UGene - Open-Source Cross Platform Bioinformatics Software

## Introduction

- UGene allows interactive visualization and manipulation of common bioinformatics file formats
- Reference: https://academic.oup.com/bioinformatics/article/28/8/1166/195474
- User manual: http://ugene.net/downloads/UniproUGENE UserManual.pdf
- Download link: http://ugene.net/download.html


## Home Screen



## Multiple Sequence Alignment View



- Multiple alignment viewer image of aligned sequences


## Adding New Files To View



- Files can be added from the right click menu

- Added files are not automatically aligned if not already prealigned
- UGene allows alignment of sequences in current project using one of multiple algorithms
- WARNING: alignment of large sequences takes prohibitively long time on slower machines


## Highlighting Options



- A selected sequence in an alignment - Sites in other sequences that are identical to or different from can be set as reference
reference can be highlighted, as well as specific mutation types, gaps or conservation level


## No highlight



## Highlighted disagreements



## Extracting Highlighted Sequences

## \&G $\quad 1$ CTAGTGAGAAAAATATTTGTT

ICTAGTGAGAAAAATATTTGTT
ICTAGTGAGAAAAATATTTGTT

- ICTAGTGAGAAAAATATTTGTT
- ICTAGTGAGAAAAATATTTGTT
- ICTAGTGAGAAAAATATTTGTT ICTAGTGAGAAAAATATTTGTT
- ICTAGTGAGAAAAATATTTGTT
-1 CTAGTGAGAAAAATATTTGTT
$\rightarrow$ ICTAGTGAGAAAAATATTTGTT
+ ICTAGTGAGAAAAATATTTGTT
- t CTAGTGAGAAAAATATTTGTT
- ICTAGTGAGAAAAATATTTGTT
- Export highlighted

Export as image
Save subalignment...
Export selected sequence(s)... Amino translation...

- The highlighted sites can be exported in tab-delimited text file
- The resulting file can be viewed in Microsoft Excel, Pages, or similar software
- The first column shows nucleotide position, the second column shows reference sequence, the remaining columns show non-aligned sites
- Gaps are shown with -, while sites identical to reference are shown with .


## Manually Editing Sequences



- Low quality sequences can cause misalignment as unidentified residues ( N in nucleotide, X in peptide) align preferentially with each other

- Sequences can be edited manually using the right click menu
- Individual sites or long stretches can be edited


## Erroneous gaps



Gaps removed


