

Tile Miner — Example Calls and Usage Guide

This document contains example calls for the functions in the Tile_miner program and their expected returns.

1. **tile_fetch_one()** creates a tile plot from a given accession code. Can be customized as indicated in the program documentation.

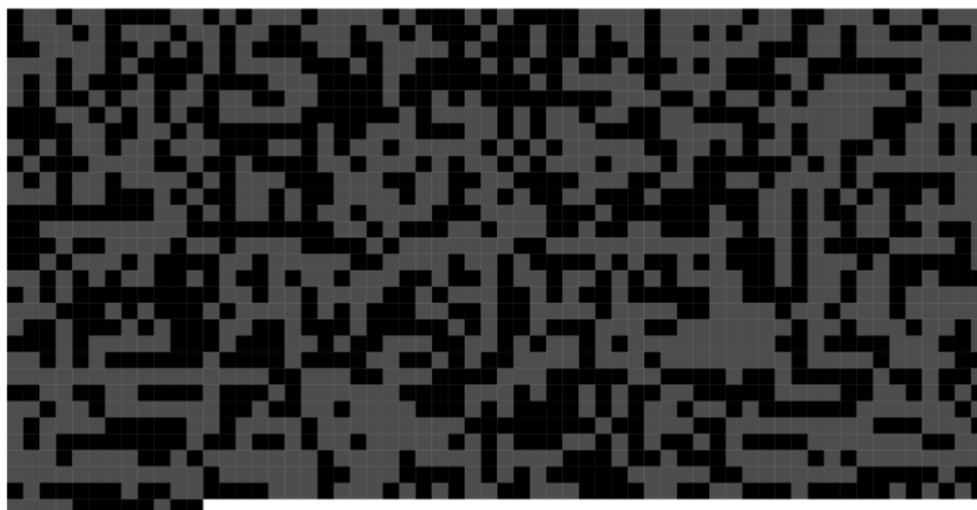
i.e.,

This call retrieves ACTB and turns the sequence into a tile plot 60 columns wide (per default). Plot will be divided into several pages if it exceeds the number of bases per page allowed by *bases_per_page* (helps in customizing resolution of the patterns).

tile_fetch_one("NM_001101.5")

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA

Width: 60 | Page: 1 of 1



Length: 1812 bp
Total Pages: 1
Columns: 60

In addition to plots, a function also returns a FASTA file of the sequence plus a summary of the search containing relevant information about the sequence and arguments used in the function.

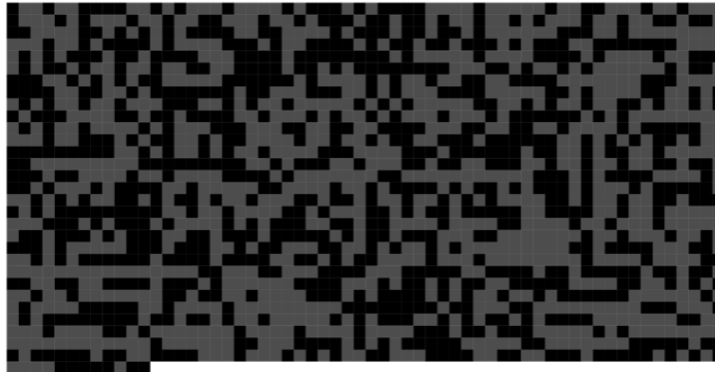
To obtain plots of different dimensions (num. of columns) or nucleotide density (resolution), the arguments *widths* or *bases-per-page* can be modified as shown below. It is important to note that the patterns formed by the tiles in a plot depend on the values of these arguments in addition to the sequence itself and the colour scheme. In this example, pyrimidines and purines have been coloured differently to show their distribution. Full colour customization is included in the program. Additional patterns will arise if colour is assigned based on other functional elements of a sequence (i.e., exons, LTRs, codons, etc.). Programs allowing manual and automatic annotation of the plots are being developed to explore these patterns.

i.e.,

This call retrieves the sequence for ACTB and plots it into three plots of varying width.

tile_fetch_one("NM_001101.5", widths = c(60, 80, 90))

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA
Width: 60 | Page: 1 of 1



Length: 1812 bp
Total Pages: 1
Columns: 60

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA
Width: 80 | Page: 1 of 1



Length: 1812 bp
Total Pages: 1
Columns: 80

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA
Width: 90 | Page: 1 of 1

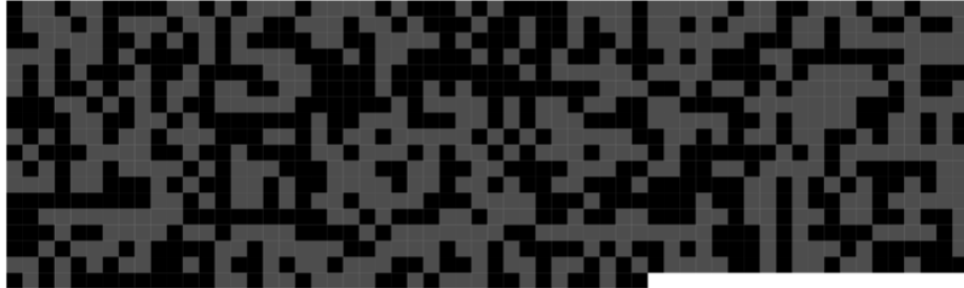


Length: 1812 bp
Total Pages: 1
Columns: 90

`tile_fetch_one("NM_001101.5", bases_per_page = 1000)` breaks the plot into two pages containing 1000 bases max.

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA

Width: 60 | Page: 1 of 2

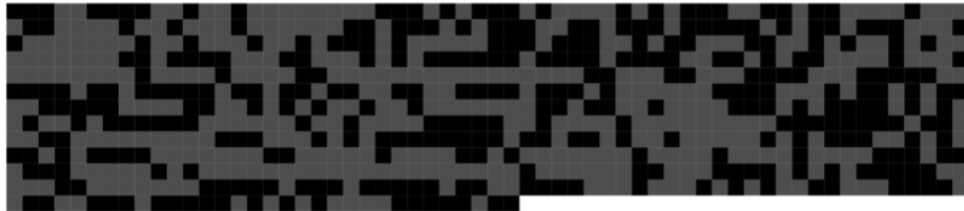


char
A
C
G
T

Length: 1812 bp
Total Pages: 2
Columns: 60

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA

Width: 60 | Page: 2 of 2



char
A
C
G
T

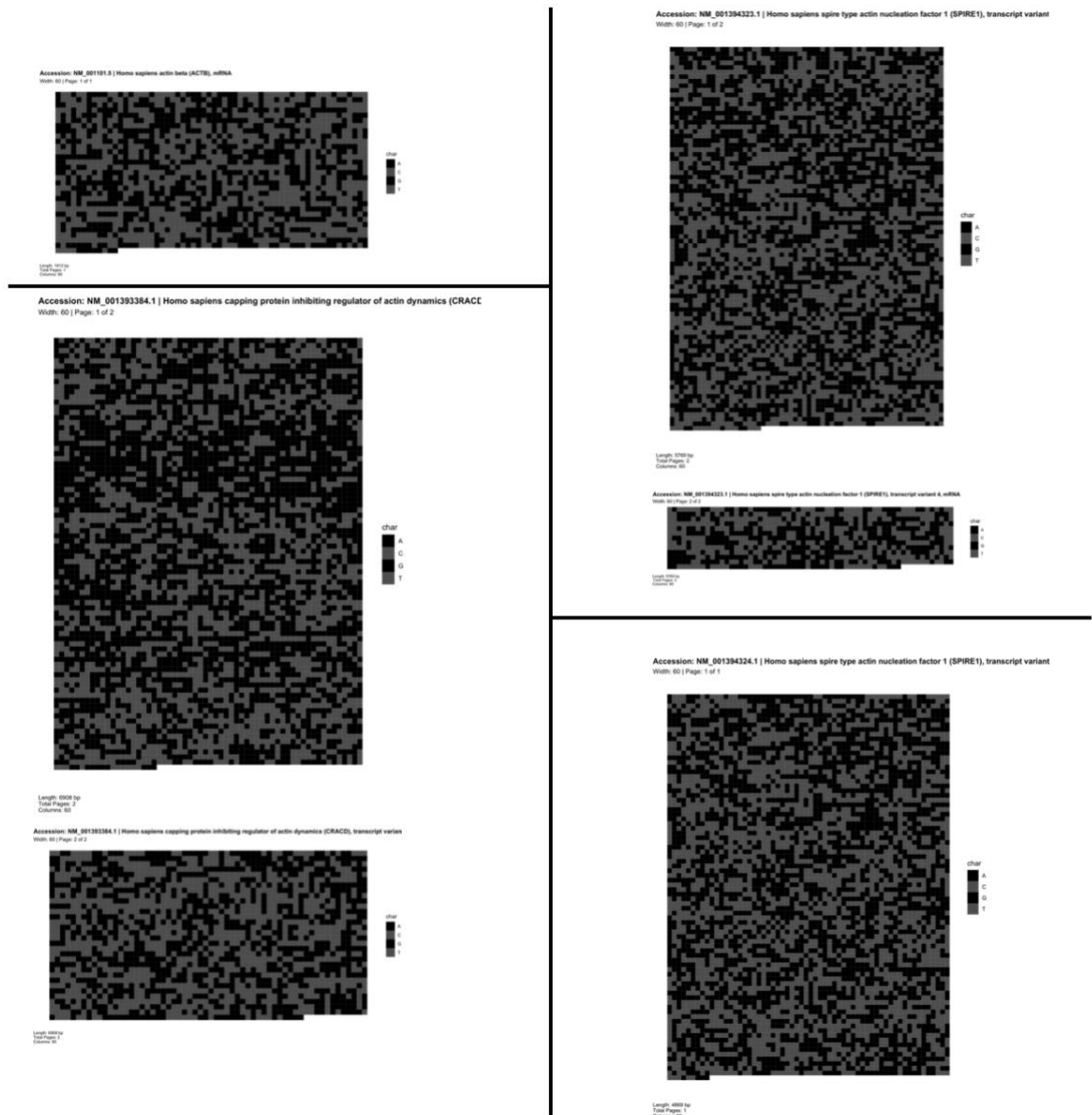
Length: 1812 bp
Total Pages: 2
Columns: 60

- The **tile_fetch_batch()** function performs a search of the NCBI's nuccore database and returns the specified range of sequences in the form of tile plots. The function uses the same filtering system used by the NCBI. Please refer to the program's documentation for further information about the arguments of this function.

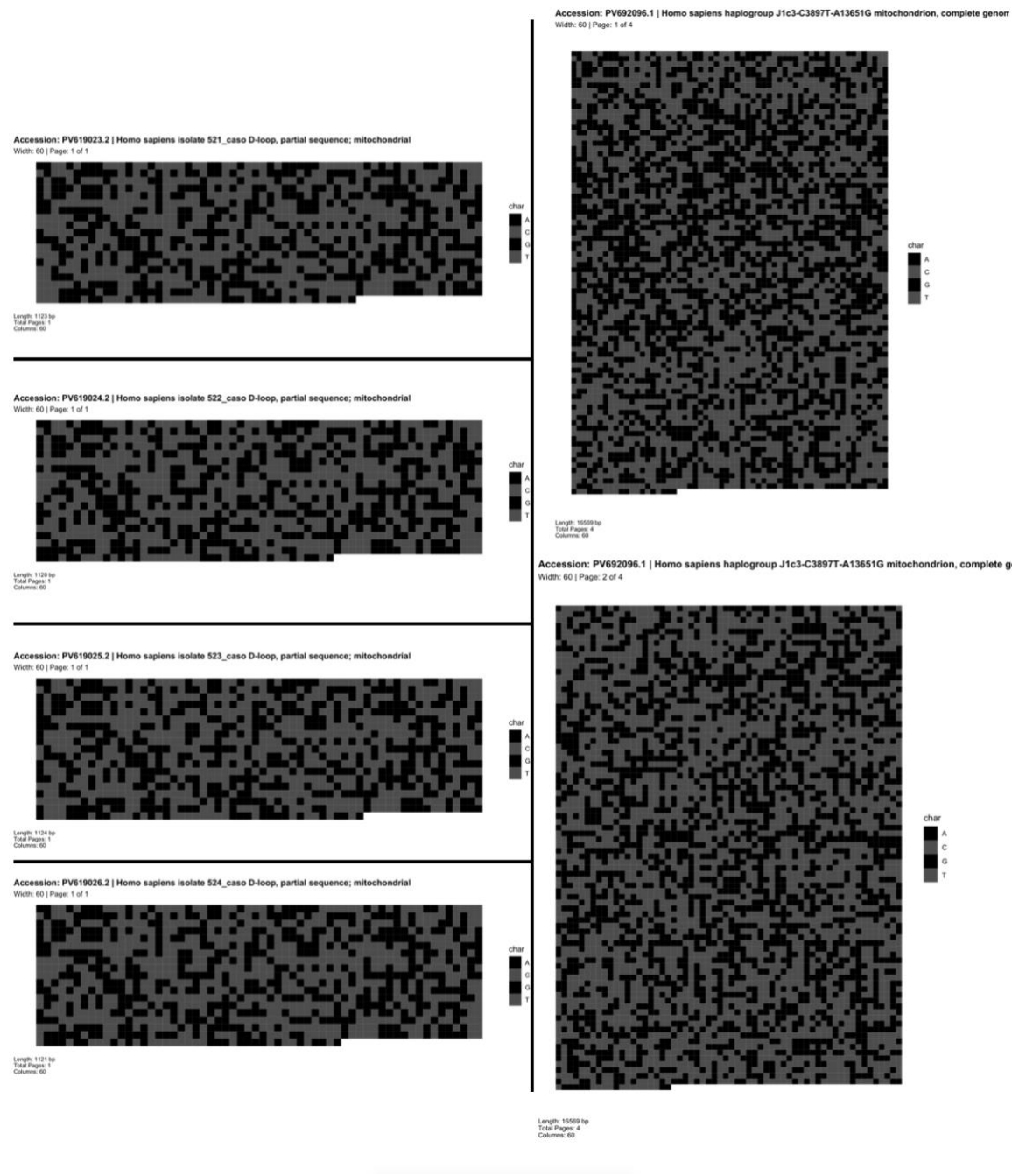
i.e.,

```
tile_fetch_batch("actin[Title] AND Homo sapiens[Organism]  
AND biomol_mrna[PROP]")
```

By default, the function retrieves the first 10 sequences in the database (shown here only the first 4, two of the sequences have been split into different plots). Please refer to the program's documentation to learn more about how to manipulate the search.



tile_fetch_batch("mitochondrion[Filter] AND Homo sapiens[Organism]")



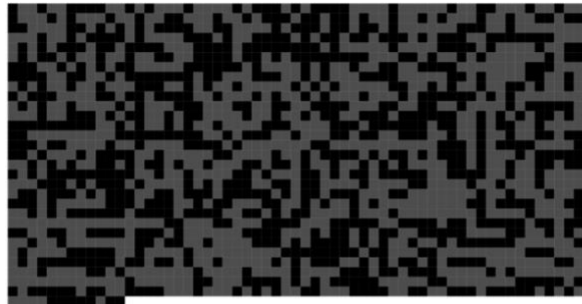
As with the single tile plotter, a FASTA file is produced for each sequence retrieved and plotted by tile_fetch_batch together with a summary file for the whole search.

3. Finally, a wrapping function is included in the program which recognizes the type of search based on the input given by the user. Please refer to the program documentation to learn more about this function.

i.e.,

```
tile_miner(  
  query = "NM_001101.5 OR NM_007393 OR NM_131031.2",  
  widths = c(60),  
  max_results = 3,  
  batch_size = 3  
)
```

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA
Width: 60 | Page: 1 of 1



Length: 1812 bp
Total Pages: 1
Column: 60

Accession: NM_007393.5 | Mus musculus actin, beta (Actb), mRNA
Width: 60 | Page: 1 of 1



Length: 1835 bp
Total Pages: 1
Column: 60

Accession: NM_131031.2 | Danio rerio actin, beta 1 (actb1), mRNA
Width: 60 | Page: 1 of 1



Length: 1730 bp
Total Pages: 1
Column: 60

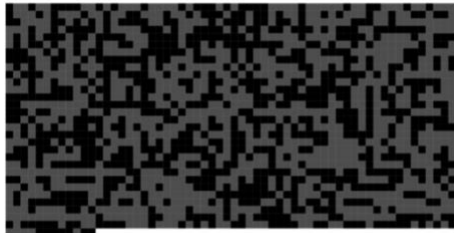
```

tile_miner(
  query = "actin beta[Title] AND (Homo sapiens[Organism] OR Mus musculus[Organism]
          ORDanio rerio[Organism]) AND biomoI_mrna[PROP] AND refseq[filter]",
  widths = c(60),
  max_results = 6,
  batch_size = 2,
  min_length = 500
)

```

Some results have been omitted.

Accession: NM_001101.5 | Homo sapiens actin beta (ACTB), mRNA
Width: 60 | Page: 1 of 1



Length: 1812 bp
Total Pages: 1
Column: 60

Accession: NM_007393.5 | Mus musculus actin, beta (Actb), mRNA
Width: 60 | Page: 1 of 1



Length: 1935 bp
Total Pages: 1
Column: 60

Accession: NM_131631.2 | Danio rerio actin, beta 1 (actb1), mRNA
Width: 60 | Page: 1 of 1



Length: 1750 bp
Total Pages: 1
Column: 60

Accession: NM_001017992.4 | Homo sapiens actin beta like 2 (ACTBL2), mRNA
Width: 60 | Page: 1 of 1



Length: 2784 bp
Total Pages: 1
Column: 60

End of Examples.

For advanced usage and filtering, see the full documentation included in the README file.