
 - Gene expression
 - Exon/intron detection

Storing alignments

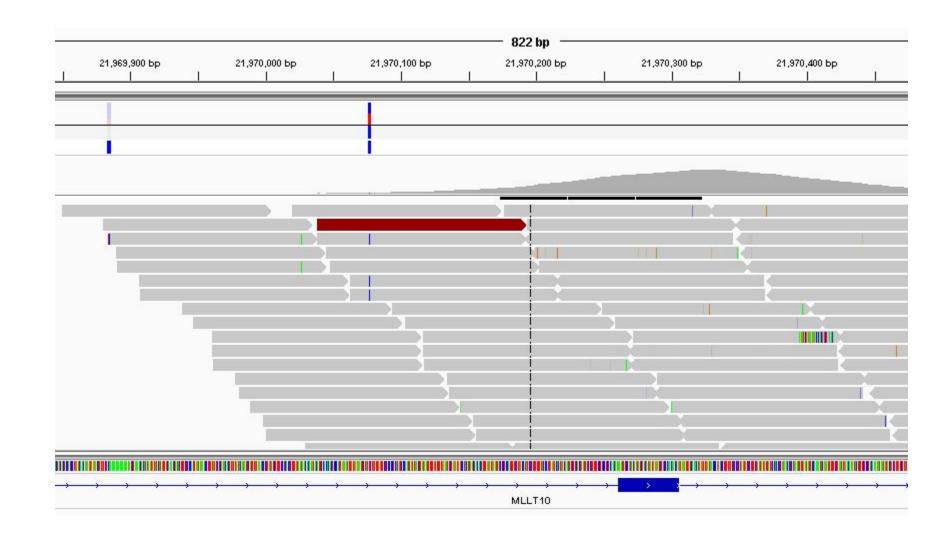
SAM/BAM files

- Read ID (QNAME)
- Reference ID (RNAME)
- Mapping position (POS)
- Mate reference ID (RNEXT)
- Mate position (PNEXT)
- Observed insert length (TLEN)
- Read sequence (SEQ)
- Read quality (QUAL)
- CIGAR string
 - 34M 1I 4M 2D 1X 3M

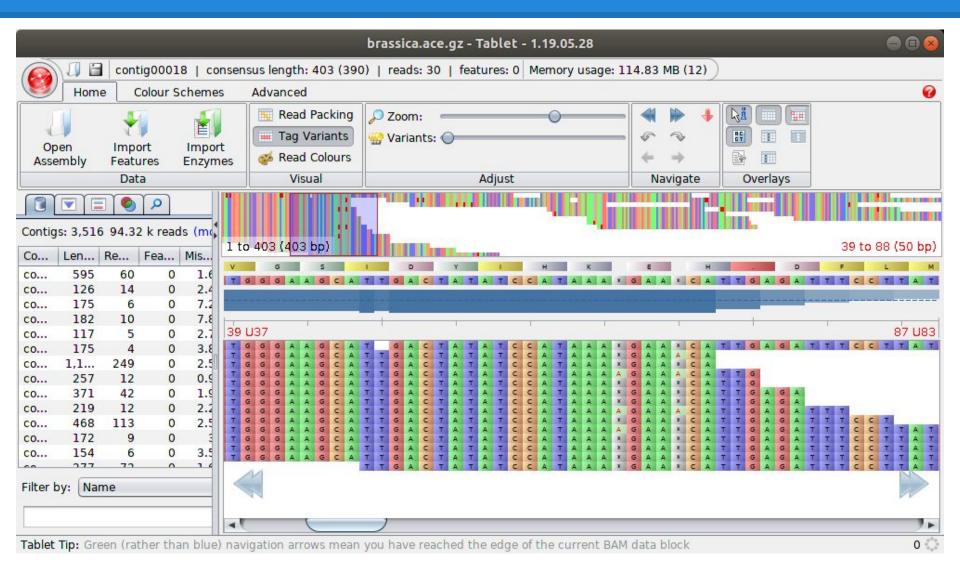
SAM files

```
@HD
      VN:1.0 SO:coordinate
@SQ
      SN:chr20
                   LN:64444167
@PG
      ID:TopHat
                   VN:2.0.14
                                CL:/srv/dna tools/tophat/tophat -N 3 --read-edit-dist 5 --read-rea
lign-edit-dist 2 -i 50 -I 5000 --max-coverage-intron 5000 -M -o out /data/user446/mapping tophat/index/chr
20 /data/user446/mapping tophat/L6 18 GTGAAA L007 R1 001.fastq
HWI-ST1145:74:C101DACXX:7:1102:4284:73714
                                      16
                                             chr20
                                                   190930 3
                                                                100M
                                                                                    0
     {\sf CCGTGTTTAAAGGTGGATGCGGTCACCTTCCCAGCTAGGCTTAGGGGATTCTTAGTTGGCCTAGGAAATCCAGCTAGTCCTGTCTCTCAGTCCCCCCTCT}
    AS: i:-15
                XM:i:3 X0:i:0 XG:i:0 MD:Z:55C20C13A9 NM:i:3 NH:i:2 CC:Z:= CP:i:55352714
HWT-ST1145:74:C101DACXX:7:1114:2759:41961
                                                                100M
                                             chr20
                                                   193953
     TGCTGGATCATCTGGTTAGTGGCTTCTGACTCAGAGGACCTTCGTCCCCTGGGGCAGTGGACCTTCCAGTGATTCCCCTGACATAAGGGGCATGGACGA
    G
                XM:i:3 XO:i:0 XG:i:0 MD:Z:60G16T18T3 NM:i:3 NH:i:1
   AS: i:-16
                                                                100M
HWI-ST1145:74:C101DACXX:7:1204:14760:4030
                                      16
                                             chr20
                                                   270877 50
     DDDDDDDDDDDDDDDDDDDDDDDEEEEEEFFFEFFEGHHHHFGDJJIHJJIJJJJIIIIIGGFJJIHIIIIJJJJJJIIGHHFAHGFHJHFGGHFFFDD@BB
   AS: i:-11
                XM:i:2 X0:i:0 XG:i:0 MD:Z:0A85G13
                                                NM:i:2 NH:i:1
HWT-ST1145:74:C101DACXX:7:1210:11167:8699
                                             chr20
                                                   271218 50
                                                                50M4700N50M
                                                                                    0
            GTGGCTCTTCCACAGGAATGTTGAGGATGACATCCATGTCTGGGGTGCACTTGGGTCTCCGAAGCAGCAGAACATCCTCAAATATGACCTCTCG
accepted hits.sam
```

Alignment visualization with IGV



Alignment visualization (Tablet)



Samtools: working with SAM/BAM

- samtools flagstat <input.bam>
- samtools view <input.bam> | less -S
- samtools sort <input.bam> -o <out.bam>
- samtools index <input.bam>
- samtools view <input.bam> "chr1:100-500"

http://www.htslib.org/doc/samtools.html

Pysam: SAM/BAM in Python

```
import pysam
samfile = pysam.AlignmentFile("ex1.bam", "rb")
for read in samfile.fetch('chr1', 10000, 20000):
     print('%s %s %d' %
           (read.query name,
            read.reference name,
            read.reference start))
```

https://pysam.readthedocs.io/en/latest/api.html

SNP calling

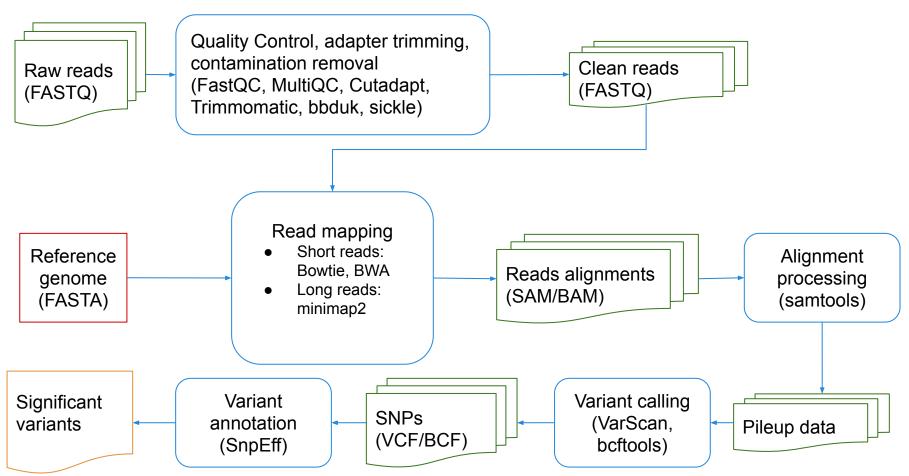
Process of detecting positions that differ from the reference genome

- Typically including an associated statistical confidence score
- Also known as "variant calling"

We need enough coverage to distinguish real variants from sequencing errors

Reference based analysis

SNP calling pipeline



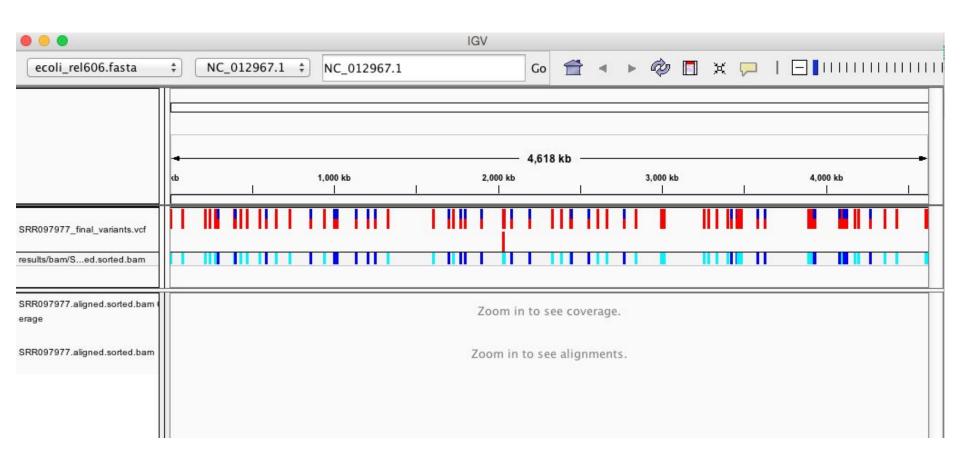
VCF/BCF files

- Chromosome (#CHROM)
- Position (POS)
- Unique identifiers where available (ID)
- Reference base(s) (REF)
- Alternate non-reference alleles (ALT)
- Phred quality score for the variant (QUAL)
- Optional filters (FILTER)
- Additional information (INFO)

VCF files

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO
1	10177		A	AC	100	PASS	AC=2130; AF=0.425319; AN=5008; NS=2504
1	10235		T	TA	100	PASS	AC=6; AF=0.00119808; AN=5008; NS=2504
1	10352	rs145072688		T	TA	100	PASS AC=2191; AF=0.4375; AN=5008; NS=2504
1	10505		A	T	100	PASS	AC=1;AF=0.000199681;AN=5008;NS=2504
1	10506		C	G	100	PASS	AC=1;AF=0.000199681;AN=5008;NS=2504
1	10511		G	A	100	PASS	AC=1;AF=0.000199681;AN=5008;NS=2504
1	10539		C	A	100	PASS	AC=3;AF=0.000599042;AN=5008;NS=2504
1	10542		C	Т	100	PASS	AC=1;AF=0.000199681;AN=5008;NS=2504
1	10579		C	A	100	PASS	AC=1;AF=0.000199681;AN=5008;NS=2504
1	10616	rs376342519		CCGCCGTTGCAAAGGCGCGCCG		GCGCGCCG	C 100 PASS AC=4973;AF=0.993011;AN=5008;NS=2504
1	10642		G	A	100	PASS	AC=21; AF=0.00419329; AN=5008; NS=2504
1	11008		C	G	100	PASS	AC=441;AF=0.0880591;AN=5008;NS=2504
1	11012		C	G	100	PASS	AC=441;AF=0.0880591;AN=5008;NS=2504
1	11063		T	G	100	PASS	AC=15; AF=0.00299521; AN=5008; NS=2504
1	13011		T	G	100	PASS	AC=3;AF=0.000599042;AN=5008;NS=2504
1	13110	8.0	G	A	100	PASS	AC=134;AF=0.0267572;AN=5008;NS=2504

SNP visualization with IGV



Tools

- Alignment and data processing
 - o samtools
 - bcftools
- SNP calling and annotation
 - VarScan
 - SnpEff
- Visualization
 - Tablet
 - o IGV
- Pipelines
 - GATK

Thank you!

Questions?