# Using DMAP

DMAP is an application that visualises and analyses the correlation between a physical sequence (pseudomolecule) and a genetic map.

### Input file format

There are three types of input and these must appear in the order below. Each line is made up of comma separated fields. There should be no spaces next to the commas.

**LINK,type,colourname,linetype(dash|solid),font**

A LINK line specifies how a particular marker type should be represented.

Type is the name given to that marker type.

Colourname is a text colour name as used in HTML/CSS/X11 (see http://en.wikipedia.org/wiki/X11\_color\_names for more details)

Linetype is either *dash* or *solid*

Font is a font description which has a face (*Helvetica* or *Times* and an option *Roman*, *Bold* or *Italic*)

**MOLECULE,molecule\_name,start,length**

A MOLECULE line describes a contiguous fragment of the physical molecule.

Molecule\_name is the label to be given to this fragment.

Start is the start coordinate

Length is the length in base pairs. No units or qualifiers should be used (ie 12000 not 12 kbp)

**MARKER,marker\_name,marker\_position,pseudomolecule\_position,markertype**

A MARKER line describes the mapping between the genetic map and the physical map for an individual sequence-located marker.

Marker\_name is a unique identifier for the specific sequence located marker.

Marker\_position is the position on the genetic map in centimorgans. There should be no units. This can be expressed as a range of two hyphen separated floating point numbers, e.g. 12.5 14.1-16.3

Pseudomolecule\_position is the base pair number that best represents the location of the marker in the physical sequence. This must be located inside a MOLECULE otherwise DMAP will exit with an error message

Markertype is a type specified in a LINK line that describes how the mapping is to be represented.

Example:

LINK,opa,blue,solid,Helvetica Roman

LINK,ssr,red,dashed,Helvetica Italic

LINK,tom,green,solid,Times Bold

MOLECULE,contig1,1,12345

MOLECULE,contig2,12500,7654

MOLECULE,contig3,22000,54321

MOLECULE,contig4,77000,3456

MARKER,opa1,1.54,3456,opa

MARKER,opa2,3.84,6644,opa

MARKER,opa3,5.234,8000,opa

MARKER,opa4,9.3,11111,opa

MARKER,tom1,14.876-20.001,25111,tom

MARKER,tom2,18.0,30111,tom

MARKER,ssr1,35.1,41111,ssr

MARKER,ssr2,59,61111,ssr

MARKER,ssr3,77,71111,ssr

## Running DMAP

options:

-infile input file

-outfile output file

-height figure height in mm

-width figure width in mm

-colour (multi) name:red,green,blue values 0-255

-chrom chromosome colour

-mol molecule colour

-minfont minimum font size for markers (default 4)

-crowd try to fit more marker labels in (default 2.5 - higher is more

labels)

-nocount Don’t include marker count.

-genbin resolution of genetic map bin (default 0.1cM)

-nosize don’t add molecule size to the plot title.

-seqbin resolution of sequence marker bin (only one marker of each type will be shown per bin) Default 100.

-title plot title.

Colours are X11/HTML/CSS colours. Font is Helvetica or Times with

options Roman Bold or Italic e.g. Helvetica Roman

Interpreting the output