

NGS解析(初～中級)  
ゲノムアセンブリ後の各種解析  
の補足資料(プラスアルファ)

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## ■ Gepardでドットプロット

- 連載第8回W5-3で最も長いsequence1同士のドットプロットを実行できなかったが、Gepardというプログラムで実行可能。
- 動かせなかったらすぐに諦めるのではなく、「少ないメモリで動かせるもっといいプログラムがあるはず!」という視点で探すべし!

## ■ BlastViewerの新しいバージョンもある

- 連載第8回W7-2でBlastViewer ver. 2.2を利用したが、よく調べるとver. 5.2.0が存在します。



# ウェブ検索

Googleで①それっぽいキーワードで検索した結果。②Wikipediaのページを眺めてみる

The screenshot shows a Google search interface in Japanese. The search bar contains the text "dot plot bioinformatics" and is marked with a red arrow and the number 1. Below the search bar, there are navigation tabs for "すべて", "画像", "ニュース", "動画", "ショッピング", "もっと見る", "設定", and "ツール". The search results are displayed below, starting with "約 108,000 件 (0.65 秒)". The first result is "Dot plot (bioinformatics) - Wikipedia", which is marked with a red arrow and the number 2. The snippet for this result reads: "In bioinformatics a dot plot is a graphical method that allows the comparison of two biological sequences and identify regions of close similarity between them. It is a type of recurrence plot." Below this, there are two more results: "Dotplots for Bioinformatics - SlideShare" and "EMBOSS: dotmatcher - Bioinformatics".

# Wikipediaのドットプロット

The screenshot shows the Wikipedia article page for 'Dot plot (bioinformatics)'. The browser address bar shows the URL 'https://en.wikipedia.org/wiki/Dot\_plot\_(bioinformatics)'. The page title is 'Dot plot (bioinformatics)'. The article text explains that a dot plot in bioinformatics is a graphical method for comparing two biological sequences. A large dot plot image is shown on the right side of the page. A red arrow with the number '1' points to the scroll bar on the right side of the page, indicating the instruction to scroll to the bottom.

# Wikipediaのドットプロット

①このあたりまで移動して、②Software to create plotsのところまで手を止める

The screenshot shows a web browser window displaying the Wikipedia page for 'Software to create plots'. The address bar shows the URL 'https://en.wikipedia.org/wiki/Dot\_plot\_(bioinformatics)'. The page title is 'Software to create plots [edit]'. A red arrow with the number '2' points to the title. The page content is a list of tools for generating dot plots, including SynMap, Genomdiff, Gepard, ANACON, and various R packages like seqinr, dotplot, dotmatcher, Dotter, and JDotter. A red arrow with the number '1' points to the bottom right corner of the page content area. At the bottom, there are category links for 'Statistical charts and diagrams' and 'Bioinformatics'.

② Software to create plots [edit]

- [SynMap](#) - An easy to use, web-based tool to generate dotplots for many species with access to an extensive genome database. Offered by the comparative genomics platform CoGe.
- [Genomdiff](#) - An open source Java dot plot program for viruses.
- [Genomdiff](#) - An open source Java dot plot program for viruses.
- [Gepard](#) - Dot plot tool suitable for even genome scale.
- [ANACON](#) - Contact analysis of dot plots.
- [General introduction to dot plots with example algorithms](#) and a [software tool to create small and medium size dot plots](#).
- [Dotlet](#) - Provides a program allowing you to construct a dot plot with your own sequences.
- [UGENE Dot Plot viewer](#) - Opensource dot plot visualizer.
- [seqinr](#) - R package to generate dot plots.
- [dotplot](#) - R package to rapidly generate dot plots as either traditional or ggplot graphics.
- [dotmatcher](#) - Web tool to generate dot plots.
- [Dotter](#) - Stand alone program to generate dot plots.
- [JDotter](#) - Java version of Dotter
- [Dotplot](#), easy (educational) HTML5 tool to generate dot plots from RNA sequences
- [lastz](#) and [laj](#), programs to prepare and visualize genomic alignments.

Categories: [Statistical charts and diagrams](#) | [Bioinformatics](#)

# Gepardよさそう

①H29年度講習会スライド94-で用いた seqinrというRパッケージもちゃんとリストアップされている。②genome scaleの大きさの配列に対してもドットプロットしてくれる③Gepardというものもあるようだ

Wikipedia page titled "Software to create plots" with the URL [https://en.wikipedia.org/wiki/Dot\\_plot\\_\(bioinformatics\)](https://en.wikipedia.org/wiki/Dot_plot_(bioinformatics)). The page lists various software tools for creating dot plots. Red arrows with numbers 1, 2, and 3 point to specific items in the list.

## Software to create plots [\[ edit \]](#)

- [SynMap](#) - An easy to use, web-based tool to generate dotplots for many species with access to an extensive genome database. Offered by the comparative genomics platform CoGe.
- [Genomdiff](#) - An open source Java dot plot program for viruses.
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- [JDotter](#) - Java version of Dotter
- [Dotplot](#), easy (educational) HTML5 tool to generate dot plots from RNA sequences
- [lastz](#) and [laj](#), programs to prepare and visualize genomic alignments.

Categories: [Statistical charts and diagrams](#) | [Bioinformatics](#)



# 原著論文もある

①PubMed上で、②「gepard dotplot」で検索すると、③原著論文が見つかりました

The screenshot shows the PubMed website interface. The search bar contains the text 'gepard dotplot'. The search results section displays two items. The second item, 'Gepard: a rapid and sensitive tool for creating dotplots on genome scale', is highlighted with a red arrow and the number 3. The search details section shows the search query: 'gepard[All Fields] AND dotplot[All Fields]'. The left sidebar contains various filters and options, including 'Article types', 'Text availability', 'PubMed Commons', 'Publication dates', and 'Species'.

① PubMed

② gepard dotplot

③ [Gepard: a rapid and sensitive tool for creating dotplots on genome scale.](#)

Search results

Items: 2

1. [Phage cluster relationships identified through single gene analysis.](#)  
Smith KC, Castro-Nallar E, Fisher JN, Breakwell DP, Grose JH, Burnett SH.  
BMC Genomics. 2013 Jun 19;14:410. doi: 10.1186/1471-2164-14-410.  
PMID: 23777341 **Free PMC Article**  
[Similar articles](#)

2. [Gepard: a rapid and sensitive tool for creating dotplots on genome scale.](#)  
Krumsiek J, Arnold R, Rattei T.  
Bioinformatics. 2007 Apr 15;23(8):1026-8. Epub 2007 Feb 19.  
PMID: 17309896  
[Similar articles](#)

Search details

gepard[All Fields]  
AND dotplot[All Fields]

Search See more...

Recent Activity

# 原著論文もある

① ページ下部に移動すると、100回以上引用されていることがわかります。② このURLにアクセスすればいいようだ

The screenshot shows a web browser displaying a PubMed article. The browser's address bar shows the URL <https://www.ncbi.nlm.nih.gov/pubmed/17309896>. The page header includes the NCBI logo and navigation links. The article title is "Gepard: a rapid and sensitive tool for creating dotplots on genome scale." by Krumsiek J<sup>1</sup>, Arnold R, Rattei T. The abstract describes Gepard as a user-friendly application for creating dotplots. The availability section provides the URL <http://mips.gsf.de/services/analysis/gepard>. The PMID is 17309896 and the DOI is [10.1093/bioinformatics/btm096](https://doi.org/10.1093/bioinformatics/btm096). On the right side, there are sections for "Full text links" (Oxford Academic), "Save items" (Add to Favorites), and "Similar articles" (JDotter, PhyloGena, Idiographica, VEGA, UCSC genome browser). Two red arrows with numbers 1 and 2 point to the "Help" link in the top right and the DOI link in the bottom left, respectively.

<http://mips.gsf.de/services/analysis/gepard>



# Gepardのページ

①Gepardのページにアクセスしたところ。②ここでも原著論文情報がありますね。③ページ下部に移動してプログラムをダウンロードできる場所を探す

The screenshot shows the web browser interface for the Gepard website. The address bar displays the URL <http://cube.univie.ac.at/gepard>. The page header includes the 'Cube Computational Systems Biology' logo and a search bar. A dark navigation bar contains a menu icon and the word 'NAVIGATION'. The main content area is divided into sections: 'GENOME PAIR RAPID DOTTER (GEPARD)', 'CUBE NEWS', and 'LATEST PUBLICATIONS'. Three red arrows with numbers 1, 2, and 3 point to specific elements: arrow 1 points to the 'GENOME PAIR RAPID DOTTER (GEPARD)' section header; arrow 2 points to the reference text 'Reference: Krumsiek J, Arnold R, Rattei T. Gepard: A rapid and sensitive tool for creating dotplots on genome scale. Bioinformatics 2007; 23(8): 1026-8. PMID: 17309896'; and arrow 3 points to the search bar.

GENOME PAIR RAPID DOTTER (GEPARD)

Gepard (German: "cheetah", Backronym for "GENome PAir - Rapid Dotter") allows the calculation of dotplots even for large sequences like chromosomes or bacterial genomes. Reference: Krumsiek J, Arnold R, Rattei T. Gepard: A rapid and sensitive tool for creating dotplots on genome scale. *Bioinformatics* 2007; 23(8): 1026-8. PMID: [17309896](#)

USE CASES

Local comparison two of nucleotide or amino acid sequences from user-specified files. Batch dotplot functionality provided by command line access to Gepard.

FEATURES

CUBE NEWS

- » [Symposium "Computational Approaches in Precision Medicine" Jul 27/28 in Vienna](#)  
27.07.17
- » [FIRST RELEASE OF 45 PICA MODELS READY FOR DOWNLOAD](#)  
12.06.17
- » [Dr. rer. nat. Thomas Eder](#)  
18.04.17

LATEST PUBLICATIONS

- » [The desert plant \*Phoenix dactylifera\* closes stomata via nitrate-regulated](#)

# GepardはJavaプログラム

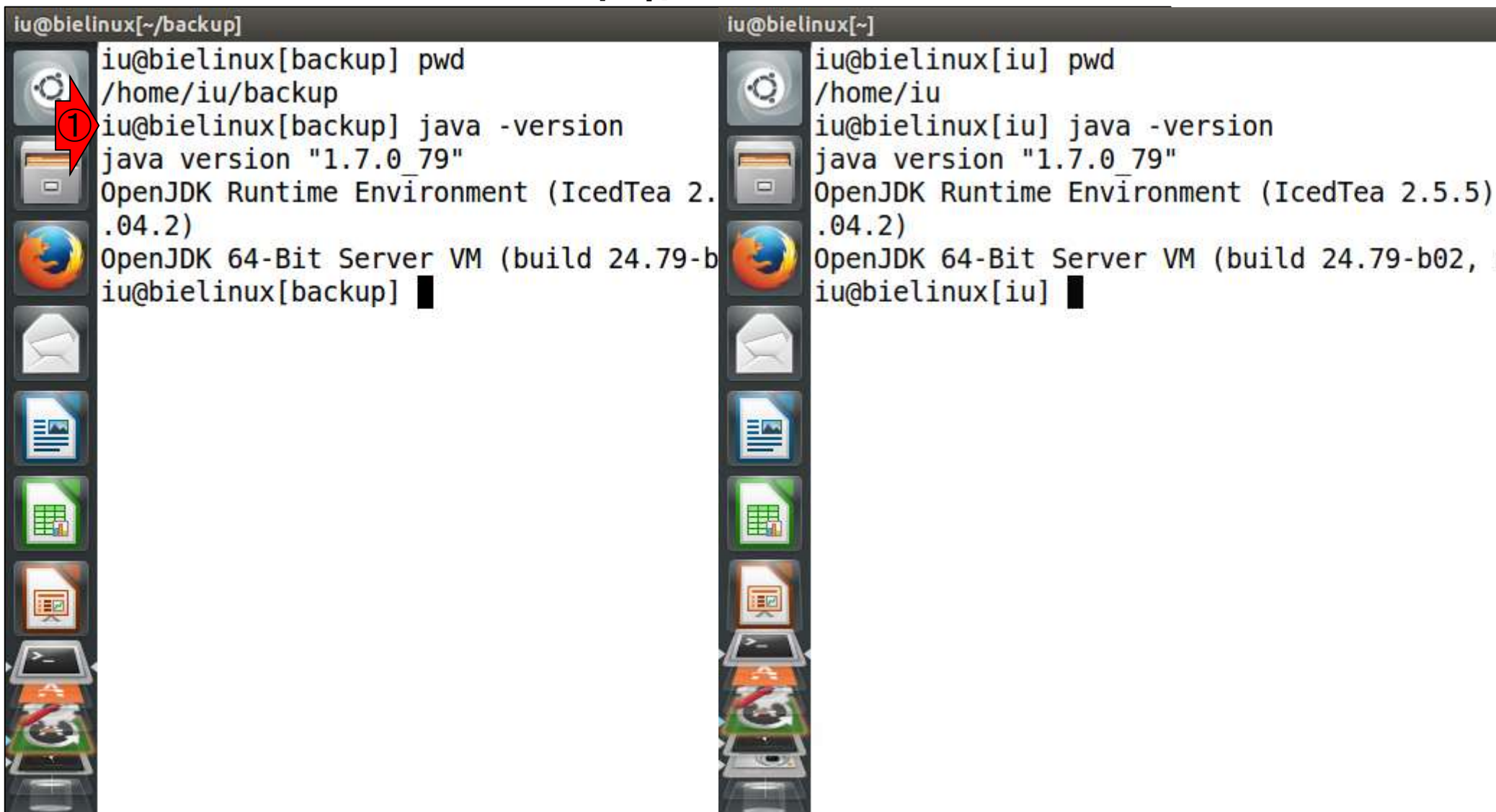
①GepardはJavaプログラムであることがわかります。②Version 5.0以上という条件があるようです

The screenshot shows a web browser window with the URL <http://cube.univie.ac.at/gepard>. The page content includes:

- A privacy notice: "Gepard guarantees the privacy of all input data, does not store user data remotely and does not contain any form of malware."
- A red arrow labeled "1" points to the "SYSTEM REQUIREMENTS" section.
- A red arrow labeled "2" points to the text "Gepard requires the Java Runtime Environment Version 5.0 or later (<http://www.java.com/download/>). It has been tested on the following operating systems:"
- A list of operating systems: Microsoft Windows XP and later, Linux/Un\*x systems, and MacOS 10.x.
- A "DOWNLOAD" section with instructions: "Please download the **jar file** if you want to run gepard on your computer (java needs to be installed). On MacOS, navigate to your Downloads folder and open the jar file via right-click. Confirm the execution of this program."
- A "SOURCE CODE" section: "The source code is available in our GitHub repository [gepard](#)."
- A "TUTORIAL" section.
- A "CONTACT" section with phone numbers (+43 1 4277 76681, +43 1 4277 876681) and email (contact.cube@univie.ac.at).

# Javaバージョン確認

Linux上でのJavaのバージョン確認は  
①「java -version」です(第4回W9-2)



```
iu@bielinux[~/backup]
iu@bielinux[backup] pwd
/home/iu/backup
iu@bielinux[backup] java -version
java version "1.7.0_79"
OpenJDK Runtime Environment (IcedTea 2.
.04.2)
OpenJDK 64-Bit Server VM (build 24.79-b
iu@bielinux[backup] █

iu@bielinux[~]
iu@bielinux[iu] pwd
/home/iu
iu@bielinux[iu] java -version
java version "1.7.0_79"
OpenJDK Runtime Environment (IcedTea 2.5.5)
.04.2)
OpenJDK 64-Bit Server VM (build 24.79-b02,
iu@bielinux[iu] █
```

# Javaバージョン確認

- ① java version 1.7.0\_79は、Java Runtime Environment 7.0という意味。
- ② 要求(5.0 or later)を満たしています

```
iu@bielinux[~/backup]
iu@bielinux[backup] pwd [ 4:50午後 ]
/home/iu/backup
iu@bielinux[backup] java -version [ 4:50午後 ]
java version "1.7.0 79"
OpenJDK Runtime Environment (IcedTea 2.5.5) (7u79-2.5.5-0ubuntu0.14.04.2)
OpenJDK 64-Bit Server VM (build 24.79-b02, mixed mode)
iu@bielinux[backup] [ 4:58午後 ]
```

SYSTEM REQUIREMENTS

Gepard requires the Java Runtime Environment Version 5.0 or later (<http://www.java.com/download/>). It has been tested on the following operating systems:

- Microsoft Windows XP and later
- Linux/Un\*x systems
- MacOS 10.x

## ダウンロード

①DOWNLOADの、②jar fileのところでクリックして、(移動が楽なので共有フォルダに)③保存

http://cube.univie.ac.at/gepard

- GeparD guarantees the privacy of all input data, does not store user data remotely and does not contain any form of malware.

### SYSTEM REQUIREMENTS

GeparD requires the Java Runtime Environment Version 5.0 or later (<http://www.java.com/download/>). It has been tested on the following operating systems:

- Microsoft Windows XP and later
- Linux/Un\*x systems
- MacOS 10.x

**①** DOWNLOAD

Please download the **jar file** if you want to run gepard on your computer (Java needs to be installed). On MacOS, navigate to your Downloads folder and open the jar file via right-click. Confirm the execution of this program.

### SOURCE CODE

The s

TUTC

raw.githubusercontent.com から GeparD-1.40.jar (160 KB) を開くか、または保存しますか?

③

ファイルを開く(O) 保存(S) キャンセル(C)



# ダウンロード

- ①共有フォルダ (~ / Desktop / mac\_share) 上で、
- ②Gepard-1.4.0.jarが見えていればOKですが…

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[mac_share] pwd [ 5:44午後 ]
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls -l [ 5:44午後 ]
total 13002
-rwxrwxrwx 1 iu iu 164270 8月 4 17:44 Gepard-1.40.jar
drwxrwxrwx 1 iu iu 20480 7月 5 12:46 result
-rwxrwxrwx 1 iu iu 13128969 6月 7 17:16 result.zip
iu@bielinux[mac_share] [ 5:44午後 ]
```



# ダウンロード

```
iu@bielinux[~/backup]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup]
```

# 実行

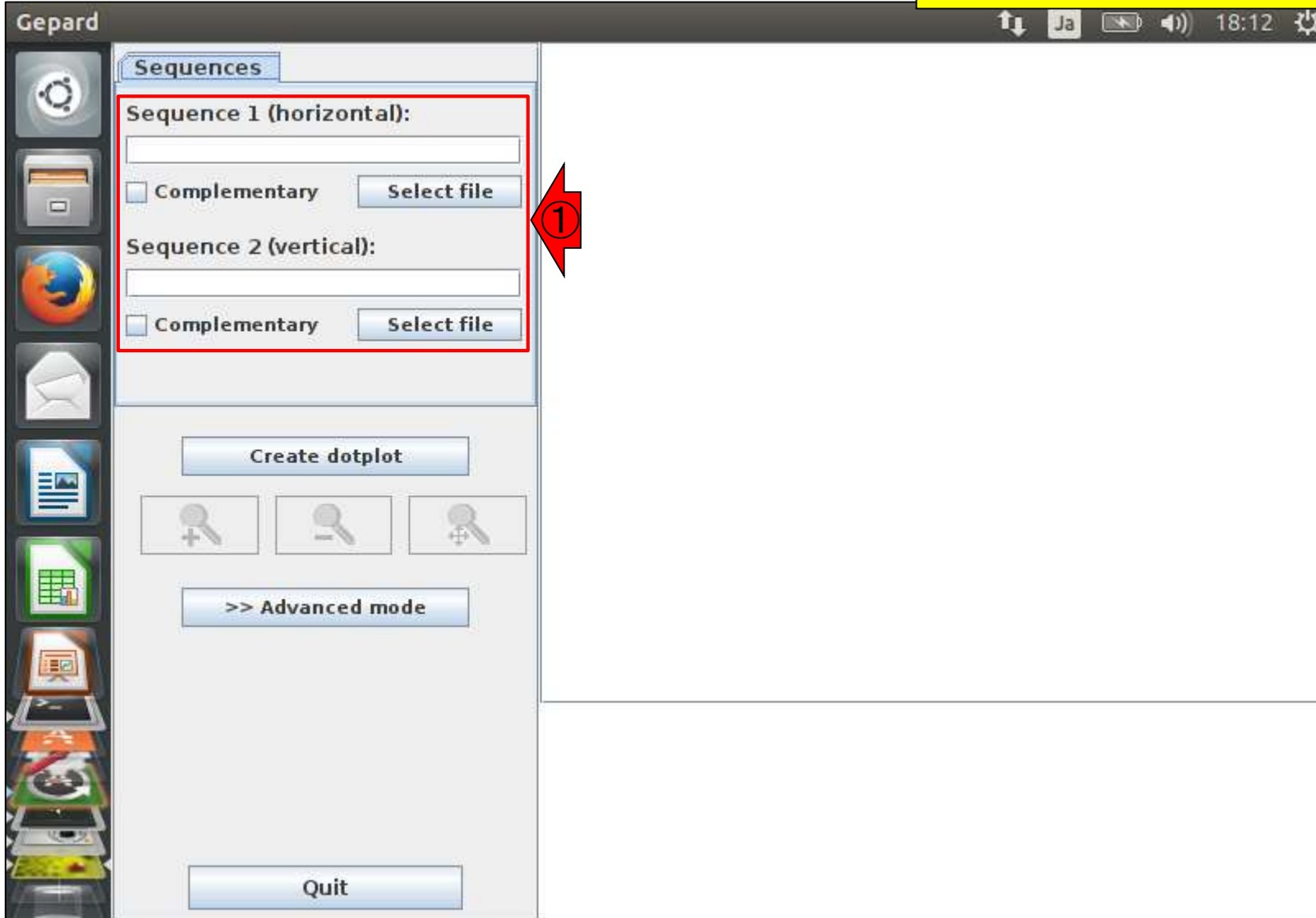
①お約束の呪文(`java -jar ファイル名`)を唱えて起動。ここではLinux上で起動していますが、ホストOS上でダブルクリックでの起動でも構いません

```
iu@bielinux[~/backup]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
```



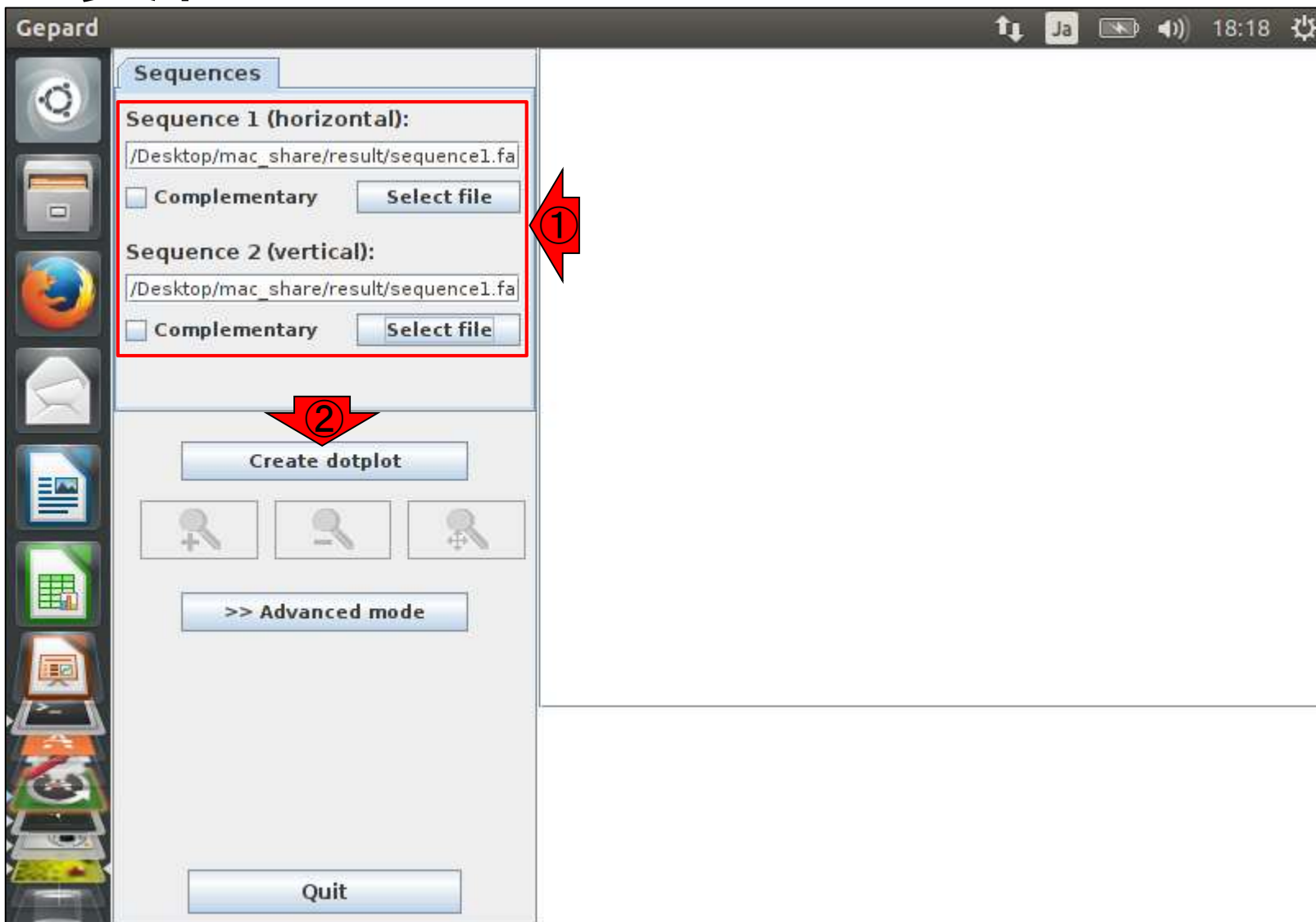
# 実行

GepardのGUI版が起動します。①ここで比較したい2つのファイルを指定します。コマンドライン上での実行方法をまだ把握していません

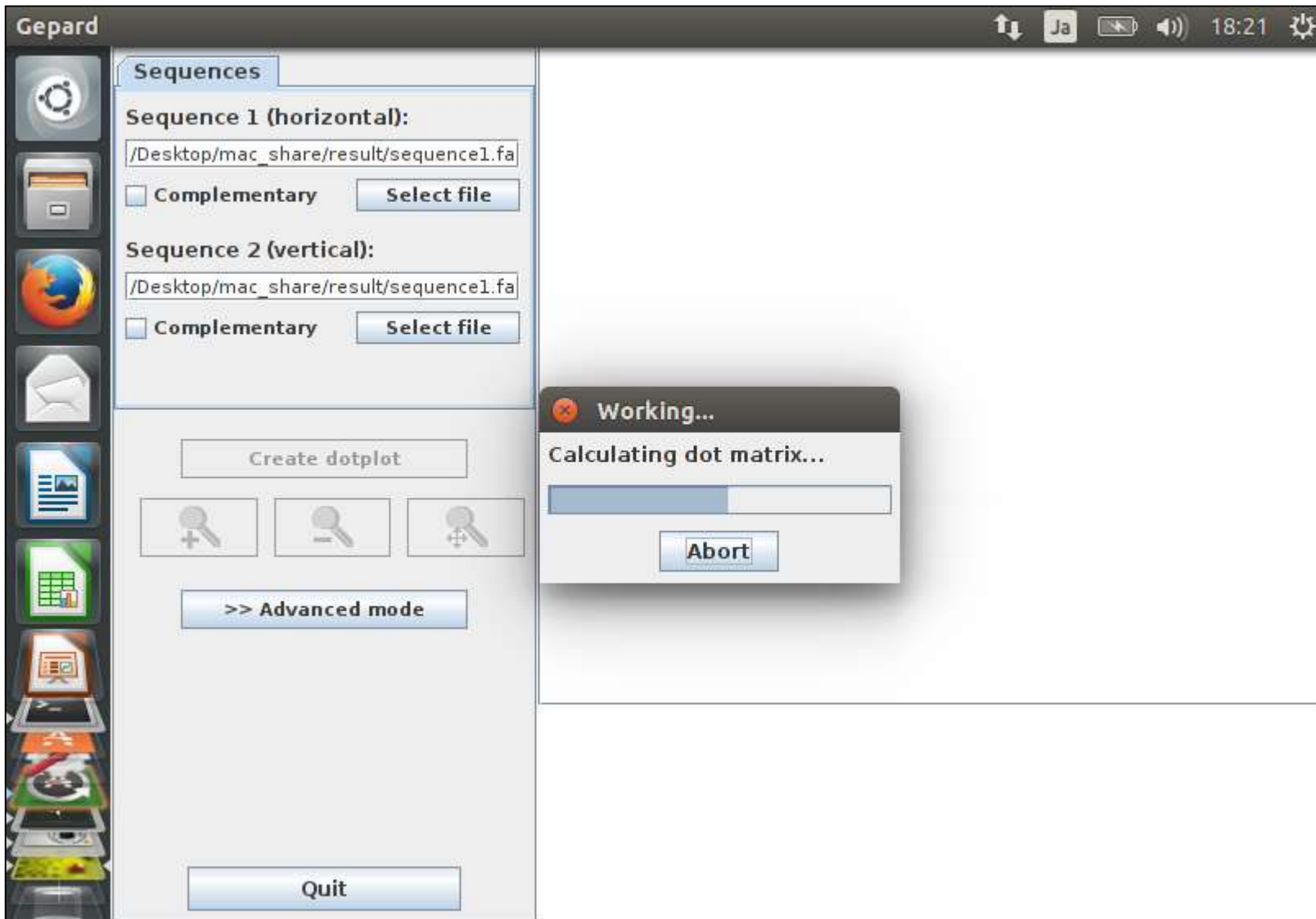


①両方に~/Desktop/mac\_share/result/sequence1.faを指定したところ。②Create dotplot

# 実行



# 作成中...



# 作成完了

確かにsequence1同士のドットプロットをあっさりと描画してくれました!



sequence1 vs. sequence1 - Gepard

Sequences

Sequence 1 (horizontal):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

Sequence 2 (vertical):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

>> Advanced mode

sequence1 vs. sequence1  
Zoom: 8236 : 1  
Word length: 10 GC ratio seq1: 0.3812  
Window size: 0 GC ratio seq2: 0.3812  
Matrix: DNA Program: Gepard (1.40 final)

0 0 sequence1 2289496

2289496

Position: 2289496, 1325996

0	32
TGTTGGGCTGCTGAATGAA CATAGCGAATTTGC	
.....	
TGTTGGGCTGCTGAATGAA CATAGCGAATTTGC	
0	32



# 部分的に拡大したい場合

①こんな感じでマウสดラッグで拡大したい領域を指定して、②update dotplot。

The screenshot shows the Gepard software interface. On the left, there are two sequence input fields, both containing the path `/Desktop/mac_share/result/sequence1.fa`. Below these are buttons for `Complementary` and `Select file`. A red arrow with the number 2 points to the `Update dotplot` button. There are also zoom control buttons (+, -, +) and an `>> Advanced mode` button. At the bottom is a `Quit` button. The main window displays a dotplot for `sequence1 vs. sequence1`. The plot has axes labeled `sequence1` and `sequence1`, with coordinates from 0 to 2289496. A red arrow with the number 1 points to a small blue square in the top-left corner of the plot, indicating the selected zoom region. Below the plot, a sequence alignment is shown with coordinates 2289463, 2289496, 831803, 831836, and 831868.

```
sequence1 vs. sequence1
Zoom: 8236 : 1
Word length: 10
Window size: 0
Matrix: DNA
GC ratio seq1: 0.3812
GC ratio seq2: 0.3812
Program: Gepard (1.40 final)

0 sequence1 2289496
0
sequence1
2289496

Position: 2289496, 2289496
2289463 2289496
| |
GTTGAATTGACTAAGGAGGAATAATTATGGAAG
: : : : :
AGATTTACATGGTTCAAACATTACTTACTCAAATTGGAACTGTTAATCAGCCCAATGAATATGTT
| |
831803 831836 831868
```

# 部分的に拡大したい場合

sequence1 vs. sequence1 - Gepard

Sequences

Sequence 1 (horizontal):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

Sequence 2 (vertical):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

sequence1 vs. sequence1  
Zoom: 415 : 1  
Word length: 10      GC ratio seq1: 0.3836  
Window size: 0      GC ratio seq2: 0.3836  
Matrix: DNA      Program: Gepard (1.40 final)

0      sequence1      115304

0

sequence1

115304

Position: 91715, 102090

# 画像を保存したい場合

sequence1 vs. sequence1 - Gepard

Sequences

Sequence 1 (horizontal):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

Sequence 2 (vertical):  
/Desktop/mac\_share/result/sequence1.fa  
 Complementary

①

sequence1 vs. sequence1  
Zoom: 415 : 1  
Word length: 10 GC ratio seq1: 0.3836  
Window size: 0 GC ratio seq2: 0.3836  
Matrix: DNA Program: Gepard (1.40 final)

0 sequence1 115304

0

sequence1

115304

Position: 91715, 102090

こんな感じになります。  
①下部に移動

# 画像を保存したい場合

The screenshot shows the Gepard software interface for comparing two sequences. The window title is "sequence1 vs. sequence1 - Gepard". The left sidebar contains several sections:

- Sequences:**
  - Sequence 1 (horizontal): /Desktop/mac\_share/result/sequence1
  - Sequence 2 (vertical): /Desktop/mac\_share/result/sequence1
- Update dotplot:** A button with a red arrow and the number 1 pointing to it.
- Display:** Sliders for "Lower color limit", "Upper color limit", and "Greyscale start".

The main window displays the following information:

- sequence1 vs. sequence1
- Zoom: 415 : 1
- Word length: 10
- Window size: 0
- Matrix: DNA
- GC ratio seq1: 0.3836
- GC ratio seq2: 0.3836
- Program: Gepard (1.40 final)

The dot plot shows a square grid with a diagonal line from the top-left corner (0, 0) to the bottom-right corner (115304, 115304). The axes are labeled "sequence1". The bottom status bar shows "Position: 0, 115304".



# 画像を保存したい場合

The screenshot shows the Gepard software interface for comparing two sequences. The window title is "sequence1 vs. sequence1 - Gepard". The main area displays a dotplot with the following parameters:

- Zoom: 415 : 1
- Word length: 10
- Window size: 0
- Matrix: DNA
- GC ratio seq1: 0.3836
- GC ratio seq2: 0.3836
- Program: Gepard (1.40 final)

The dotplot axes are labeled "sequence1" and range from 0 to 115304. A diagonal line is visible, indicating a high degree of similarity. A specific position is highlighted at the bottom of the plot: "Position: 31540, 115304".

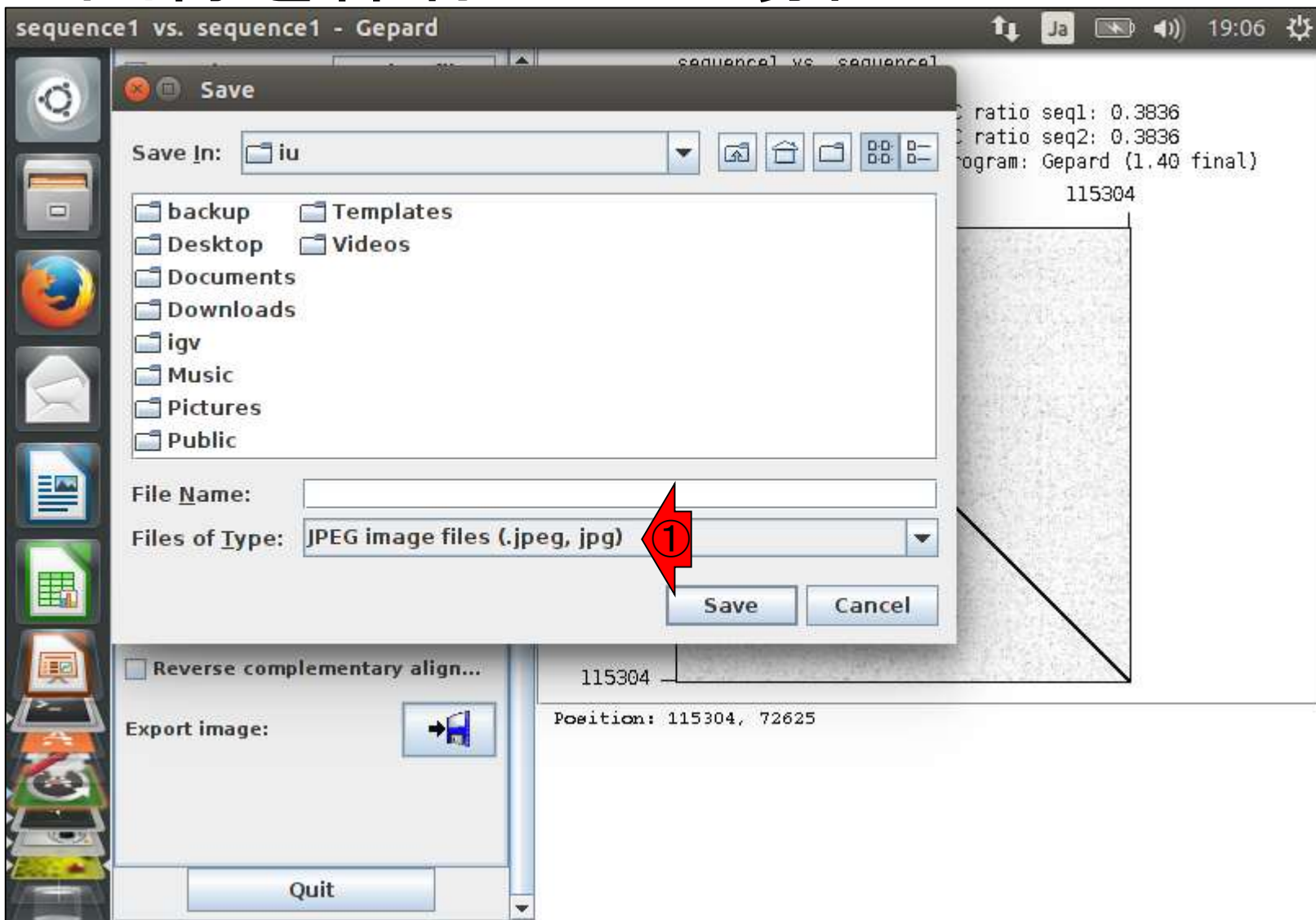
The left sidebar contains various controls:

- Complementary
- Select file
- Update dotplot
- Zoom in (+), Zoom out (-), and Pan (crosshair) buttons
- << Simple mode
- Plot, Misc, Display tabs
- Lower color limit: [slider]
- Upper color limit: [slider]
- Greyscale start: [slider]
- Reverse complementary align...
- Export image: [button with printer icon]
- Quit

A red arrow with the number "1" points to the "Export image" button, indicating the step to save the image.

# 画像を保存したい場合

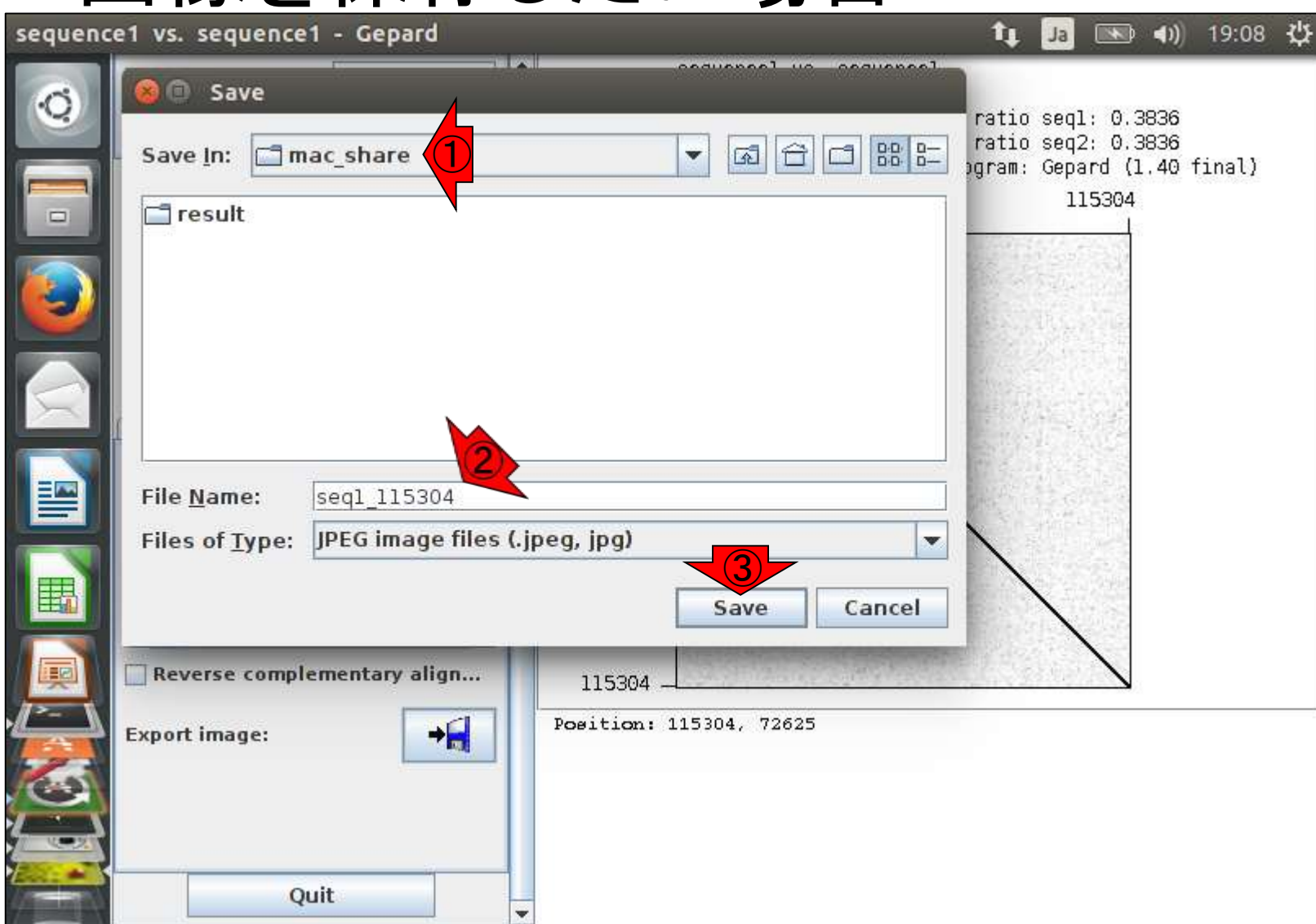
①jpeg形式で保存できるそうですね。  
ここでは共有フォルダ上に保存します





# 画像を保存したい場合

①共有フォルダ上で、②  
seq1\_115304と打って、③Save



# 画像を保存したい場合

The screenshot shows the Gepard software interface. The main window displays a dotplot comparing two sequences, 'sequence1 vs. sequence1'. The plot axes are labeled from 0 to 115304. A diagonal line of dots is visible, indicating a high degree of similarity. The interface includes a left sidebar with various icons and a top menu bar. An 'Export' dialog box is open in the center, displaying the message 'Dotplot successfully exported' and an 'OK' button. A red arrow with the number '1' points to the 'OK' button. The dialog box also shows the 'Position: 115304, 72625'.

sequence1 vs. sequence1 - Gepard

sequence1 vs. sequence1  
Zoom: 415 : 1  
Word length: 10  
Window size: 0  
Matrix: DNA

GC ratio seq1: 0.3836  
GC ratio seq2: 0.3836  
Program: Gepard (1.40 final)

0 115304  
0 sequence1  
115304

Export

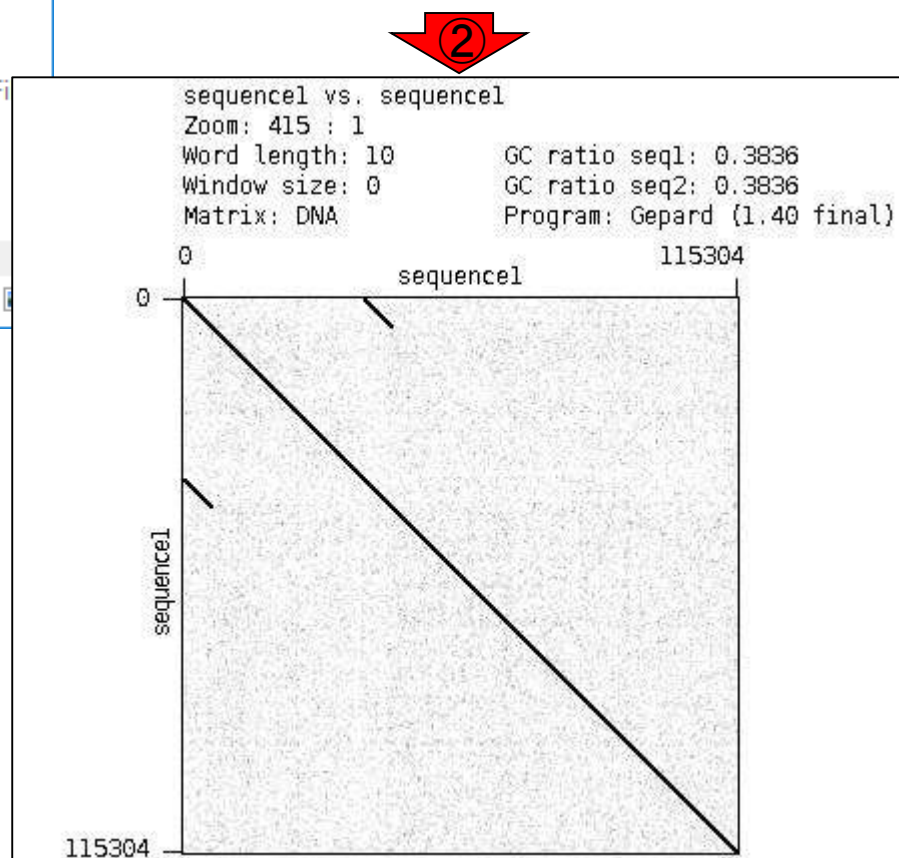
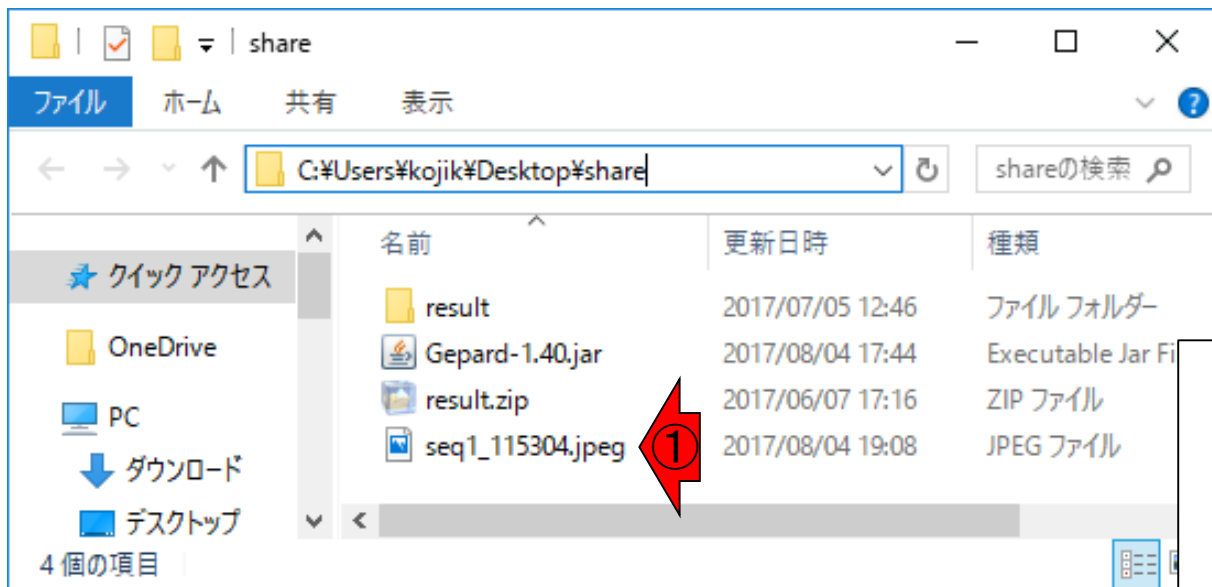
Dotplot successfully exported

OK

Position: 115304, 72625

# 保存されたファイルは

①seq1\_115304.jpegというファイル名になっていますね。②中身



# Contents

## ■ Gepardでドットプロット

- 連載第8回W5-3で最も長いsequence1同士のドットプロットを実行できなかったが、Gepardというプログラムで実行可能。
- 動かせなかったらすぐに諦めるのではなく、「少ないメモリで動かせるもっといいプログラムがあるはず!」という視点で探すべし!

## ■ BlastViewerの新しいバージョンもある

- 連載第8回W7-2でBlastViewer ver. 2.2を利用したが、よく調べるとver. 5.2.0が存在する、という話



# W7-2: BlastViewer

①Korilogというところが提供している  
BlastViewerのウェブページ。②Windows版と③  
Macintosh版ともにver. 2.2。このページは、「  
blastviewer」でウェブ検索した上位に存在します

The screenshot shows a web browser displaying the Korilog website. The page features a navigation bar with 'Download.com' and a search bar. Below the navigation bar, there is a 'Start Download' button and a list of steps: '1. Click to Start Download', '2. Run and Install', and '3. Scan for Issues'. The main content area displays the Korilog logo (marked with a red arrow ①) and a description of the company. Below the description, there are filters for 'By Price', 'By Category', and 'By Operating System'. The search results section shows two entries for 'BlastViewer'. The first entry is for the Windows version (marked with a red arrow ②), and the second entry is for the Mac version (marked with a red arrow ③). Both entries show the version number 'Version 2.2' and the date 'Added: 09/22/08'. The Windows version has 411 total downloads and 3 downloads last week, while the Mac version has 276 total downloads and 1 download last week. A 'Download' button is visible next to each entry.



# blastviewerで検索

①「blastviewer」でウェブ検索した結果。さきほどの  
②Korilogというところが提供しているBlastViewerの  
ウェブページはこちら。今着目しているBlastViewer  
ver. 5.2.0は、③ページ下部にあります

The screenshot shows a Bing search results page for the query 'blastviewer'. The search bar at the top contains the text 'blastviewer' and is marked with a red arrow and the number 1. Below the search bar, there are tabs for 'ウェブ' (Web), '画像' (Images), '動画' (Videos), '地図' (Maps), 'ニュース' (News), and '保存した項目' (Saved items). The search results show 4,220,000 items. The first result is 'NCBI Mapview - National Center for Biotechnology ...' with a URL 'www.ncbi.nlm.nih.gov/mapview'. The second result is 'BlastViewer - Free download and software reviews - ...' with a URL 'download.cnet.com/BlastViewer/3000-2054\_4-10703581.html'. This result is marked with a red arrow and the number 2. The third result is 'DDBJ | BLAST | Result viewer - DDBJ | DNA Data Bank of ...' with a URL 'ddbj.nig.ac.jp/blastviewer?lang=ja'. The fourth result is 'BlastViewer 2.2 Free Download - FreewareFiles.com - ...' with a URL 'freewarefiles.com'. The fifth result is 'DDBJ | BLAST | Result viewer - DDBJ | DNA Data Bank of ...' with a URL 'ddbj.nig.ac.jp/blastviewer?lang=en'. A red arrow and the number 3 point to the bottom of the page, indicating the location of the version 5.2.0 information.



①今着目しているBlastViewer ver. 5.2.0は、こちらのGitHubのサイト

# blastviewerで検索



## BlastViewer for Mac - Free download and software ...

[download.cnet.com/BlastViewer/3000-2054\\_4-10703575.html](https://download.cnet.com/BlastViewer/3000-2054_4-10703575.html) このページを翻訳

From Korilog: BlastViewer provides an interactive graphical user interface for the analysis of the reports produced by the blast sequence database search system. BlastViewer is an easy to use software designed for everyday ...

## GitHub - pgdurand/BlastViewer: This package contains ...

<https://github.com/pgdurand/BlastViewer> このページを翻訳

2017/03/17 · README.md BlastViewer Introduction This is the BlastViewer Tool. It aims at displaying in a graphical way results from the NCBI BLAST software. Requirements Use a Java Virtual Machine 1.7 (or above) from Oracle. ...

## Epos » Blast Viewer - Lehrstuhl für Bioinformatik an der ...

<https://bio.informatik.uni-jena.de/epos/blast-viewer> このページを翻訳

UPDATE: This version of the blast viewer is no longer maintained. The Blast Viewer is contained in the full Epos Framework. Please consider using the full framework to get the current version of the Blast Viewer. The Blast Viewer is ...

## BlastViewer for Mac : Free Download : MacUpdate

[www.macupdate.com/app/mac/30803](http://www.macupdate.com/app/mac/30803) このページを翻訳

BlastViewer for Mac : Free Download - Designed for BLAST biological sequence analysis. Download the latest versions of the best Mac apps at MacUpdate ... Change the way you install and update apps with the all new MacUpdate ...

**blast viewer** の検索結果を含めています。

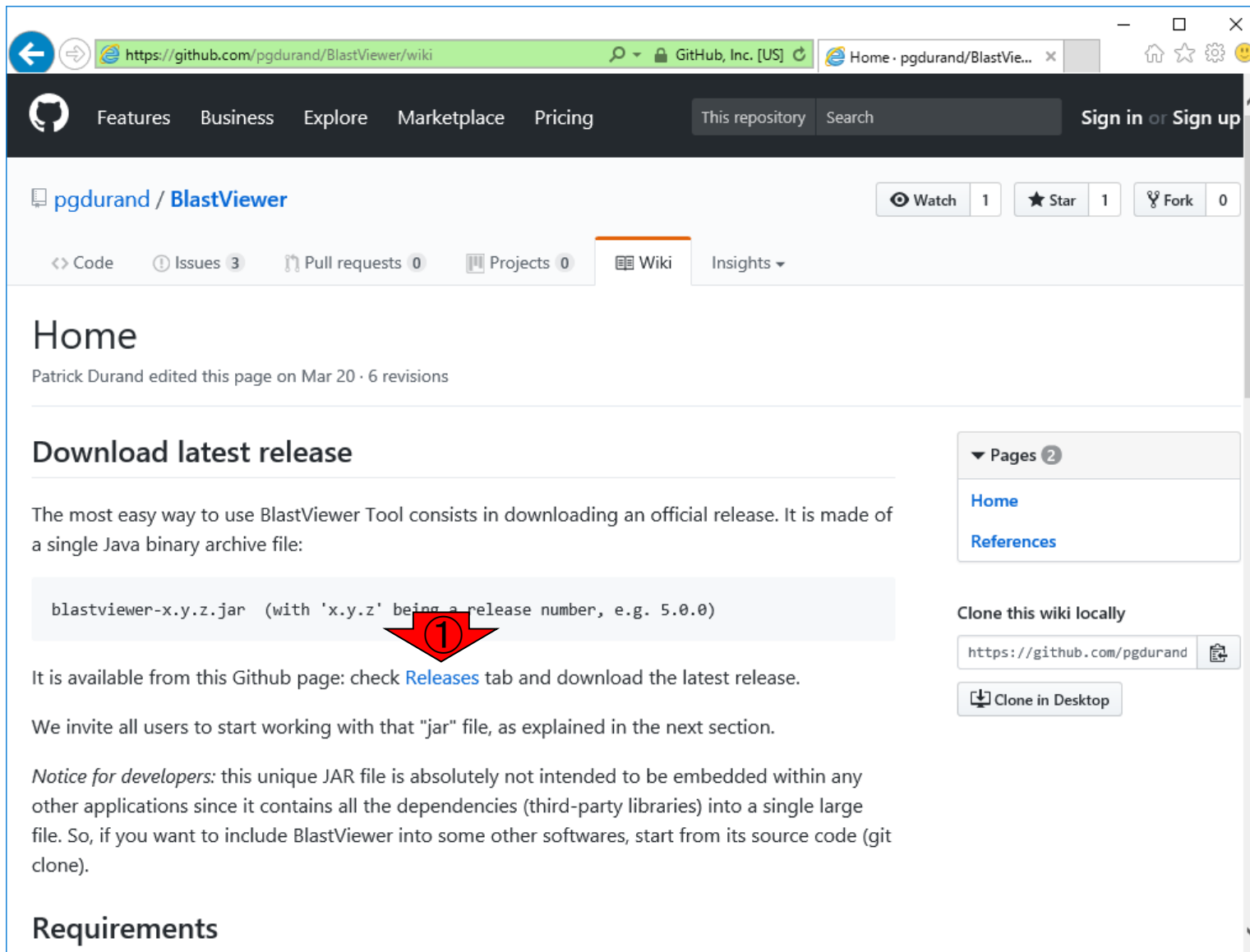
[blast viewer](#) の検索結果のみを表示しますか?

1 2 3 4 5 →

# GitHubのBlastViewer

The screenshot shows the GitHub interface for the repository `pgdurand/BlastViewer`. At the top, the navigation bar includes links for Features, Business, Explore, Marketplace, Pricing, and a search bar. The repository name and navigation tabs (Code, Issues, Pull requests, Projects, Wiki, Insights) are visible. A red arrow with a circled '1' points to the 'Wiki' tab. Below the navigation bar is a promotional banner for GitHub with a 'Sign up' button. The main content area shows the repository description: 'This package contains the BLAST Viewer Tool.' It lists tags for `blast-searches` and `bioinformatics-pipeline`. Below this, repository statistics are shown: 14 commits, 1 branch, 3 releases, 1 contributor, and AGPL-3.0 license. At the bottom, there is a 'Clone or download' button and a list of recent commits, including one by `pgdurand` to 'add TravisCI badge'.

# GitHubのBlastViewer



https://github.com/pgdurand/BlastViewer/wiki

Features Business Explore Marketplace Pricing This repository Search Sign in or Sign up

pgdurand / BlastViewer

Watch 1 Star 1 Fork 0

Code Issues 3 Pull requests 0 Projects 0 Wiki Insights

## Home

Patrick Durand edited this page on Mar 20 · 6 revisions

### Download latest release

The most easy way to use BlastViewer Tool consists in downloading an official release. It is made of a single Java binary archive file:

```
blastviewer-x.y.z.jar (with 'x.y.z' being a release number, e.g. 5.0.0)
```

It is available from this Github page: check [Releases](#) tab and download the latest release.

We invite all users to start working with that "jar" file, as explained in the next section.

*Notice for developers:* this unique JAR file is absolutely not intended to be embedded within any other applications since it contains all the dependencies (third-party libraries) into a single large file. So, if you want to include BlastViewer into some other softwares, start from its source code (git clone).

### Requirements

Pages 2

- Home
- References

Clone this wiki locally

https://github.com/pgdurand

Clone in Desktop

# GitHubのBlastViewer

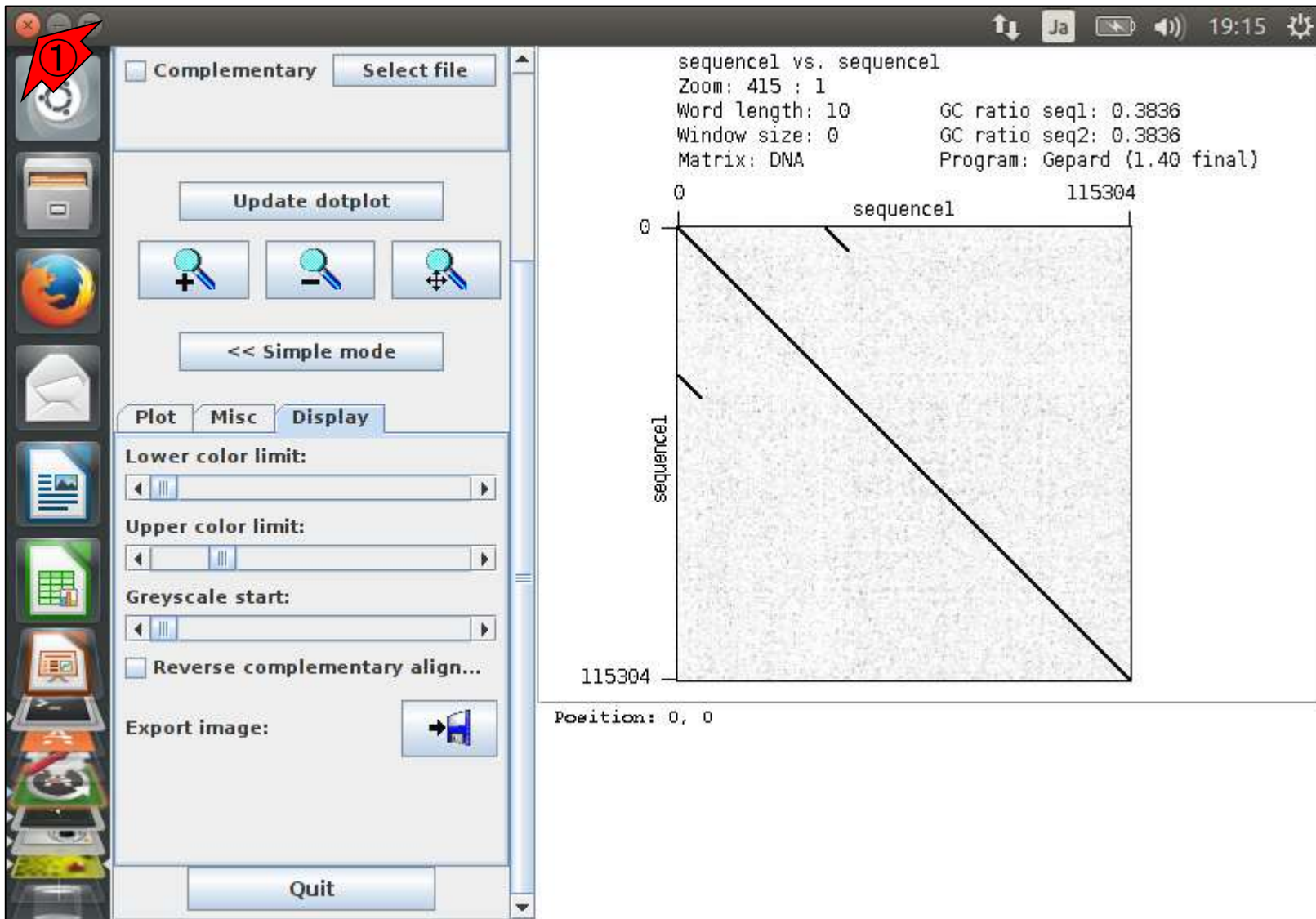
①これ (blastviewer-5.2.0.jar) をダウンロードすれば使えます

The screenshot shows the GitHub repository page for BlastViewer. The browser address bar displays the URL <https://github.com/pgdurand/BlastViewer/releases>. The repository name is pgdurand / BlastViewer. The page features a navigation bar with links for Features, Business, Explore, Marketplace, Pricing, and a search bar. Below the navigation bar, there are buttons for Watch (1), Star (1), and Fork (0). The main content area is divided into two tabs: Releases (selected) and Tags. Under the Releases tab, the latest release is highlighted with a green box and labeled "Latest release". It is version v5.2.0, identified by commit hash 72fd738. The release title is "Display annotated BLAST". The release description states: "This new release is aware of the 'annotate BLAST results' available in BeeDeeM software. You can try BlastViewer with the attached '1433S\_HUMAN.zml' file: this is a BLAST file containing hits annotated with Human Swissprot data." Below the description is a "Downloads" section with a table of files:

File Name	Size
<a href="#">1433S_HUMAN.zml</a>	52.2 KB
<a href="#">blastviewer-5.2.0.jar</a>	9.97 MB
<a href="#">Source code (zip)</a>	
<a href="#">Source code (tar.gz)</a>	

A red lightning bolt icon with the number 1 inside is positioned over the [blastviewer-5.2.0.jar](#) download link, indicating it is the file to be downloaded.


# Bio-Linux上でやると...



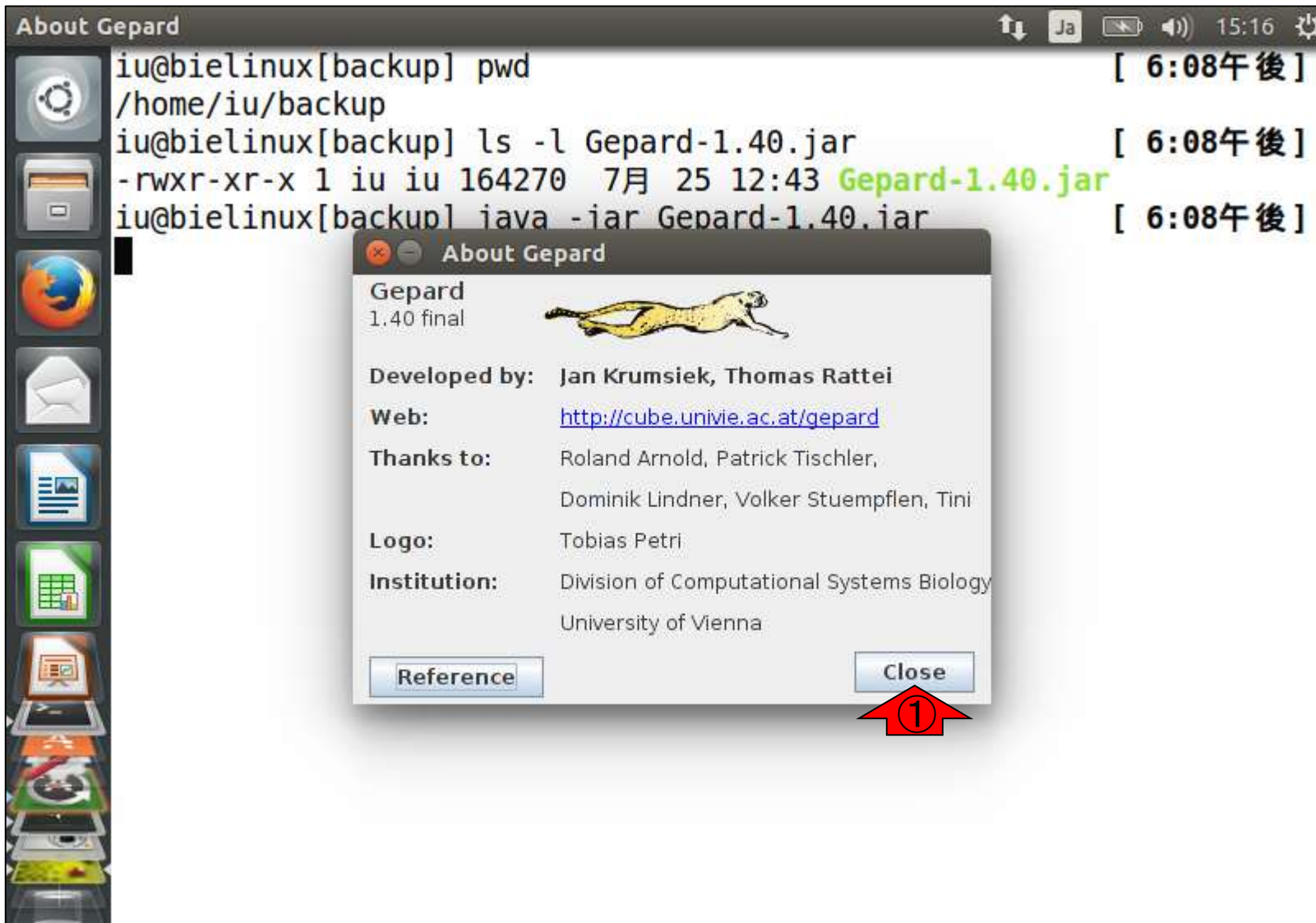
The screenshot shows the Gepard software interface. On the left is a sidebar with various icons and a red circle with the number '1' pointing to the top icon. The main window displays a dotplot alignment of 'sequencel vs. sequencel'. The plot shows a strong diagonal line from the top-left to the bottom-right, indicating a high degree of sequence similarity. The axes are labeled 'sequencel' and range from 0 to 115304. The top status bar shows 'Zoom: 415 : 1', 'Word length: 10', 'Window size: 0', 'Matrix: DNA', 'GC ratio seq1: 0.3836', 'GC ratio seq2: 0.3836', and 'Program: Gepard (1.40 final)'. The bottom status bar shows 'Position: 0, 0'. The interface includes a 'Complementary' checkbox, a 'Select file' button, an 'Update dotplot' button, zoom controls, a '<< Simple mode' button, and a 'Quit' button at the bottom.

sequencel vs. sequencel  
Zoom: 415 : 1  
Word length: 10      GC ratio seq1: 0.3836  
Window size: 0      GC ratio seq2: 0.3836  
Matrix: DNA      Program: Gepard (1.40 final)

0      sequencel      115304  
0  
sequencel  
115304  
Position: 0, 0


Complementary    Select file  
Update dotplot  
+   -   ↻  
<< Simple mode  
Plot   Misc   Display  
Lower color limit:  
Upper color limit:  
Greyscale start:  
 Reverse complementary align...  
Export image:      
Quit

# Bio-Linux上でやると...



```
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
```

**About Gepard**

Gepard  
1.40 final 

**Developed by:** Jan Krumsiek, Thomas Rattei

**Web:** <http://cube.univie.ac.at/gepard>

**Thanks to:** Roland Arnold, Patrick Tischler,  
Dominik Lindner, Volker Stuempflen, Tini

**Logo:** Tobias Petri

**Institution:** Division of Computational Systems Biology  
University of Vienna

Reference Close



# 共有フォルダに移動

この状態から、場所はどこでもいいといえいいのですが、とりあえず共有フォルダに移動します

```
iu@bielinux[~/backup]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup] [ 3:17午後 ]
```

# 共有フォルダに移動

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup] cd ~/Desktop/mac_share [ 3:17午後 ]
iu@bielinux[mac_share] pwd [ 3:20午後 ]
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls [ 3:20午後 ]
Gepard-1.40.jar result result.zip seq1_115304.jpeg
iu@bielinux[mac_share] [ 3:20午後 ]
```

①

# wget

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup] cd ~/Desktop/mac_share [ 3:17午後 ]
iu@bielinux[mac_share] pwd [ 3:20午後 ]
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls [ 3:20午後 ]
Gepard-1.40.jar result result.zip seq1_115304.jpeg
iu@bielinux[mac_share] wget -c [ 3:20午後 ]
```

①

# wget

①そのままjarファイルを共有フォルダにダウンロードするのもよいが、ここでは右クリックで②ショートカットのコピーでwgetに必要なURL情報をコピーした

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[backup] pwd
/home/iu/backup
iu@bielinux[backup] ls -l Gepard
-rwxr-xr-x 1 iu iu 164270 7月 2
iu@bielinux[backup] java -jar Ge
iu@bielinux[backup] cd ~/Desktop
iu@bielinux[mac_share] pwd
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls
Gepard-1.40.jar result result.
iu@bielinux[mac_share] wget -c
```

pgdurand / BlastViewer

Latest release

v5.2.0

72fd738

### Display annotated BLAST

pgdurand released this on Mar 12 · 3 commits to master since this release

This new release is aware of the "annotate BLAST results" available in BeeDeeM software.

You can try BlastViewer with the attached '1433S\_HUMAN.zml' file: this is a BLAST file containing hits annotated with Human Swissprot data.

### Downloads


File	Size
1433S_HUMAN.zml	52.2 KB
blastviewer-5.2.0.jar	9.97 MB

- 開く(O)
- 新しいタブで開く(W)
- 新しいウィンドウで開く(N)
- 対象をファイルに保存(A)...
- 対象を印刷(P)
- 切り取り
- コピー(C)
- ショートカットのコピー(T)
- 貼り付け(P)



# wget

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup] cd ~/Desktop/mac_share [ 3:17午後 ]
iu@bielinux[mac_share] pwd [ 3:20午後 ]
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls [ 3:20午後 ]
Gepard-1.40.jar result result.zip seq1_115304.jpeg
iu@bielinux[mac_share] wget -c [ 3:20午後 ]
```



- Open Terminal
- Open Tab
- Close Window
- Copy
- Paste ①
- Profiles
- ✓ Show Menubar



# wget

```
iu@bielinux[~/Desktop/mac_share]
iu@bielinux[backup] pwd [ 6:08午後 ]
/home/iu/backup
iu@bielinux[backup] ls -l Gepard-1.40.jar [ 6:08午後 ]
-rwxr-xr-x 1 iu iu 164270 7月 25 12:43 Gepard-1.40.jar
iu@bielinux[backup] java -jar Gepard-1.40.jar [ 6:08午後 ]
iu@bielinux[backup] cd ~/Desktop/mac_share [ 3:17午後 ]
iu@bielinux[mac_share] pwd [ 3:20午後 ]
/home/iu/Desktop/mac_share
iu@bielinux[mac_share] ls [ 3:20午後 ]
Gepard-1.40.jar result result.zip seq1_115304.jpeg
iu@bielinux[mac_share] wget -c https://github.com/pgdurand/BlastView
er/releases/download/v5.2.0/blastviewer-5.2.0.jar
```



# wget完了

①lsで確かに約10MBのjarファイルがあることを確認。作業ディレクトリは共有フォルダなので?!、デフォルトでjarファイルに実行権限がついている

```
iu@bielinux[~/Desktop/mac_share]
T065231Z&X-Amz-Expires=300&X-Amz-Signature=c2573bf91e58a80a7770a916
e92b1914f3333af72f2c10824f27d26702f95c38&X-Amz-SignedHeaders=host&a
ctor_id=0&response-content-disposition=attachment%3B%20filename%3Db
lastviewer-5.2.0.jar&response-content-type=application%2Foctet-stre
am
Resolving github-production-release-asset-2e65be.s3.amazonaws.com (
github-production-release-asset-2e65be.s3.amazonaws.com)... 52.216.
81.48
Connecting to github-production-release-asset-2e65be.s3.amazonaws.c
om (github-production-release-asset-2e65be.s3.amazonaws.com)|52.216
.81.48|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 10450992 (10.0M) [application/octet-stream]
Saving to: 'blastviewer-5.2.0.jar'

100%[=====>] 10,450,992  2.31MB/s   in 5.8s

2017-08-07 15:52:39 (1.70 MB/s) - 'blastviewer-5.2.0.jar' saved [10
450992/10450992]

iu@bielinux[mac_share] ls -l bla*                                [ 3:52午後 ]
-rwxrwxrwx 1 iu iu 10450992  5月 25 23:37 blastviewer-5.2.0.jar
iu@bielinux[mac_share] █                                        [ 3:52午後 ]
```





# 実行

①jarファイルのありかはここなので、②cdでホームディレクトリに移動した状態でも、③のような感じで相対パス指定すればblastviewer-5.2.0.jarファイルを実行できます

```
iu@bielinux[~]
github-production-release-asset-2e65be.s3.amazonaws.com)... 52.216.81.48
Connecting to github-production-release-asset-2e65be.s3.amazonaws.com (github-production-release-asset-2e65be.s3.amazonaws.com)|52.216.81.48|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 10450992 (10.0M) [application/octet-stream]
Saving to: 'blastviewer-5.2.0.jar'

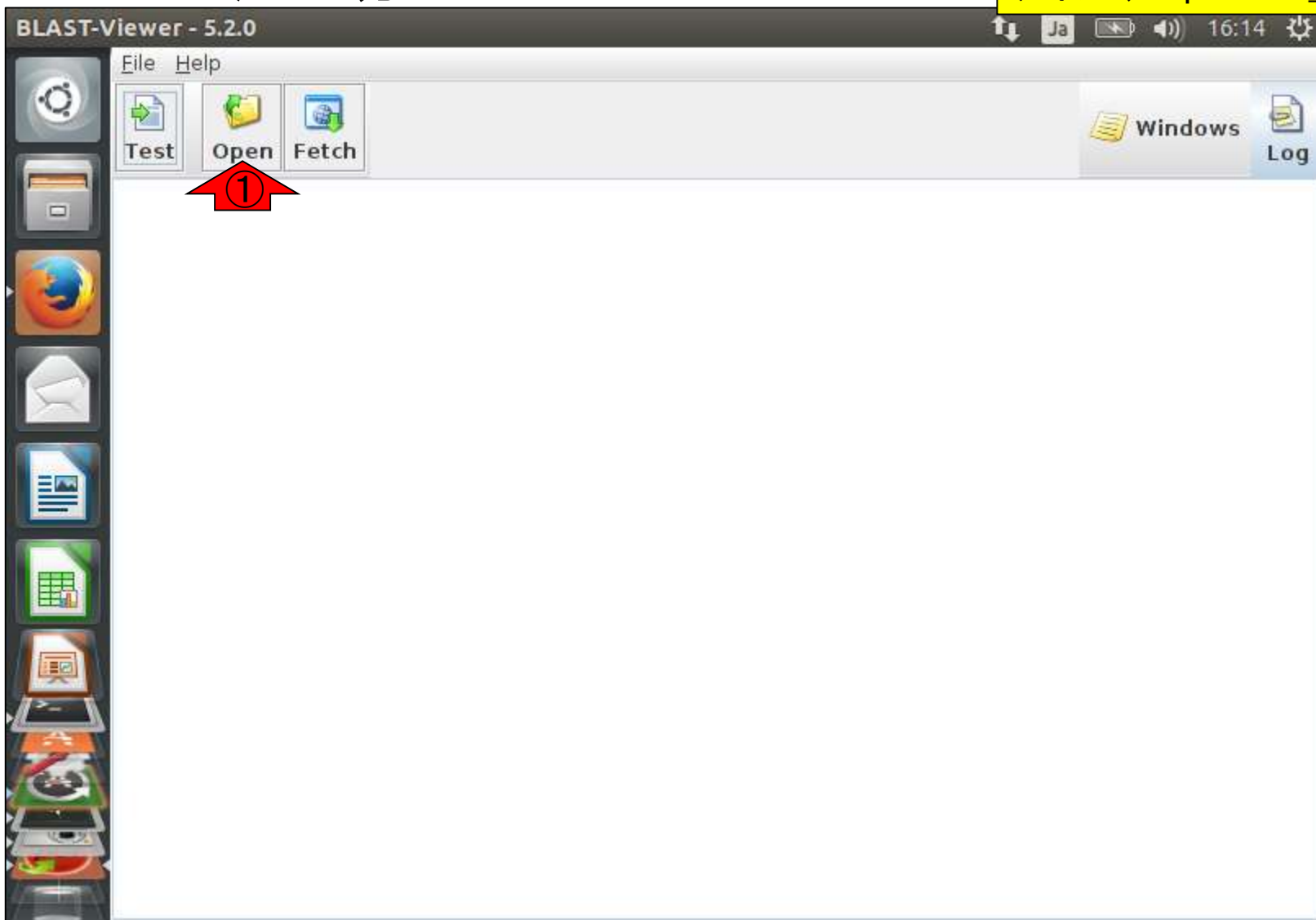
100%[=====>] 10,450,992  2.31MB/s   in 5.8s

2017-08-07 15:52:39 (1.70 MB/s) - 'blastviewer-5.2.0.jar' saved [10450992/10450992]

iu@bielinux[mac_share] ls -l bla*                                [ 3:52午後 ]
-rwxrwxrwx 1 iu iu 10450992  5月 25 23:37 blastviewer-5.2.0.jar
① iu@bielinux[mac_share] pwd                                    [ 3:52午後 ]
/home/iu/Desktop/mac_share
② iu@bielinux[mac_share] cd                                    [ 4:08午後 ]
iu@bielinux[iu] pwd                                           [ 4:08午後 ]
/home/iu
③ iu@bielinux[iu] java -jar ~/Desktop/mac_share/blastviewer-5.2.0.jar
```

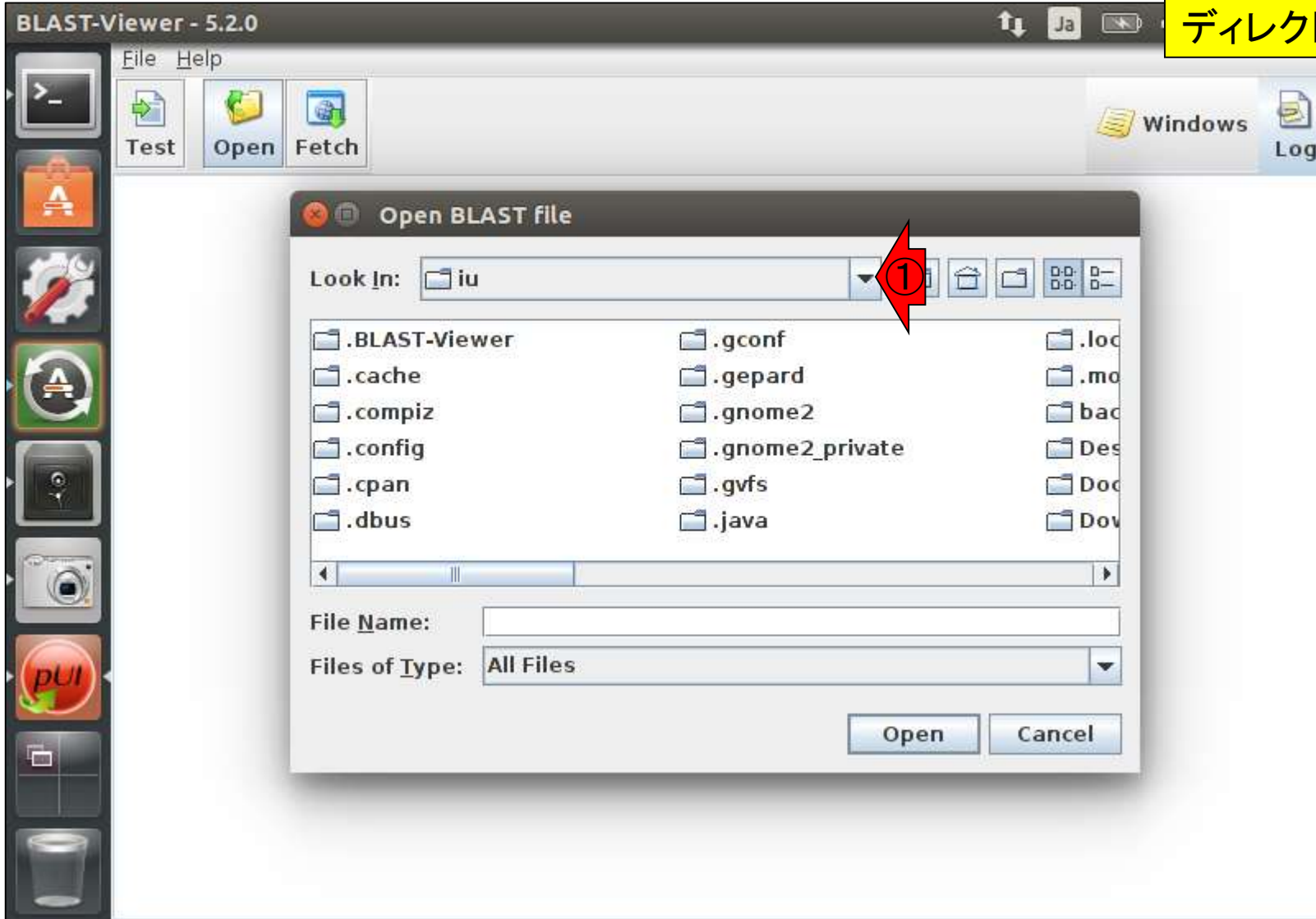
# GUI起動

BlastViewer ver. 5.2.0起動直後の状態。  
①Openで、Blast実行結果のxml形式ファイル(sequence1\_blast.xml)を読み込む



# 読み込み

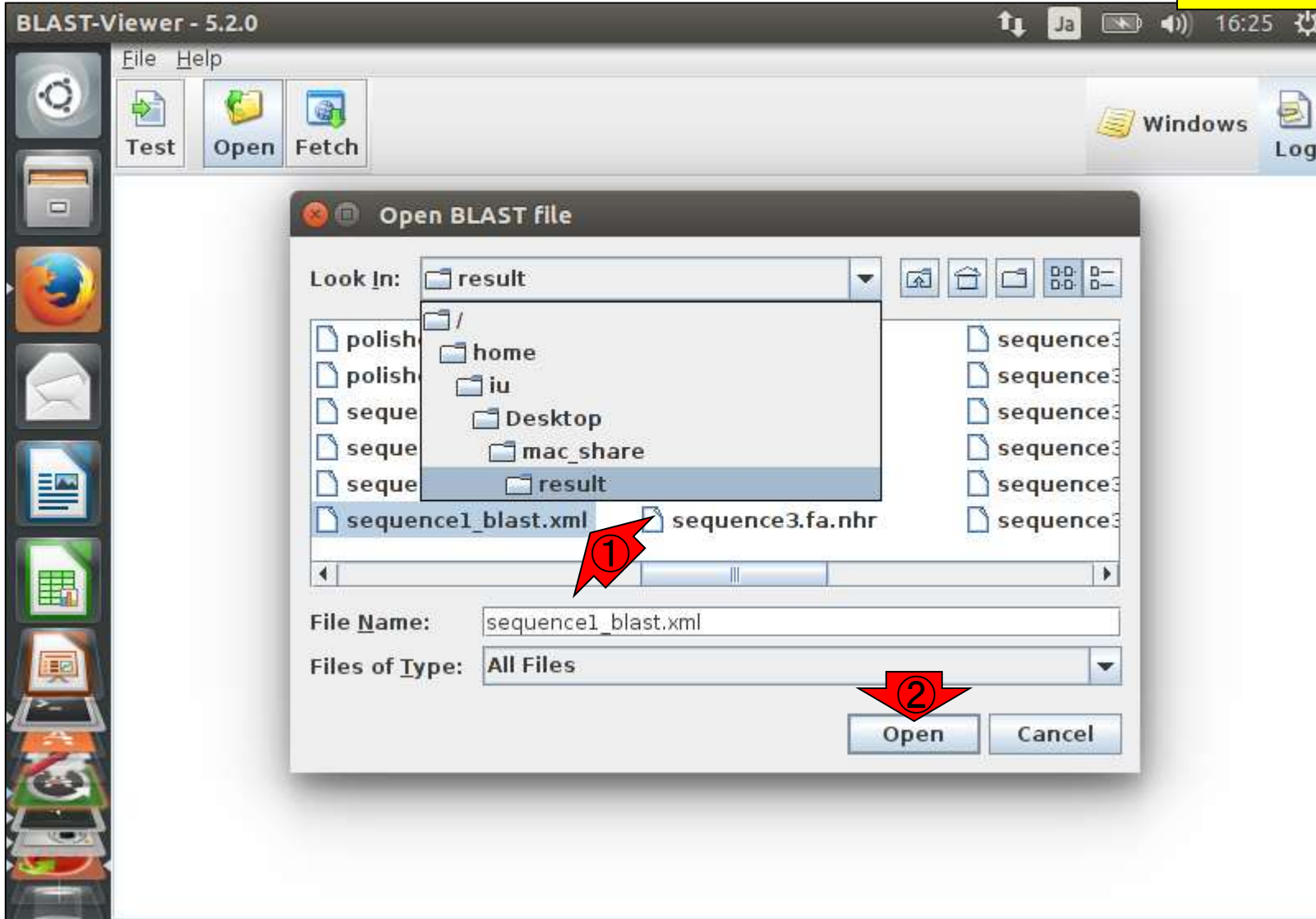
Blast実行結果のxml形式ファイル(sequence1\_blast.xml)は、~/Desktop/mac\_share/resultディレクトリにあります





# 読み込み

①Blast実行結果のxml形式ファイル(sequence1\_blast.xml)を選択して、②Open



# 読み込み後

BLAST-Viewer - 5.2.0

File Help

Test Open Fetch

Windows Log

sequence1\_blast.xml

Hits Graphic MSA

Hits Results for: [1] sequence: 4 h... Hits: 4 HSPs: 1351

#	Accession ...	E-Value	Quality	# HSPs	Identity	Positive	Query Coverage	Hit Coverage
1	0 ...	0	😊	1347	100%	100%	100%	100%
2	3 ...	0	😊	2	99.5%	99.5%	0.5%	92.5%

Alignment: Query (2289497 nuc) vs. 0 (2,289,497 nuc)

HSP Map Definition Statistics Alignment

Alignment Features

```

Query
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
HSP(s)
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
0
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

T G T T G G G C T G C T G A A T G
| | | | | | | | | | | | | | | |
T G T T G G G C T G C T G A A T G
| | | | | | | | | | | | | | | |
10
HSP: < 1/1347 >

```