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MARTITRACKS MANUAL

PUBLISHED BY THE AUTHORS

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LIFE AND EARTH HAVE EVOLVED TOGETHER

LEON CROIZAT

ANALYSES AND SOFTWARE HAVE TO EVOLVE TOGETHER

THE AUTHORS

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*Dedicated to those who appreciate good
Biogeography and love dogs.*

Forewords

This manual is intended to be a clear and comprehensive introduction to Panbiogeography and geometric track analyses, using the program *MartiTracks*. The book is divided into four main chapters and some appendices. First chapter is a general introduction to Panbiogeography and related terms, second chapter presents *MartiTracks*' algorithm while third chapter is devoted to commands used. The fourth and final chapter presents some theoretical and empirical data and its analyses to explore *MartiTracks* options.

° <http://ciencias.uis.edu.co/labsist/pantrack>

The program was developed using FreePascal, as Pascal is an intuitive and easy to handle language for programming, the debate is open to consider whether C/C++ or Python/Perl/Java are more suitable languages for this kind of problem. As a free software project, feel free to criticize the code or the algorithm, and if you improve it, we will be more than delighted and thankful.

° <http://www.freepascal.org>

This manual has been developed using Tufte-L^AT_EX, maybe (in our humble opinion), the best environment to write a book or a handout.

We are grateful to many people,

° <http://code.google.com/p/tufte-latex>

We are open to new ideas or suggestions to improve our analyses, the program, and this manual itself.

Introduction

Panbiogeography

Panbiogeography is a unique and very useful approach to capture any distributional pattern/structure in studies that use geographical data. Mapping biogeographic tracks is a cost efficient way to reduce the initial complexity that we find in the data sets (Craw, 1989b), as Croizat's tracks analysis (Croizat, 1952, 1958) provides a conceptual framework for understanding the biogeographic structure and the relationships of areas.

Panbiogeography was developed by Croizat in his books, "Manual of phytogeography"(Croizat, 1952), "Panbiogeography"(Croizat, 1958) and "Space, Time, Form: The Biological Synthesis"(Croizat, 1964). Panbiogeography was inspired by Croizat's idea of connecting two essential elements in evolution: Space and Time: Earth and Life evolve together, which means that biotas evolve together with the geographic barriers (Morrone and Crisci, 1995; Morrone, 2000).

Croizat's panbiogeography constituted a unique critique to Darwin's biogeography ideas about natural selection, means of dispersal and geographic distribution (Craw, 1987). This approach challenged the idea that means of dispersal are the principal factors responsible for the evolution of the distribution (Craw, 1989a; Craw *et al.*, 1999).

Panbiogeography assumes that taxa distribution evolves through two stages: mobilism and immobilism. The interaction of these two states is called vicariant form-making model. Within the mobil-

ism stage, an ancestor taxon expands to establish on new territory through its means of dispersal ("means of survival") when the geographic and climatic factors are favorable. Later, when the range geographic is established (immobilism) the appearance of barriers allows the isolation and differentiation of taxa (vicariant form-making) (Grehan, 1988; Michaux, 1989; Craw *et al.*, 1999; Crisci and Morrone, 1992).

Panbiogeography has been considered an independent research program because is the only approach that focuses on the spatial or geographical sector as a fundamental pre-condition to any analysis of the patterns and processes of evolutionary change (Craw *et al.*, 1999; Grehan, 1994, 2001a).

The assumptions that make the Panbiogeography different from other historical biogeography approaches are (Craw *et al.*, 1999, :19): "1. Distribution patterns constitute an empirical databases for biogeographical analysis.

2. Distribution patterns provide information about where, when, and how animals and plants evolve;

3. The spatial and temporal component of these distribution patterns can be graphically represented;

4. Testable hypothesis about historical relationship between the evolution of distributions and Earth history can be derived from geographic correlations between distribution graphs as geological/geomorphic features."

Track analysis

Panbiogeography as a biogeographic method is called track analysis. There are four principal concepts within this method: track, node, main massing, and baseline (Crisci and Morrone, 1992; Craw *et al.*, 1999; Grehan, 2001a; Espinos-Organista *et al.*, 2002).

Individual tracks are the basic units of panbiogeography. These

are lines drawn on a map that connect different localities or distribution points of a particular taxon or group of taxa, so that the sum of the segment lengths that connect all the distribution points is the smallest possible. In the graph theory words, the individual track is a minimum spanning tree (Craw *et al.*, 1999; Morrone, 2004; Page, 1987)

Generalized tracks or standard tracks are called repetitive patterns because summarized distributions of diverse individual taxa (Michaux, 1989). These are lines on a map resulting from the superimposition of the individual tracks. Generalized tracks are interpreted as distributional patterns of ancestral biota that had been fragmented by tectonic and climatic events (Craw, 1988b). These panbiogeographic element is considered conjectures on a common biogeography history or primary biogeography homology sensu Morrone (2001), which means that analyzed taxa are spatiotemporally integrated in a biota (Craw, 1983; Morrone, 2001, 2004).

Nodes are areas or localities where two or more generalized tracks are overlapped. These are complex areas or tectonic and biotic convergence zones (Craw, 1988a; Crisci and Morrone, 1992; Morrone, 2004; Page, 1987). The nodes are considered priority areas for conservation or sites of biological endemism because represented localities of high diversity, distribution boundaries, disjunction, incongruence and recombination, specimens that are difficult to identify and unusual hybrids (Craw *et al.*, 1999; Morrone and Espinosa, 1998; Grehan, 1993).

The Panbiogeographic method involves basically main three steps (Morrone, 2004): Firstly, construction of two or more taxon individual tracks (minimum spanning tree from distributional localities). Secondly, delimitation of generalized tracks through geographic congruence between individual tracks. Finally, determination of nodes within the intersection areas between generalized tracks.

There are different approaches within panbiogeographic method. Croizat's manual reconstruction (Croizat, 1958, 1964), Page's Spanning graphs (Page, 1987), Craw's Track compatibility (Craw, 1989b) and PAE ("Parsimony Analysis of Endemicity") (Rosen, 1984; Craw *et al.*, 1999; Luna-Vega *et al.*, 2000; Morrone and Marquez, 2001)

Croizat's manual reconstruction

Croizat's manual reconstruction is done by drawing on a map taxon's individual tracks and then overlapping them to determinate generalized tracks. Basically the method consists of the following steps (Morrone, 2004):

1. Connect the disjunct areas of distribution by lines forming individual tracks,
2. The individual tracks are oriented using baselines,
3. Overlap individual tracks to determinate generalized tracks,
4. Recognize the nodes where two or more generalized tracks are intersected,
5. Indicate on a map the generalized tracks, baselines and nodes.

Page's Spanning graphs

Page's Spanning graphs was the first attempt to quantify the panbiogeographic analysis using graph theory. Its main methodological steps are (Page, 1987):

1. connect the disjunct areas of distribution through a MST (Minimum Spanning Trees) forming an individual track for each species,
2. Construct incidence and connectivity matrices for individual tracks to recognized shared elements and track congruence,
3. Construct a connectivity matrix for all tracks together to search circuits that indicate incongruence tracks,
4. Indicate on a map the generalized tracks, baselines and nodes.

Craw's tracks compatibility analysis

Craw's tracks compatibility analysis (Craw, 1989b) involves finding the largest clique of compatible tracks through a locality/distribution per track matrix (Craw *et al.*, 1999). In general, its algorithm involves the following steps (Craw, 1989b; Grehan, 2001b; Morrone, 2004):

1. Construct individual tracks for different taxa from distribution localities using a MST,
2. Generate an areas matrix for individual tracks where the presence of the areas is represented by "1" and absence by "0".
3. Find the largest clique for compatible individual tracks which is considered the generalized track.
4. Evaluate statistically the generalized track,
5. Indicate on a map the generalized tracks, baselines, and nodes.

Parsimony Analysis of Endemicity

PAE ("Parsimony Analysis of Endemicity") has been considered a panbiogeographic method (Craw *et al.*, 1999; Luna-Vega *et al.*, 2000; Morrone and Marquez, 2001; Morrone, 2004). Its algorithm includes the following steps (Morrone, 2004):

1. Construct individual tracks for different taxa from distribution localities using a MST,
2. Generate an areas matrix for individual tracks where the presence of a species is represented by "1" and the absence by "0".

Within this step, an extra area is added with "0" (all species absence) for polarized areas cladogram,

3. Analyze the matrix using a parsimony algorithm. Each clade formed by at least two individual tracks is considered a generalized track,
4. "Disconnect" or delete the species that support the different clades and reanalyze the matrix to search clades that are supported by other taxa,

5. Indicate on a map the generalized tracks, baselines and nodes.

Since Croizat (1958, 1964) presented his panbiogeographic method, the above mentioned quantitative techniques had been proposed, Page's graph theory method (Page, 1987), Henderson's analysis (Henderson, 1989), which is similar to Page's analysis, and Craw's compatibility track analysis (Craw, 1989b). These techniques have emerged taking into account Croizat's framework for analysis: individual tracks congruence to define generalized tracks (Page, 1987; Henderson, 1989; Craw, 1989a). Page (1987) suggested a quantitative approach using graph theory by incidence and connectivity matrices, but this method has not been applied to real data, perhaps because of its difficult calculation and computational complexity. Craw (1989b) proposed the compatibility track analysis based on distributional compatibility which is analogous with Meacham's character compatibility approach (Meacham, 1984) to phylogenetic systematics (Craw *et al.*, 1999). Within the latter method, two or more individual tracks are considered compatible if either one is included within or replicated by the other. Morrone and Crisci (1995) claimed that the compatibility in Panbiogeography is used in a restricted way depending on the method. "Non-overlapping tracks" are incompatible according to compatibility track analysis and should be compatible in Croizat's track analysis by geographic proximity.

Within the quantitative techniques proposed in the history of the panbiogeography (Page, 1987; Craw, 1989b; Henderson, 1989), only Craw's compatibility tracks analysis has been implemented and now part of the algorithm, the minimal spanning tree, has been automated in the software package "Croizat" (Cavalcanti, 2009).

Grid analysis such as PAE (Parsimony Analysis of Endemicity) has been considered a panbiogeographic approach (Craw *et al.*, 1999; Luna-Vega *et al.*, 2000; Morrone and Marquez, 2001; Morrone, 2004), but some authors do not consider it a historical biogeography

method (Humphries, 2000; Garcia-Barros *et al.*, 2002). Although this method has been widely used (Luna-Vega *et al.*, 2000; Morrone and Marquez, 2001; Huidobro *et al.*, 2006; Mihoc *et al.*, 2006; Espinosa-Perez *et al.*, 2009; Contreras-Medina *et al.*, 2007), its implementation to the panbiogeographic analysis was secondary. Its direct objective is the analysis of endemism and its relation to the track analysis sensu Croizat could become ambiguous.

Despite of these methods, Croizat's manual reconstruction has been the most used in panbiogeographic studies because its simplicity and the alleged direct connection to Croizat's panbiogeographic concept. Nevertheless, the debate about the reliability of the manual reconstruction is still valid. The method turns to be ambiguous and generates subjective results with large data set due to overcrowded points (Franco-Rosselli, 2001; Liria, 2008).

Suggested literature

- *Craw et al.* (1999) is a good summary of theories and methods, while the empirical approach could be flawed.
- *Crisci* (2001) is an historical account of biogeography, and is illustrative of the so called forces that shaped present biogeographic thought.

MartiTracks, the program

Definitions

MartiTracks algorithm has been presented in our paper (cite), therefore we suggest you to read the paper first.

The program tracks MST or segments, therefore you can conduct your analysis in either of those two ways.

The program and its calculations

If you use MST, the species' MST will be compared to all species MST, comparing each segment but outputting the answer by species, so you can expect at most nsp possible tracks, where nsp is the number of initial species.

If you use segments each segment will be compared to all species MST, comparing each segment and outputting the answer by segments/points, so you can expect at most nsegs, where nseg is

$$\sum_{j=1}^{nsp} MST(j) \rightarrow nsp \text{ i=number of segments } MST(j)$$

As all segments or MST are not congruent, the real number of answers lies in a number smaller than those.

MartiTracks files. General information

The program uses two input files,

1. -the input file with the distributional data. (Only the input file is mandatory).

° If you are not familiar with graph theory you might find these links useful:

http://en.wikipedia.org/wiki/Minimum_spanning_tree

http://en.wikipedia.org/wiki/Glossary_of_graph_theory

° nsp = number of species

2. -the parameters/orders file with the values for parameters and the commands to be executed in bash and creates a kml output file

MartiTracks input file

MartiTracks accepts as an input, a text file comprised of three columns, labels lat long separated by tabs or spaces but not commas (,), most spreadsheet and sig programs can output such text files, or you can use awk/bash to reshape them.

As an example we include

-a bash+awk command file that converts a comma delimited file in a *mt05inputfile* (csv2pt.sh)

-a bash+awk command file that converts a GlobalMapper output in a *mt05inputfile* (gm2pt.sh)

mt05output file

MartiTracks writes kml files, with or without the initial tracks. With all the analyses made before closing, in the form of tracks or points. The output is easily readable using google-earth or gis programs as QGIS. As some programs may or may not read the output, we only keep compatibility with google-earth/QGIS. If your beloved gis program does not read the output, please consider read it with google-earth.

Download the program and a data set

You must download a binary for your platform of choice, from <http://tux.uis.edu.co/labsist/martitracks> or <http://code.google.com/p/martitracks/>

Binaries are provided for Linux 64, Win 32 and 64

° a valid data set = testo.dat

sp1	1	9
sp1	3	11
sp1	6	12
sp2	1	9
sp2	1	10
sp2	3	10
sp2	4	11
sp2	5	12
sp2	6	12
sp3	4	13
sp3	5	11
sp3	8	8
sp4	4	12
sp4	6	11
sp4	7	8
sp5	8	8
sp5	7	6
sp5	8	2
sp6	8	8
sp6	7	5
sp6	8	3

° note: if your label field includes inner tabs/spaces, these will be considered as field separator therefore are NOT allowed, you can replace such character by an underscore or delete them all (*mt05* converts the dash to underscore)

° A common mistake is different labels for the same species, although *mt05* is not case sensitive, it is (quite) sensitive to misspellings therefore *Simulium* and *simulium* are the same, while *Simulium*, *Simulium* or *Simulium* are not.

and the data sets at <http://tux.uis.edu.co/labsist/martitracks/data-example.zip>

° For linux version, you might need to convert the file `mt05-xx` to an execute file by typing in a command-line window:

```
$ chmod +x mt05
```

Command modes

MartiTracks has two uses-interfaces: 1. A text user interface, and 2. a command-line interface.

in the text user interface (TUI), the user can choice among different options including: changes of parameters for analysis, track a pair, groups or the whole data, find the index of congruence (IC) between pairs of tracks, or among several tracks. print kml file, etc. The command line interface was created for search strategies previously defined. The input file, output file and parameters files must be defined.

° http://en.wikipedia.org/wiki/Text_user_interface#TUI_under_Unix-like_systems

Text user interface

You can use the text interface by simply typing at the prompt:

```
$ ./mt05
```

for Linux, and

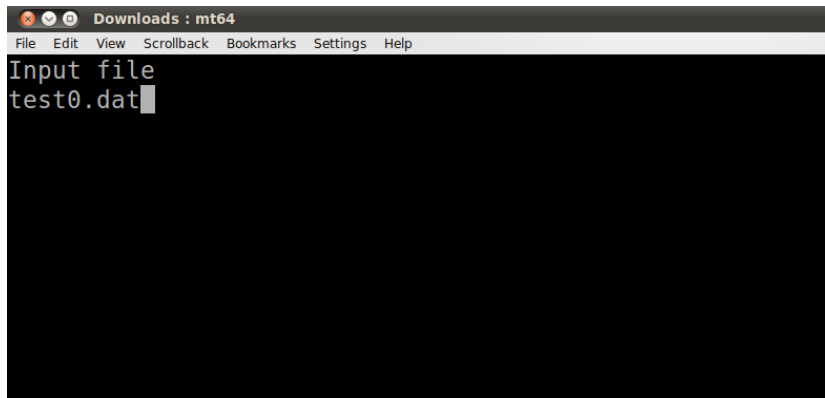
```
$ mt05-winXX.exe
```

for Windows in a command-line window

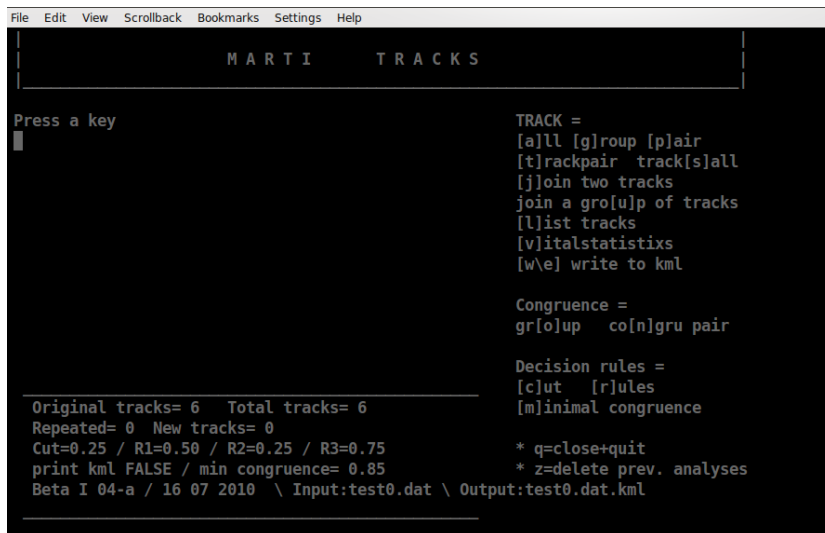
or by clicking on the *MartiTracks* icon (win. only).

1. Enter the input name: As soon as you open `mt05`, it asks for the input file name:

° TUI typography: commands will be **[C]**ut, to indicate that the instruction is cut and the letter to be pressed is c]



2. **Set up the analysis:** Once you specified the input name, a list of commands help the users to set up the analysis.



Then we must define the values of the parameters, to be used in this analysis.

There are five parameters: [c]ut value,

three [r]ules of decision, and the value for [m]inimal congruence.

And we are ready to conduct our analysis. As we might have similar initial MSTs, we need to joint those MST that are the same according to the minimum value of [m]inimal congruence fixed. We must press [u], to join the gro[u]p. The program will ask thenumber of the initial and final track to be joint. Now we must use [a]ll, to

find the congruent segments and define the generalized tracks or distributional patterns of species.

Finally, we need to eliminate those redundant generalized tracks, typing again [**u**], but joint from the track number 7 to the track 9, because first six tracks are individual tracks.

If, we want to write our results in a kml file, we must type [**k**] and [**+**] to activate the output to the kml file. The kml info must change from FALSE to TRUE. Then, we will use [**w**] if we want to write the whole information of the analysis including: individual tracks, and generalized tracks, or we can type [**e**] to write only the generalized tracks into the kml file.

For the command-line user interface we need to specified: the input file, output file, and parameters file.

```
$ ./mt05-64 <input file> <output file> <parameters file>
```


° You must download the program and the example data set, please see to page 22.

Worked example: *testo.dat*

Testo.dat

First of all, we must open the program (see page 23), read the data set and define the values of the parameters, to be used in this analysis.

There are five parameters: [c]ut value, three [r]ules of decision, and the value for [m]inimal congruence.

For *testo.dat* we will use the following values:

[c]ut	0.25
[r]ules	0.75 0.5 1
[m]inimal congruence	0.8

° please remember:
to set each of these parameters you have to type the letters inside the square brackets [] and write the corresponding value followed by and enter

3. Search options: Once the parameters have been defined, we will search the general patterns of distribution.

As we might have similar initial MSTs, we need to find the similarity among the individual tracks to join a group of tracks according to the minimum value of [m]inimal congruence fixed

In the case of *testo.dat*, we group from the track number 1 [first] to the track number 6 [last]. Thus, we find whether there are similar individual tracks that can be considered like the same track, and those tracks will be joint.

Later, we need to redefine the values of the parameters, in the case of *testo.dat* we will set:

[c]ut	0.5
[r]ules	1.5 1 2
[m]inimal congruence	0.8

Then, Typing [a]ll, we will find the congruent segments for each individual tracks in order to delimitate the generalized tracks or distributional patterns of species.

Finally, we need to eliminate those redundant generalized tracks, typing again [u], but joint from the track number 7 to the track 9, because first six tracks are individual tracks.

4. write a kml file

Now, we need to write our results (the generalized tracks) in a kml file. To do that, first we must type [k] and [+] to activate the output to the kml file. The kml info must change from FALSE to TRUE. Then, we will use [w] if we want to write the whole information of the analysis including: individual tracks, and generalized tracks, or we can type [e] to write only the generalized tracks into the kml file.

Command line interface

For the command-line user interface we need to specified: the input file, output file, and parameters file.

For linux 64 bits:

```
$ ./mt05-64 <input file> <output file> <parameters file>
```

For Windows 64 bits:

```
$ mt05-64.exe <input file> <output file> <parameters file>
```

For Windows 32 bits:

```
$ mt05-32.exe <input file> <output file> <parameters file>
```

Output file: it must have an extension .kml.

parameters file: This interface was designed for parameters/searching strategies defined previously. These search strategies have to be set in the parameters file. There are two main predefined strategies, *croizato*, and *croizat1*.

° .kml file extension is mandatory with googleeearth, otherwise googleeearth will complain and will not open the file

° CL typography: commands will be *croizato*, to indicate that the instruction is named Croizato and you must type *croizato* in your parameter file, the command could be written using lower or upper case.

The framework of *croizato* is:

1. Find similar individual tracks [= [**u**]] from the first, to the last individual track
2. Calculate the congruent segments among individual tracks (delimitate generalized tracks) [= [**a**]]
3. Find similar generalized tracks [= [**u**]] from the first, to the last generalized tracks

Therefore, our analysis made with the TUI is a *croizato* analysis.

The framework of *croizat1* is:

1. Calculate the congruent segments among individual tracks (delimitate generalized tracks) by [**a**]
2. Find similar generalized tracks by [**u**] from the first, to the last generalized tracks

Possible **parameters** values are:

[c]ut		set cut <real value 0-360>
[r]ules	lmax	set lmax <real value 0-360>
	lmin	set lmin <real value 0-360>
	maxline	set maxline <real value 0-360>
[m]inimal congruence		set ci <real value 0-1>

° * cut value is a real <0 - 360> value expressed in degrees
 [0.0] = no cut - [360.0] = all points will be collapsed to one.
 * rules are real <0 - 360> values expressed in degrees
 * minimal congruence is a real <0 - 1> value.
 [0.0] = no congruence - [1.0] = totally congruent.
 please refer to our paper (cite) for further information

These values are used to calculate the similarity among individual tracks in any analysis, joint or track.

Thus, the commands for the analysis of `test0.dat`, using `par1-search1.txt` are:

For linux 64 bits:

```
$ ./mt05-64 test0.dat test0.kml par1-search1.txt
```

For linux 32 bits:

```
$ ./mt05-32 test0.dat test0.kml par1-search1.txt
```

For Windows 64 bits:

```
$ mt05-64.exe test0.dat test0.kml par1-search1.txt
```

For Windows 32 bits:

```
$ mt05-32.exe test0.dat test0.kml par1-search1.txt
```

Results of `test0.dat` analysis

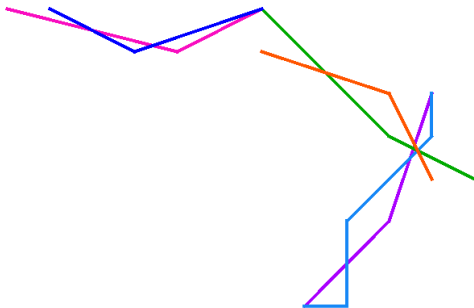


Figure 1: Individual tracks from `test0.dat`

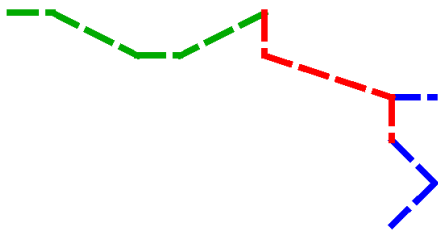


Figure 2: Generalized tracks from
testo.dat

MartiTracks commands

Text interface mode

general

[l] == list List all tracks

comparing *tracks*

[a] == all Track all the species using MSTs to compare

[g] == group Track a group of contiguous species

[p] == pair Track a pair of species (contiguous or not)

In all the three cases a new MST=track will be created if the species compared are congruent, while in a [p]air comparison only a single track could be created. In an [a]ll/[g]roup comparison, there could be more than one track.

comparing *segments*

[s] == all Track all the species using segments to compare

[t] == pair Track a pair of species (contiguous or not)

join

[u] == join group Join a group of contiguous tracks if a given pair

has a minimal congruence equal or higher than the

minimal congruence inputed in the value file or

the default value used in the TUI. If you want to join

a group regardless of the minimal congruence value,

reduce the min. cong. value to 0.0. After this late

analysis, replace the original min. cong. value

[j] == join pair Join two, contiguous or not, tracks independent of

the minimal congruence value

congruence calculation

[o] == Congr. group Calculate the congruence by pairs of a contiguous group,

as the output is a list, it is easier to read a small group than a large group

[n] == Congr. pair Calculate the congruence of a single pair
modify decision rules

[c] == cut Change the minimal cut value

[r] == rules Modify rules

[m] == min. cong. Change the minimal congruence value (see join)

Bash command mode

A bash command is an instruction that will perform an analysis equal to the analysis made in the text user interface [see page 33]. This mode is more appropriated to medium to huge data sets, where the analysis could last more than a few minutes or to test different parameter values.

The commands are given in the equivalence of the TUI, with a short explanation.

kmlgen == write to the kml file ONLY the generalized tracks (default). Must be in the file before the analysis.

kmlall == write to the kml file all, individual and generalized tracks. Must be in the file before the analysis.

croizat0 ==

join (individual tracks),

track (individual tracks),

join (generalized tracks)

= **[u]** (1 - # individual tracks), **[a]**, **[u]** (individual tracks + 1) total tracks

```

croizat1 ==
track (individual tracks)
join (generalized tracks)
= [a], [u] (individual tracks +1) total tracks

```

A sample command file is

```

set cv 1.5
set lmax 2.0
set lmin 0.6
set maxline 3.0
set ci 0.80
kmlall
croizat0

```

So, these seven lines in a file will change the default parameters to $cv = 1.5$, $lmax = 2.0$, $lmin = 0.6$, $maxline = 3.0$, $ci = 0.80$, and will use these values to join the individual tracks if the congruence value of the two MSTs compared is larger than 0.80, then *MartiTracks* will track those resulting MST to obtain the generalized tracks and will eliminate (joint) those redundant tracks using the same rule used before ($ci = 0.80$), and will output the individual and the generalized tracks.

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