

Primer on Reading Frames and Phase

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A genomic sequence has 6 reading frames

- 3 reading frames per strand (+ / -)

Score = 57.0 bits (136), Expect = 1e-18
 Identity = 25/25 (100%), Positives = 25/25 (100%), Gaps = 0/25 (0%)
 Frame = 12

Query 2 VEKYSIVFHFDIFPITVICNSNAY 76
 VEKYSIVFHFDIFPITVICNSNAY
 Sbjct 1 VEKYSIVFHFDIFPITVICNSNAY 25

- Frame: base to start translation relative to the first base of the sequence
 - 1: Start translation at **first** base of sequence
 - 2: Start translation at **second** base of sequence
 - 3: Start translation at **third** base of sequence

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A codon could be derived from nucleotides in adjacent exons

Spliced mRNA: CTG AGA GAT TTT CCG

Phase 0 | Phase 0

CTG AGA GT AG GAT TTT CCG

Phase 1 | Phase 2

CTG AGA G GT AG AT TTT CCG

Phase 2 | Phase 1

CTG AGA GA GT AG T TTT CCG

Donor Intron Acceptor

3

Splice donor and acceptor phases

- Phase: Number of bases between the complete codon and the splice site
 - Donor phase: Number of bases between the **end of the last complete codon** and the splice donor site (GT/GC)
 - Acceptor phase: Number of bases between the splice acceptor site (AG) and the **start of first complete codon**
- Phase **depends on the reading frame** of the CDS

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Phase depends on the reading frame

3305 | 3300 | 3295 | 3290 | 3285 | 3280

G T T T A T T T T C A G C G S T T A C G C C A A T

G F V I F F S Q S L R Q

V L F F S Q S L R Q

Splice acceptor

- Acceptor phase:
 - Phase 2 relative to **frame 1**
 - Phase 0 relative to **frame 2**
 - Phase 1 relative to **frame 3**

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Compatibility of donor and acceptor site

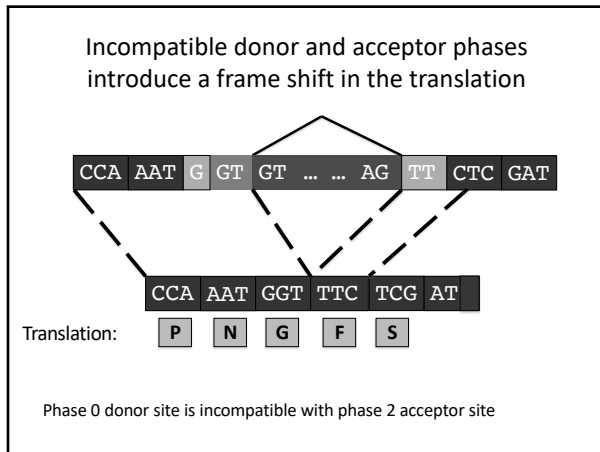
- Donor and acceptor phases of adjacent exons must be **compatible** with each other:
 Donor phase + acceptor phase = 0 or 3

CCA AAT G GT AG TT CTC GAT

CCA AAT GTT CTC GAT

Translation: P N V L D

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Calculating the exon acceptor phase

$$P_i = (3 - ((L_{i-1} - P_{i-1}) \% 3)) \% 3$$

where: $i > 1$

- P_i = Acceptor phase of exon i
- L_{i-1} = Length of previous exon
- P_{i-1} = Acceptor phase of previous exon

- $L_{i-1} - P_{i-1}$ = Previous exon length starting from the first complete codon
- $(L_{i-1} - P_{i-1}) \% 3$ = Donor phase of previous exon
- $3 - ((L_{i-1} - P_{i-1}) \% 3)$ = Acceptor phase of current exon
- $(3 - ((L_{i-1} - P_{i-1}) \% 3)) \% 3$ = Change to phase 0 if acceptor phase is 3

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