

Manual for Sondovač 0.6

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Sondovač is a script to create orthologous low-copy nuclear probes from transcriptome and genome skim data for target enrichment.

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Sondovač is a script to create orthologous low-copy nuclear probes from transcriptome and genome skim data for target enrichment. For information and download see <https://github.com/V-Z/sondovac/wiki>. For paper introducing Sondovač see Schmickl et al.

Abstract

Phylogenetics benefits from using a large number of putatively independent nuclear loci and the combination with other datasets such as the plastid and mitochondrial genome. Selecting such orthologous low-copy nuclear (LCN) loci is still a challenge for non-model organisms. Meanwhile it is common to select LCN genes for phylogenies based on a comparison of transcriptomes, but automated bioinformatic pipelines for the selection of those genes are largely absent. We created a user-friendly, automated and interactive script named Sondovač to LCN loci by a comparison between transcriptome and genome skim data. The script is licensed under open-source license GPL v.3 allowing further modifications. The script runs on major Linux distributions and Mac OS X. Strong bioinformatic skills and access to high-performance computer clusters are not required; it runs on a standard desktop computer equipped with modern CPU like Intel i5 or i7 within several hours.

1 Introduction

Phylogenetics benefits from using a large number of putatively independent nuclear loci and their combination with other sources of information, such as the plastid and mitochondrial genomes. Currently, target enrichment (sequence capture) of hundreds of loci in combination with genome skimming is becoming increasingly popular in phylogenetics. In animal phylogenomics non-exonic or partly exonic ultraconserved elements and their quite variable flanking regions are often utilized. For plant phylogenetics, low-copy nuclear (LCN) genes are targeted due to the paucity of ultraconserved nuclear sequences. Due to sequence divergence, target sequencing strategies for plant nuclear genomes are largely lineage-specific, requiring the de novo design of target enrichment probes. We developed a novel probe design pipeline for targeting orthologous LCN loci for phylogenetic reconstruction by using genome skim and transcriptome data. We implemented our software workflow in the user-friendly, automated and interactive BASH script Sondovač.

Sondovač workflow is divided into three parts (see details at page 4 and Figure 1):

1. Raw input data are analyzed by `sondovac_part_a.sh`.
2. Obtained sequences are assembled by Geneious.
3. Final probes are produced by `sondovac_part_b.sh`.

1.1 Pipeline – how the data are processed

A transcriptome assembly and paired-end genome skim raw data are combined to get hundreds of orthologous LCN loci. Enrichment of multi-copy loci is minimized by using unique transcripts only, which are obtained by comparing all transcripts and removing those sharing $\geq 90\%$ sequence similarity using BLAT. Before matching the genome skim data against those unique transcripts, reads of plastid (and mitochondrial) origin are removed with Bowtie 2, SAMtools and bam2fastq utilizing reference sequences. Paired-end reads are subsequently combined with FLASH. These processed reads are matched against the unique transcripts sharing $\geq 85\%$ sequence similarity with BLAT. Transcripts with >1000 BLAT hits, indicating repetitive elements, and BLAT hits containing masked nucleotides are removed before de novo assembly of the BLAT hits to larger contigs with Geneious, using the medium sensitivity / fast setting. After assembly, only those contigs that comprise exons of a minimum bait length (usually ≥ 120 bp in case of probe design for phylogenies) and have a certain minimum total locus length (multiple of the bait length, should not be too short in order to obtain sufficient phylogenetically informative signal; we recommend at least ≥ 600 bp) are retained. To ensure that probes do not target multiple similar loci, any probe sequences sharing $\geq 90\%$ sequence similarity are removed using cd-hit-est, followed by a second filtering step for contigs containing exons of a minimum bait length and totaling minimum loci length (see comments above). To ensure that plastid sequences are absent from the probes, the probe sequences are matched against the plastome reference sharing $\geq 90\%$ sequence similarity with BLAT and the hits removed from the probe set. The workflow of Sondovač is summarized in the Figure 1. The direction of the workflow is indicated by arrows. Optional removal of reads of mitochondrial origin from the genome skim data is marked by light background. The required input files of Sondovač are highlighted in bold.

For comprehension improvement the steps of Sondovač are consecutively numbered. Sondovač has three parts: two script parts and an intermediate part using Geneious. The workflow is as follows:

A. `sondovac_part_a.sh`: Covers steps 1 to 6.

1. Removal of transcripts sharing $\geq 90\%$ sequence similarity.
2. Removal of reads of plastid origin.
3. Removal of reads of mitochondrial origin (optional).
4. Combination of paired-end reads.
5. Matching of the unique transcripts and the filtered, combined genome skim reads sharing $\geq 85\%$ sequence similarity.
6. Filtering of BLAT output:
 - 6.1. Choice of transcript or genome skim sequences for further processing.
 - 6.2. Removal of transcripts with >1000 BLAT hits.
 - 6.3. Removal of transcript or genome skim BLAT hits [depending on the selection in (6.1)] containing masked nucleotides.

Input files for `sondovac_part_a.sh` are FASTA transcriptome data, FASTQ paired-end genome skim reads and a plastome (and possible as well mitochondriome) reference. The input file for Geneious is the output of `sondovac_part_a.sh`.

B. Geneious: Covers step 7 (see below and PDF manual).

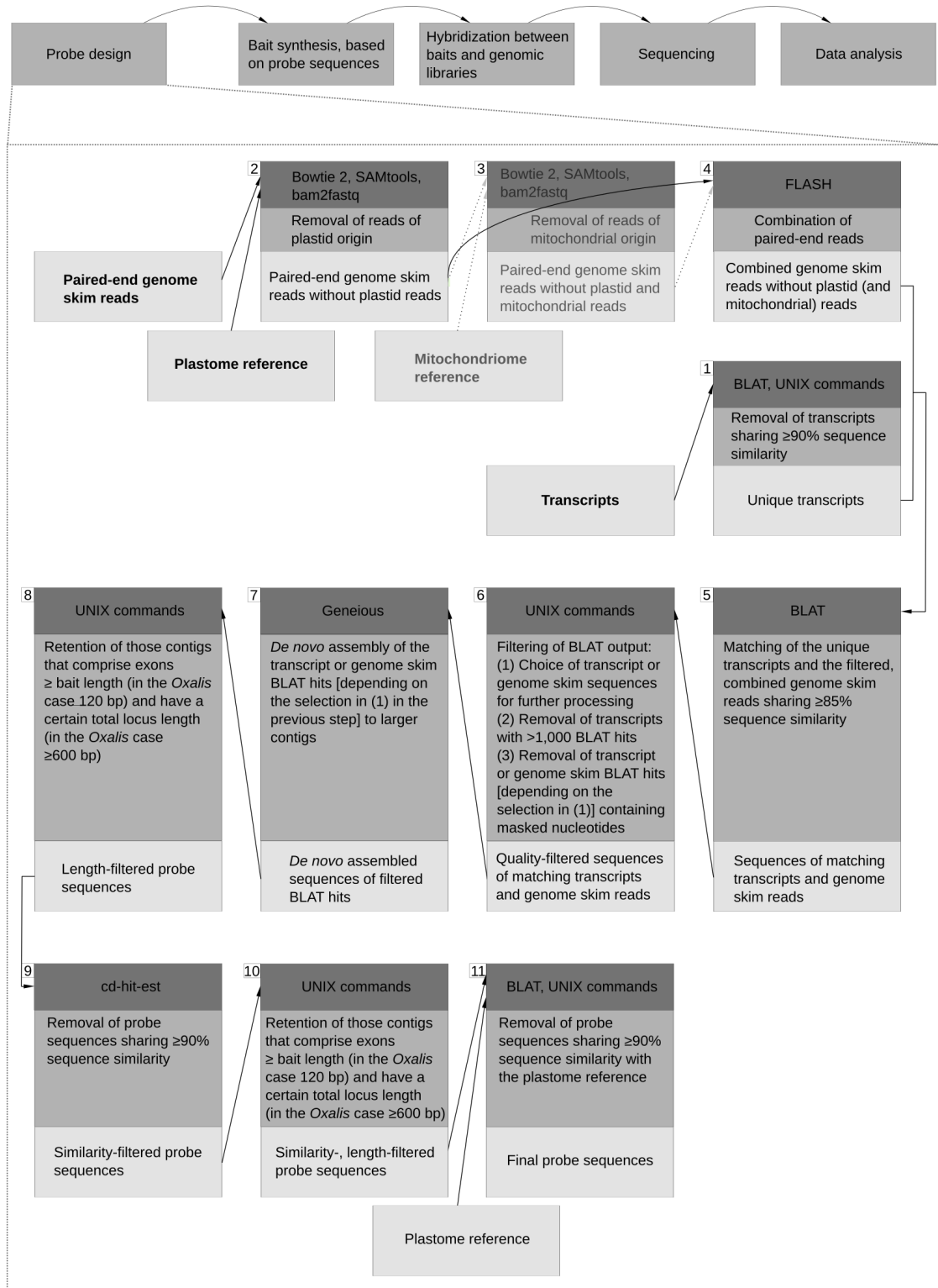


Figure 1: Workflow of the probe design script Sondovač. An overview on the main steps of Hyb-Seq are given in the top part of the figure; probe design is the first one. Each step of Sondovač is numbered and illustrated by three boxes each: Software is highlighted in dark gray, a summary of each step is given in medium gray, and input/output of each step is depicted in light gray. Optional removal of reads of mitochondrial origin from the genome skim data is marked by decoloration of the text. The required input files of Sondovač are highlighted in bold. The direction of the workflow is indicated by arrows.

7. De novo assembly of the transcript or genome skim BLAT hits [depending on the selection in (6.1)] to larger contigs. Note you need a copy of Geneious for this step.

The output files of Geneious are input files for `sondovac_part_b.sh`.

C. `sondovac_part_b.sh`: Covers steps 8 to 11.

8. Retention of those contigs that comprise exons \geq bait length and have a certain total locus length.
9. Removal of probe sequences sharing $\geq 90\%$ sequence similarity.
10. Retention of those contigs that comprise exons \geq bait length and have a certain total locus length.
11. Removal of probe sequences sharing $\geq 90\%$ sequence similarity with the plastome reference.

The output file of `sondovac_part_b.sh` is the final list of probes.

2 Installation of Sondovač

Sondovač is simple BASH script, but it requires some software. The script will check for presence of all required software and if needed, it will offer installation. The most easy way is just to launch the script (see chapter 2.2 at page 7) and yet yourselves to be guided through whole needed process.

2.1 Requirements to run Sondovač

Sondovač is currently tested on the Linux distributions Ubuntu and openSUSE. Testing on Mac OS X and other major Linux distributions is on the way and full support will be added soon. Thank you for patience and reporting¹ any problems and wishes.

In order to run Sondovač you need a UNIX-based operating system (preferably Linux or Mac OS X) equipped with BASH or compatible shell interpreter (this should be by default available for any Linux distribution, Mac OS X and any other UNIX-based operating system like Solaris, BSD and its variants etc). You should use the current operating system version supported by upstream. Otherwise we will not be able to help you in case of problems. Older operating systems can have different versions of shell and system libraries, which can cause various problems and incompatibilities.

Sondovač is using several scientific software packages (namely bam2fastq, BLAT, Bowtie2, CD-HIT, FASTX toolkit, FLASH, htsjdk, libgtextutils, Picard and SAMtools – see required versions and links below), and basic UNIX tools. Sondovač will check if those programs are installed – available in the PATH (i.e. if the shell application can locate and launch respective binaries). If you have those packages installed (in current versions), ensure their binaries are in PATH. This should not be a problem for basic tools available in any UNIX-based operating system, as basic installation usually contains all needed tools. If you are lacking some of the required tools, the script will notify you, and you will have to install them manually. If this will be needed, check the documentation for your operating system.

If required scientific programs are not installed, Sondovač will offer you installation. You can use precompiled binaries available together with the script or (sometimes) from the web.

¹You can report any problems at <https://github.com/V-Z/sondovac/issues>. We will try to help you.

This is the recommended way. In case you would like to compile required software yourselves, the script will guide you through this process. Anyway, it is recommended only for advanced users, as compilation might sometimes be very tricky. It is currently fully implemented only for the Linux distributions Ubuntu and openSUSE. Support for other Linux distributions and Mac OS X will be added soon. For compilation you need Apache Ant, GNU G++, GNU GCC, GIT, Java, libpng developmental files and zlib developmental files. Ensure you have those tools available – they should be readily available for any UNIX-based operating system.

2.2 First launch of Sondovač

Download the latest version from <https://github.com/V-Z/sondovac/releases/> and unpack the archive. You can run Sondovač from any directory. In command line navigate to the directory with the unpacked Sondovač files (see Figure 2):

```
1 cd /path/to/directory_with_sondovac
```

and start it by

```
1 ./sondovac_part_a.sh -h
```

to see basic usage instructions. See chapter 3 at page 12 for more information.

2.2.1 Examples (see further for explanation of command line parameters)

Basic and the most simple usage (running in interactive mode, see chapter 3 at page 12):

```
1 ./sondovac_part_a.sh -i
```

Specify some of required input files, otherwise run interactively:

```
1 ./sondovac_part_a.sh -i -f input.fa -t reads1.fastq -q reads2.fastq
```

Running in non-interactive automated way (parameter "-n", see chapter 3 at page 12) with example data downloaded from <https://github.com/V-Z/sondovac/wiki/Sample-data>:

```
1 ./sondovac_part_a.sh -f input1_JHCN_Oxalis_corniculata_transcriptome_data.fa \
2 -c input2_Ricinus_communis_reference_plastid_genome.fsa -m \
3 input5_Ricinus_communis_reference_mitochondrial_genome.fasta -t \
4 input3_J12_Oxalis_obtusa_genome_skim_data_R1.fastq -q \
5 input4_J12_Oxalis_obtusa_genome_skim_data_R2.fastq -n
```

Modify parameter "-a", otherwise run interactively:

```
1 ./sondovac_part_a.sh -i -a 300
```

Run in non-interactive mode (parameter "-n", see chapter 3 at page 12) – in such case user must specify all required input files (parameters "-f", "-c", "-m", "-t" and "-q"). Moreover, parameter "-y" is modified:

```
1 ./sondovac_part_a.sh -n -f input.fa -c referencecp.fasta \
2 -m referencemt.fsa -t reads1.fastq -q reads2.fastq -y 90
```

Modifying parameter "-s". Note interactive mode "-i" is implicit and does not need to be specified explicitly:

```
1 ./sondovac_part_a.sh -s 950
```



```
script : bash - Konsole
File Edit View Bookmarks Settings Help
vojta@veles:~> cd dokumenty/botanak/oxalis/south_africa_target_enrichment_genome_s
kimming/script_probe_design_pipeline/
vojta@veles:~/dokumenty/botanak/oxalis/south_africa_target_enrichment_genome_skim
ing/script_probe_design_pipeline> ls sample_data/
input1_JHCN_Oxalis_corniculata_transcriptome_data.fa
input2_Ricinus_communis_reference_plastid_genome.fsa
input3_J12_Oxalis_obtusa_genome_skim_data_R1.fastq
input4_J12_Oxalis_obtusa_genome_skim_data_R2.fastq
input5_Ricinus_communis_reference_mitochondrial_genome.fasta
vojta@veles:~/dokumenty/botanak/oxalis/south_africa_target_enrichment_genome_skim
ing/script_probe_design_pipeline> cd script/
vojta@veles:~/dokumenty/botanak/oxalis/south_africa_target_enrichment_genome_skim
ing/script_probe_design_pipeline/script> ls -lha
total 500K
drwxr-xr-x 7 vojta users 4.0K Sep 30 18:17 .
drwxr-xr-x 6 vojta users 4.0K Aug 31 19:26 ..
drwxr-xr-x 6 vojta users  54 May 31 15:42 bin
-rwxr-xr-x 1 vojta users 1.4K Jul 23 16:54 geneious_column_separator.pl
drwxr-xr-x 8 vojta users 4.0K Sep 30 18:16 .git
-rw-r--r-- 1 vojta users  51 Aug  6 15:48 .gitignore
-rw-r--r-- 1 vojta users  16 Aug  6 15:48 .gitignore~
-rw-r--r-- 1 vojta users 114 Aug 10 18:38 .info
-rw-r--r-- 1 vojta users 114 Aug 10 18:38 .info~
-rw-r--r-- 1 vojta users 11K Sep 30 11:16 INSTALL
-rw-r--r-- 1 vojta users 11K Sep 30 11:16 INSTALL~
-rw-r--r-- 1 vojta users 93K Sep 30 11:18 LICENSE
-rw-r--r-- 1 vojta users 93K Sep 30 11:18 LICENSE~
drwxr-xr-x 2 vojta users 4.0K Sep 30 18:16 manual
drwxr-xr-x 5 vojta users 135 Aug  7 15:20 pkgs
-rw-r--r-- 1 vojta users 14K Sep 30 17:53 README
-rw-r--r-- 1 vojta users 14K Sep 30 17:53 README~
-rw-r--r-- 1 vojta users 659 Sep 30 18:16 .README.kate-swp
-rw-r--r-- 1 vojta users 29K Sep 30 12:45 sondovac_functions
-rw-r--r-- 1 vojta users 29K Sep 30 12:45 sondovac_functions~
-rwxr-xr-x 1 vojta users 45K Sep 30 08:54 sondovac_part_a.sh
-rwxr-xr-x 1 vojta users 45K Sep 30 08:54 sondovac_part_a.sh~
-rwxr-xr-x 1 vojta users 23K Sep 29 17:48 sondovac_part_b.sh
-rwxr-xr-x 1 vojta users 23K Sep 29 17:48 sondovac_part_b.sh~
drwxr-xr-x 10 vojta users 4.0K May 31 17:03 src
vojta@veles:~/dokumenty/botanak/oxalis/south_africa_target_enrichment_genome_skim
ing/script_probe_design_pipeline/script> ./sondovac_part_a.sh
```

Figure 2: Starting terminal and navigating to Sondovač. First look at the terminal (command-line, shell) window, navigation to directory with Sondovač (using command `cd`), listing directory content (command `ls`) and preparing to launch Sondovač (`./sondovac_part_a.sh`).

2.3 Help for usage of terminal

If you are not familiar with the usage of command line, see some basic tutorial first. You can try some of those:

- <https://activedoc.opensuse.org/book/opensuse-start-up/chapter-17-shell-basics>
- <https://help.ubuntu.com/community/UsingTheTerminal>
- <https://www.gnu.org/software/bash/manual/> (advanced – full reference manual)
- <http://ubuntuguide.org/>
- <https://www.debian.org/doc/manuals/debian-reference/ch01.en.html>
- <https://trapa.cz/en/course-linux-command-line-2015>
- https://docs.fedoraproject.org/en-US/Fedora/22/html/System_Administrators_Guide

2.4 Geneious

For the part (2) user must have Geneious. Geneious is a DNA alignment, assembly, and analysis software and one of the most common software platforms used in genomics. It is utilized for de novo assembly in Sondovač. We plan to replace it by some free open-source command line tool in some future release of Sondovač. Visit <http://www.geneious.com/> for download, purchase, installation and usage of Geneious. It is very feature-rich application.

Geneious was tested with versions 6, 7 and 8.

Import output file of part A of the script (`sondovac_part_a.sh`): go to menu **File | Import | From File...** This file is named as:

YourInputFile_blat_unique_transcripts_versus_genome_skim_data-no_missing_fin.fsa

Select the file and go to menu **Tools | Align / Assemble | De Novo Assemble**. In **Data** frame select **Assemble by 1st (...) Underscore**. In **Method** frame select **Geneious Assembler** (if you don't have other assemblers, this option might be missing) and **Medium Sensitivity / Fast Sensitivity**

In **Results** frame check **Save assembly report**, **Save list of unused reads**, **Save in sub-folder**, **Save contigs** (do not check **Maximum**) and **Save consensus sequences**. Do not trim. Otherwise keep defaults. Run it. Geneious may warn about possible hanging because of big file. Do not use Geneious for other tasks during the assembly. Running may take long time.

Select all resulting contigs (typically named * **Contig #**) and export them (go to menu **File | Export | Selected Documents...**) as **Tab-separated table values (*.tsv)**. Save following columns (Hold **Ctrl** key to mark more fields): **# Sequences**, **% Pairwise Identity**, **Description**, **Mean Coverage**, **Name** and **Sequence Length**. If this option would be inaccessible for you, export all columns.

Select items **Consensus Sequences** and **Unused Reads** and export them as one **FASTA**. Go to menu **File | Export | Selected Documents...** and choose **FASTA file type**.

Use exported files from Geneious as input for part B of the script (`sondovac_part_b.sh`).

2.5 Software used by Sondovač

Table 1 lists all software used by Sondovač, including minimal required versions and homepages. As soon as you have recent version of your operating system and you are using automated way of installation of additional software offered by Sondovač, you do not have to worry about this. In case you installed some of required scientific packages manually, ensure you have required minimal version. Following list refers papers and web resources describing methods used by software used by Sondovač:

Table 1: Required software, its versions and homepages. "X" denotes any subversion of particular lineage and "v. >" denotes any version higher then noted. Generally, any current version should usually be fine.

Software	Version	Homepage
Apache Ant	1.9.X	https://ant.apache.org/
bam2fastq	1.1.0	http://gsl.hudsonalpha.org/information/software/bam2fastq
BASH	v. > 3	https://gnu.org/software/bash/bash.html
BLAT	v.36	http://genome.ucsc.edu/FAQ/FAQblat.html
Bowtie2	2.2.6	http://bowtie-bio.sourceforge.net/bowtie2/index.shtml
CD-HIT	4.6	http://weizhongli-lab.org/cd-hit/
FASTX, libgtextutils	0.0.13	http://hannonlab.cshl.edu/fastx_toolkit/
FLASH	1.2.11	http://sourceforge.net/projects/flashpage/
G++, GCC	v. > 4.2	http://gcc.gnu.org/
Geneious	v. > 6.1	http://www.geneious.com/
GIT	v. > 2.0	http://git-scm.com/
GNU core utils	8.X	https://gnu.org/software/coreutils/coreutils.html
Java/OpenJDK	v. > 7	https://www.java.com/ http://openjdk.java.net/
libpng	1.6.X	http://www.libpng.org/
Picard	v. > 1.137	https://broadinstitute.github.io/picard/
SAMtools, htsjdk	1.2	http://www.htslib.org/
Sondovač	0.6	https://github.com/V-Z/sondovac/wiki
zlib	1.2.8	http://zlib.net/

BLAT Kent: BLAT – the BLAST-like alignment tool, <http://genome.cshlp.org/content/12/4/656.short>

Bowtie2 Langmead and Salzberg: Fast gapped-read alignment with Bowtie 2, <http://www.nature.com/nmeth/journal/v06/n03/2009.016.full>

CD-HIT There are several papers describing CD-HIT:

- Li et al: Clustering of highly homologous sequences to reduce the size of large protein databases, <http://bioinformatics.oxfordjournals.org/content/17/3/282.short>
- Li et al: Tolerating some redundancy significantly speeds up clustering of large protein databases, <http://bioinformatics.oxfordjournals.org/content/18/1/77.short>
- Li and Godzik: Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences, <http://bioinformatics.oxfordjournals.org/content/22/13/1658.short>
- Fu et al: CD-HIT: accelerated for clustering the next generation sequencing data, <http://bioinformatics.oxfordjournals.org/content/28/23/3150.short>
- Huang et al: CD-HIT Suite: a web server for clustering and comparing biological sequences, <http://bioinformatics.oxfordjournals.org/content/26/5/680.short>

- Niu et al: Artificial and natural duplicates in pyrosequencing reads of metagenomic data, <http://www.biomedcentral.com/1471-2105/11/187>
- Li et al: Ultrafast clustering algorithms for metagenomic sequence analysis, <http://bib.oxfordjournals.org/>

FASTX toolkit Gordon and Hannon: FASTX-Toolkit. FASTQ/A short-reads pre-processing tools, http://hannonlab.cshl.edu/fastx_toolkit/

FLASH Magoč and Salzberg: FLASH: fast length adjustment of short reads to improve genome assemblies, <http://bioinformatics.oxfordjournals.org/content/27/21/2957.abstract>

SAMtools There are several papers describing SAMtools:

- Li et al.: The Sequence alignment/map (SAM) format and SAMtools, <http://bioinformatics.oxfordjournals.org/>
- Li: A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data, <http://bioinformatics.oxfordjournals.org/>
- Li et al: Improving SNP discovery by base alignment quality, <http://bioinformatics.oxfordjournals.org/>

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2.6 Vocabulary

Binary An application in form understandable by the computer, but usually not transferable among operating systems and/or hardware platforms. Binaries in Windows usually have extension *.exe, in UNIX there use to be no extension.

BASH "The command line" – fully featured programming scripting language accessible through terminal of any UNIX-based operating system (any Linux, Mac OS X, Solaris, any variant of BSD and more). BASH scripts usually have extension *.sh.

BSD Group of popular UNIX-based operating systems. See https://en.wikipedia.org/wiki/Berkeley_Software_Distributions

compilation "Translation" of software application from the source code (text readable by human programmer) into binary form launchable by the computer. It requires special tools, and it usually must be done for every operating system and hardware platform.

Console See "Shell".

GNU Major project providing free software widely used in many operating systems, see <https://gnu.org/>.

Library Pack of software tools and functions used by another applications.

Linux One of the most common variants of UNIX-based operating systems. Linux kernel is used by many developers, so that there are plenty of Linux distributions ("flavors") from various sources (e.g. Ubuntu and derivatives, openSUSE, SLE, Debian, Linux Mint, Fedora, Centos, RedHat etc.). They share many features although on the first look they can look differently. See <https://en.wikipedia.org/wiki/Linux>.

Mac OS X Popular operating system produced by Apple. The system kernel is based on UNIX, see <https://www.apple.com/osx/>.

openSUSE Popular Linux distribution, see <https://www.opensuse.org/>.

Operating system Basic system running on your computer – typically MS Windows (not supported by Sondovač, although it might be working), Mac OS X or some Linux distribution (Ubuntu and derivatives, openSUSE, SLE, Debian, Linux Mint, Fedora, Centos, RedHat etc.).

Parameter(s) Option(s) passed to any function/command line application to modify its usage. Some can be required, some are optional and some can be used only in particular cases. In case of shell applications, parameters are usually given in way like "application -X", "application -parameter", "application -Param SomeValue" and so on. See manual for particular application (e.g. "man application"), in case of Sondovač see XXX.

PATH Directories in the computer where the system is looking for installed software (in a UNIX-based system you can view it by the command "echo \$PATH"). If you need to modify it manually, see the documentation for your operating system.

Script Software application. It requires an interpreter (application installed on the computer that is able to launch scripts written in a particular language), but the application itself is portable among operating systems and hardware architectures, and it is written in plain text, so that developers can easily modify it. Common examples are Python, Perl or BASH.

Shell "The command line" – the interface to interact with software using commands typed into the terminal window (See Figure 2).

Solaris Popular (mainly on servers) UNIX-based operating system, now developed by Oracle and including several independent clones. See <http://distrowatch.com/table.php?distribution=solaris>.

Terminal see "Shell".

Ubuntu Popular Linux distribution, see <http://www.ubuntu.com/>.

Upstream Developers usually support (e.g. by fixing of bugs) only newer versions of an application. If you use an older version and you encounter problems, no one will probably help you. Moreover, using old versions of software can be a security risk because of security issues fixed in newer versions.

UNIX (UNIX-like, UN*X, *nix, ...) Family of operating systems sharing the same logic, software architecture and plenty of tools. See <https://en.wikipedia.org/wiki/Unix-like> for details.

3 Usage of Sondovač

3.1 Command line parameters

Sondovač has some parameters useful especially for advanced users, on remote servers, for repeated analysis and so on. We recommend to start with basic interactive usage – script will ask for input files and when needed also for installation of additional software.

```
1 # Go to directory with unpacked Sondovač (in terminal):
2 cd /path/to/directory_with_sondovac
3 # Run sondovac_part_a.sh in basic interactive mode:
```

```

4 ./sondovac_part_a.sh -i
5 # Then run Geneious and continue with sondovac_part_b.sh:
6 ./sondovac_part_b.sh -i

```

3.1.1 General parameters

Shared by `sondovac_part_a.sh` as well as `sondovac_part_b.sh`.

- h, -v** Print help message and exit.
- u** Check for updates. If there is newer version of Sondovač available on <https://github.com/V-Z/sondovac/releases/> download of newer version will be offered to the user.
- l** Display LICENSE for license information (this script is licensed under GNU GPL v.3, other software under variable licenses). Exit viewing by pressing the Q key.
- r** Display README for detailed usage instructions. Exit viewing by pressing the Q key.
- p** Display INSTALL for detailed installation instructions. Exit viewing by pressing the Q key. See also page 6.
- e** Display detailed citation information and exit.
- i** Running in interactive mode – script will on-demand ask for required input files, installation of missing software etc. This is recommended default value (the script runs interactively without explicit using option **-n**).
- n** Running in non-interactive mode. User must provide at least required input files (see below). You can use only one of parameters **-i** or **-n** (not both of them). If script fails to find some of required software packages, it will exit. This is recommended for batch or repeated analysis, on remote servers and for more advanced users. User must be sure that all required software is installed (see page 6).

3.1.2 Input files

Those parameters are required when running in non-interactive mode. The parameters are optional in default interactive mode. Please, use file names without spaces and without special characters.

-f FILE Transcriptome input file in FASTA format.

- `sondovac_part_a.sh`

-c FILE Plastome reference sequence input file in FASTA format.

- `sondovac_part_a.sh`, `sondovac_part_b.sh`
- Plastome reference sequences from taxa up to the same order of the studied plant group are suitable. See Straub et al. 2012, <http://www.amjbot.org/content/99/2/349.short>.

-m FILE Mitochondriome reference sequence input file in FASTA format (optional).

- `sondovac_part_a.sh`

- This step is facultative, as plant mitochondrial genomes have largely variable sizes and high rearrangement rates.

-t FILE Paired-end genome skim input file in FASTQ format (first file).

- `sondovac_part_a.sh`

-q FILE Paired-end genome skim input file in FASTQ format (second file).

- `sondovac_part_a.sh`

-x FILE Input file in TSV format (output of Geneious assembly).

- `sondovac_part_b.sh`

-z FILE Input file in FASTA format (output of Geneious assembly).

- `sondovac_part_b.sh`

3.1.3 Optional parameters

See page 4 and Figure 1 for steps referred here. If those parameters are not provided, default values are used and it is not possible to change them any time later (not even in interactive mode).

-a ### Read length of paired-end genome skim reads (parameter -M of FLASH, see its manual for details).

- Step 4 of Sondovač, `sondovac_part_a.sh`.
- Ensure to use a certain insert size of the genome skim genomic library in combination with an appropriate read length for sequencing in order to enable merging of the paired-end genome skim reads.
- DEFAULT: 250
- OPTIONS: 125, 150, 250, 300

-y ## Sequence similarity between unique transcripts and the filtered, combined genome skim reads (parameter -minIdentity of BLAT, see its manual for details).

- Step 5 of Sondovač, `sondovac_part_a.sh`.
- Consider the trade-off between probe specificity and number of remaining matching sequences for probe design. Sequence similarity is in percent.
- DEFAULT: 85
- OPTIONS: Integer ranging from 70 to 100

-s #### Number of BLAT hits per transcript when matching unique transcripts and the filtered, combined genome skim reads.

- Step 6.2 of Sondovač, `sondovac_part_a.sh`.
- Transcripts with a high number of BLAT hits, indicating repetitive elements, need to be removed from the putative probe sequences.
- DEFAULT: 1000

- OPTIONS: Integer ranging from 100 to 10000
- b ###** Minimum exon (bait) length.
- Steps 8 and 10 of Sondovač, `sondovac_part_b.sh`.
 - The minimum exon length should not fall below the bait length in order to facilitate specific binding between genomic libraries and baits during hybridization.
 - DEFAULT: 120 (optimal length for phylogeny).
 - OPTIONS: Integer ranging from 120 to 200
- d 0.##** Sequence similarity between probe sequences (parameter -c of cd-hit-est, see its manual for details).
- Step 9 of Sondovač, `sondovac_part_b.sh`.
 - Too similar probe sequences will interact with each other during hybridization and thereby reduce enrichment efficiency.
 - DEFAULT: 0.9 (highly recommended).
 - OPTIONS: Decimal ranging from 0.85 to 0.95

3.2 Input and output files

XXX

4 Questions not covered here, reporting bugs and wishes

If you have any question or you encounter some problem, please, see <https://github.com/V-Z/sondovac/issues> and feel free to ask any question and/or express any wish. The authors will do their best to help you.

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