Title	Otter/ZMap/SeqTools: A productive alternative to web browser genome visualisation
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License	GNU General Public License (GPL)

We believe our set of integrated software tools offers our annotators a genome visualisation and annotation environment that cannot be matched in a browser application. The software's features have evolved over many years to support complex vertebrate annotation using a workflow which pulls together genomic data from around the world.

Otter coordinates the annotation workflow, manages local editing session caches, and records and audits annotation edits. Otter performs on-the-fly alignments to allow annotators to verify new and remapped evidence. Otter's filters can re-map data sources between different sequence assemblies.

ZMap is a high-performance standalone genome browser/editor written in C/C++. Its vertical columns allow for side-by-side comparison of many tens of data sources, drawn from local and remote resources in standard formats including GFF3 and BAM. ZMap allows split panels to be scrolled in unison, and has a rich set of highlighting, searching and filtering options for coping with large-volume alignment and feature sources. ZMap also provides a "remote control" interface that allows another program (e.g. otter) to exchange information with it, so that it can be integrated into existing software.

Otter and ZMap launch Blixem, an interactive browser which provides display of features from ZMap in the context of one-to-many pairwise alignments at individual amino acid or nucleotide base level. Blixem is supported by Dotter for graphical dot-matrix comparison of sequences and by Belvu for viewing of multiple sequence alignments and phylogenetic trees. Blixem, Dotter and Belvu can also be run standalone using standard file formats such as GFF3, FASTA, Stockholm etc.