

Converting Alignment

To convert an alignment from DNA to RNA or from RNA to DNA alphabet use the *Advanced Convert to RNA (TU)* context menu or use the General tab of Options Panel:

The screenshot displays the Jvarkit software interface. At the top, a bar chart shows sequence coverage across positions 60 to 82. Below this, a sequence alignment is shown with the reference sequence **C A A A T t T A t A A t G T + A T t g T t A C**. The alignment consists of 18 sequences, with positions 60-82 labeled at the bottom. A context menu is open over the alignment, listing options: Appearance, Navigation, Add, Copy/Paste, Edit, Sort, Align, Tree, Statistics, Export, Advanced (highlighted), Set this sequence as reference, and Consensus mode... The 'Advanced' menu is further expanded, showing options: Convert to RNA alphabet (T->U), Build HMMER2 profile, and Build HMMER3 profile. On the right, the 'General' settings panel is visible, showing 'Reference sequence' (Select and add), 'Alignment info' (Alphabet: Standard DNA, Length: 604, Sequences: 18), 'Consensus mode' (Consensus type: Default, Threshold: 100%), and 'Copy (custom format)' (Format: ...). A red arrow points to the 'RNA' button in the 'Alignment info' section.