

VitisOmics

(see contributors below)

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Contents

1	Overview	2
1.1	Contributors	3
1.2	References	3
2	Data	4
2.1	URGI	4
2.2	NCBI	5
2.3	EBI	6
2.4	CRIBI	6
2.5	Genoscope	6
3	Results	6
3.1	Comparisons of original "assembly" files	6
3.2	Comparisons of annotations	8
3.3	Manipulations of files from URGI	9
3.3.1	Reformat sequence headers for VITVI_PN40024_8x_chroms_URGI	9
3.3.2	Reformat sequence headers for VITVI_PN40024_12x_v0_scaffolds_EMBL_r102	11
3.3.3	Reformat sequence headers for VITVI_PN40024_12x_v0_chroms_URGI	11
3.3.4	Reformat sequence headers for VITVI_PN40024_12x_v2_chroms_URGI	12
3.3.5	Format VITVI_PN40024_8x_chroms_URGI for BLAST	13
3.3.6	Format VITVI_PN40024_12x_v0_chroms_URGI for BLAST	13
3.3.7	Format VITVI_PN40024_12x_v2_chroms_URGI for BLAST	14
3.3.8	Index VITVI_PN40024_12x_v0_chroms_URGI for BWA	14
3.3.9	Index VITVI_PN40024_12x_v2_chroms_URGI for BWA	14
3.3.10	Prepare VITVI_PN40024_12x_v2_chroms_URGI for SAMtools and Picard	14
3.3.11	Index VITVI_PN40024_12x_v0_chroms_URGI for Bowtie2	14
3.3.12	Index VITVI_PN40024_12x_v2_chroms_URGI for Bowtie2	15

3.3.13	Index VITVI_PN40024_12x_v2_chroms_URGI for Bowtie2 compatible with Tassel	15
3.3.14	Translate CRIBI annotations from 12x.0 to 12x.2	15
3.3.15	Convert SNP data of the 18K Illumina array from <code>xls</code> to <code>txt.gz</code>	15
3.3.16	Align Illumina probes on PN40024 assemblies	16
3.4	Manipulations of files from NCBI	16
3.4.1	Reformat sequence headers for VITVI_PN40024_8x_scaffolds_NCBI	16
3.4.2	Reformat sequence headers for VITVI_PN40024_12x_v0_scaffolds_NCBI	17
3.4.3	Format VITVI_PN40024_8x_scaffolds_NCBI for BLAST	17
3.4.4	Format VITVI_PN40024_12x_v0_scaffolds_NCBI for BLAST	18
3.4.5	Convert <code>gbs</code> files to <code>GFF3</code>	18
3.5	Creation of R/Bioconductor packages	19
3.5.1	BSgenome IGGP12Xv2 package	20
3.5.2	BSgenome IGGP12Xv0 package	21
3.5.3	BSgenome IGGP8x package	22
3.5.4	TxDb IGGP8X package from Genoscope annotations	23
3.5.5	TxDb IGGP12Xv0 package from NCBI annotations	23

1 Overview

This document describes the "VitisOmics" project. This project aims at handling "omics" data in the genus *Vitis* (e.g. grapevine) in an open and reproducible way. Nevertheless, it requires some basic knowledge and skills about bioinformatics on GNU/Linux computers.

A large amount of such "omics" data are already available, and several committes from the IGGP (International Grape Genome Program) strive at improving interoperability. However, several issues remain, among which:

- partially-overlapping data present at multiple locations (URGI, CRIBI, NCBI, EBI, etc);
- data downloadable as files in various formats not always easy to interchange (fasta, genbank, gff3, gtf, etc);
- data often available without meta-data inside the file;
- large files not always available in compressed form;
- main efforts dedicated to wet-labs grapevine biologists.

These have consequences in terms of ambiguity, inefficiency, potential mistakes, etc. Therefore, I hope that my attempt, via the usage of git and GitHub, could prove for the community to be a useful addition to the IGGP efforts.

The repository can be easily cloned from GitHub:

```
git clone https://github.com/timflutre/VitisOmics.git
```

The project directory is organized as advised by Noble (PLoS Computational Biology 2009). On any Unix-like system, it can be easily compressed and transferred (ignoring large data files):

```
cd ..; tar -czvf VitisOmics.tar.gz \
--exclude=VitisOmics/data --exclude=VitisOmics/results \
--exclude="*~" --exclude=".*" VitisOmics
```

In order to concretely promote collaborative editing in a distributed manner, the content of the "VitisOmics" repository should be based on plain text files. As a consequence, this document is written in the org format, and can thus be automatically exported, best by emacs, but also by pandoc, into the pdf and html formats for easy reading. A choice is also made to use as much as possible softwares widely available on any GNU/Linux computer, such as bash, awk, etc, but of course it may sometimes be much easier to use R (with Bioconductor), Python (with Biopython), etc.

Last but not least, feel free to contribute, by reporting issues or forking the repository!

1.1 Contributors

The person roles comply with R's guidelines (The R Journal Vol. 4/1, June 2012).

- Timothée Flutre (cre,aut)
- Gautier Sarah (ctb)
- ...

1.2 References

The NCBI has web pages about genome assembly:

- Assembly information;
- NCBI Genome Assembly Model;
- AGP specification.

The original article for grapevine (PN40024) is a must read:

- Jaillon, et al. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature 449, 463-467 (2007).

About genome annotations:

- Grimplet et al. Comparative analysis of grapevine whole-genome gene predictions, functional annotation, categorization and integration of the predicted gene sequences. BMC Research Notes 5, 213+ (2012).
- Grimplet et al. The grapevine gene nomenclature system. BMC Genomics 15, 1077+ (2014).
- Vitulo et al. A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype. BMC Plant Biology 14, 99+ (2014).

2 Data

```
mkdir -p data; cd data/
```

TODO: retrieve genome data from other cultivars than PN40024, e.g. Sultanina

2.1 URGI

- <https://urgi.versailles.inra.fr/Species/Vitis>

```
mkdir -p urgi; cd urgi/  
../../src/download_urgi.bash
```

Remarks:

- when needed, the script decompresses zip files and compress them again but with gzip instead;
- the AGP file for the PN40024 8x assembly is not available at URGI's web site.

At the bottom of this page, one can find the following assemblies summary.

12x.2 assembly:

- contigs: 14642
- scaffolds (> 2kb): 2059
- mapped scaffolds: 366 (coverage of the genome: 95%)

12X.0 assembly:

- contigs: 14642
- scaffolds (> 2kb): 2059
- mapped scaffolds: 211 (coverage of the genome: 91.2%)

8X assembly:

- contigs: 19577
- scaffolds: 3514
- mapped ultracontigs: 191 (coverage of the genome: 68.9%)

N. Choisne from URGI (personal communication, 13/10/2015):

- "mapped scaffolds": scaffolds anchored on the linkage groups (i.e. chromosomes) using the markers from the reference genetic map;
- unmapped scaffolds hence are unanchored, and gathered into chrUn;
- "supercontig" is a synonym of "scaffold";
- "ultracontig": one level above supercontigs; localized and orientated according to data from BAC libraries.

N. Choisne from URGI on the 18K SNP chip (personal communication, 09/02/2016): let's take an example

- identifier chr1_27655_C_T;
- probe sequence TTGTCTACGAAGTTTGACAATTTCTATTTTTCATAAGTTTACACAAATTA[T/C]TGAACAGTGAGTTAGTGAC
- SNPs on the 18K Illumina Infinium microarray are named so that the first allele (here, C) corresponds to the reference (PN40024 12x.0) and the second allele (here, T) to the variant (almost sure for the "species" SNPs and should also be the case for the "vinifera" SNPs);
- in the sequence, the fact that the T comes before the C only reflects the fact that the chip is an Infinium II, with 2 beads, only allowing loci A/G, A/C, T/G, T/C, whereas the Infinium I only allows A/T et C/G.

2.2 NCBI

- <http://www.ncbi.nlm.nih.gov/genome/401>
- ftp://ftp.ncbi.nlm.nih.gov/genomes/Vitis_vinifera/

```
mkdir -p ncbi; cd ncbi/  
../../src/download_ncbi.bash
```

Remarks:

- the important file `scaffold_names` provides the correspondence between original scaffold names (i.e. from the sequencing center) and various NCBI identifiers (RefSeq, GenBank, etc);
- in `ARCHIVE/`, `BUILD.1.1/` corresponds to the 8x genome sequences of PN40024.

2.3 EBI

```
mkdir -p ebi; cd ebi/
../../src/download_ebi.bash
```

Remarks:

- a genome soft-masked by RepeatMasker is available.

2.4 CRIBI

- <http://genomes.cribi.unipd.it/grape/>

```
mkdir -p cribi; cd cribi/
../../src/download_cribi.bash
```

2.5 Genoscope

- <http://www.genoscope.cns.fr/spip/Vitis-vinifera-whole-genome.html>
- http://www.genoscope.cns.fr/externe/Download/Projets/Projet_ML/data/

```
mkdir -p genoscope; cd genoscope/
../../src/download_genoscope.bash
```

3 Results

```
mkdir -p results; cd results/
```

TODO: compress fasta files with `bgzip` instead of `gzip`

3.1 Comparisons of original "assembly" files

Files from URGI:

```

cd urgi/
zcat VV_8X_embl_98_WGS_contigs.fsa.gz | grep -c ">" # 19577
zcat VV_8X_embl_98_Scaffolds.fsa.gz | grep -c ">" # 3514
zcat VV_chr8x.fsa.gz | grep -c ">" # 35
zcat VV_12X_embl_102_WGS_contigs.fsa.gz | grep -c ">" # 14642
zcat VV_12X_embl_102_Scaffolds.fsa.gz | grep -c ">" # 2059
zcat VV_chr12x.fsa.gz | grep -c ">" # 33
cat 12x0_chr.agp | wc -l # 390
cat 12x0_scaffolds.lg | wc -l # 2059
cat 12x0_chr.lg | wc -l # 33
zcat 12Xv2_grapevine_genome_assembly.fa.gz | grep -c ">" # 20

```

Files from NCBI:

```

cd ncbi/
ls ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr*.fa.gz | grep -v "Pltd" | while read f; do
  zcat $f; done | grep -c ">" # 3514
ls ARCHIVE/BUILD.1.1/Assembled_chromosomes/vvi_ref_chr*.fa.gz | while read f; do
  zcat $f; done | grep -c ">" # 19
zcat ARCHIVE/BUILD.1.1/allcontig.agp.gz | grep -v "#" | cut -f 5 | sort | uniq -c #
F=1 N=16063 W=19577
cat ARCHIVE/BUILD.1.1/scaffold_names | sed 1d | wc -l # 3514
ls CHRS/vvi_ref_12X_chr*.fa.gz | grep -v -E "Pltd|MT" | while read f; do zcat $f;
done | grep -c ">" # 2059
ls Assembled_chromosomes/vvi_ref_12X_chr*.fa.gz | grep -v -E "Pltd|MT" | while read
f; do zcat $f; done | grep -c ">" # 19
cat scaffold_names | sed 1d | wc -l # 2061

```

See also the script `src/vitisomics.R` using R and Bioconductor. It confirms that the 12x scaffolds have the exact same sequence, whether they come from the URGI or the NCBI. Note however that the file from the NCBI allows to know easily on which chromosome a placed sequences is.

Remarks concerning PN40024 at URGI:

- the file `12x0_chr.agp.info` doesn't correspond to `12x0_chr.agp` (it doesn't even correspond to the description of a proper AGP file, as specified here);
- no mitochondrial nor chloroplastic data are available.

Remarks concerning PN40024 at NCBI:

- contig `NC_007957.1` in `ARCHIVE/BUILD.1.1/allcontig.agp.gz` (with `fragment_type=F` for "finished") corresponds to the chloroplast;

- **scaffold_names** contains all 2059 scaffolds of nuclear DNA as well as the assembled genome of the mitochondria and the chloroplast.

For its build 1.1 (corresponding to the 8x sequences of the PN40024 variety), the NCBI has one file per assembled chromosome. However, all unlocalized and unplaced scaffolds are gathered in a single file **chrUn**. This is not the case at URGI which has unlocalized scaffolds in files as **chr3_random** and a **chrUn_random** file with all unplaced scaffolds (and only them). Unfortunately, the NCBI has the annotation of the 8x (in the GenBank format), but the URGI hasn't.

3.2 Comparisons of annotations

The Genoscope annotated the 8x and 12x.v0 assemblies with the Gaze software:

```
zcat 8X/annotation/Vitis_vinifera_annotation_v1.gff.gz | cut -f2 | sort | uniq -c #
234890 Gaze_filter
zcat 12X/annotation/Vitis_vinifera_annotation.gff.gz | cut -f2 | sort | uniq -c #
245272 Gaze
```

Both GFF files contain several types of annotations:

```
zcat 8X/annotation/Vitis_vinifera_annotation_v1.gff.gz | cut -f3 | sort | uniq -c
zcat 12X/annotation/Vitis_vinifera_annotation.gff.gz | cut -f3 | sort | uniq -c
```

assembly	gene	mRNA	UTR	CDS
8x	30434	30434	24671	149351
12x.0	26346	26346	35815	156765

For both 8x and 12x.0 assemblies, gene identifiers all start with GSVIVG, and by GSVIVT for mRNA:

```
zcat 8X/annotation/Vitis_vinifera_annotation_v1.gff.gz | awk -F"\t" '{if($3=="gene")
{split($9,a," "); print substr(a[2],1,6)}}' | sort | uniq -c
zcat 8X/annotation/Vitis_vinifera_annotation_v1.gff.gz | awk -F"\t" '{if($3=="mRNA")
{split($9,a," "); print substr(a[2],1,6)}}' | sort | uniq -c
zcat 12X/annotation/Vitis_vinifera_annotation.gff.gz | awk -F"\t" '{if($3=="gene"){
split($9,a," "); print substr(a[2],1,6)}}' | sort | uniq -c
zcat 12X/annotation/Vitis_vinifera_annotation.gff.gz | awk -F"\t" '{if($3=="mRNA"){
split($9,a," "); print substr(a[2],1,6)}}' | sort | uniq -c
```

The NCBI annotated the 8x and 12x.0 assemblies with the GNOMON software.

TODO: convert NCBI annotation files from gbs into gff3 (see work in progress below)

3.3 Manipulations of files from URGI

```
mkdir -p urgi; cd urgi/
```

3.3.1 Reformat sequence headers for VITVI_PN40024_8x_chroms_URGI

Launch script:

```
ln -s ../../data/urg/uv_chr8x.fsa.gz .
echo "../../src/reformat_uv_chr8x.bash" \
| qsub -cwd -j y -V -N reformat_uv_chr8x -q normal.q
```

Check:

```
zcat uv_chr8x.fsa.gz | wc -l # 8291865
zcat uv_chr8x.fsa.gz | grep -c ">" # 35
zcat VITVI_PN40024_8x_chroms_URGI.fa.gz | wc -l # 8291865
zcat VITVI_PN40024_8x_chroms_URGI.fa.gz | grep -c ">" # 35
diff <(zcat uv_chr8x.fsa.gz) <(zcat VITVI_PN40024_8x_chroms_URGI.fa.gz)
```

Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_8x_chroms_URGI.fa.gz | md5sum # 4b6ea1cb4ff189ac587fa269077885b5
```

Length of each sequence:

```
zcat VITVI_PN40024_8x_chroms_URGI.fa.gz \
| awk 'BEGIN{RS=">"} {split($0,a,"\n");
if(length(a)==0)next;
sum=0; for(i=2;i<=length(a);++i){sum+=length(a[i])};
print a[1]": "sum; sumTot+=sum} END{print sumTot}'
```

header	length (bp)
chr1 CU462738 Vitis vinifera PN40024 assembly8x chromosome1	15630816
chr10 CU462747 Vitis vinifera PN40024 assembly8x chromosome10	9647040
chr10 _{random}	2206354
chr11 CU462748 Vitis vinifera PN40024 assembly8x chromosome11	13936303
chr11 _{random}	1958407
chr12 CU462749 Vitis vinifera PN40024 assembly8x chromosome12	18540817
chr12 _{random}	2826407
chr13 CU462750 Vitis vinifera PN40024 assembly8x chromosome13	15191948
chr13 _{random}	1580403
chr14 CU462751 Vitis vinifera PN40024 assembly8x chromosome14	19480434
chr14 _{random}	5432426
chr15 CU462752 Vitis vinifera PN40024 assembly8x chromosome15	7693613
chr15 _{random}	4297576
chr16 CU462753 Vitis vinifera PN40024 assembly8x chromosome16	8158851
chr16 _{random}	4524411
chr17 CU462754 Vitis vinifera PN40024 assembly8x chromosome17	13059092
chr17 _{random}	1763011
chr18 CU462755 Vitis vinifera PN40024 assembly8x chromosome18	19691255
chr18 _{random}	5949186
chr19 CU462756 Vitis vinifera PN40024 assembly8x chromosome19	14071813
chr19 _{random}	1912523
chr1 _{random}	5496190
chr2 CU462739 Vitis vinifera PN40024 assembly8x chromosome2	17603400
chr2 _{random}	60809
chr3 CU462740 Vitis vinifera PN40024 assembly8x chromosome3	10186927
chr3 _{random}	1343266
chr4 CU462741 Vitis vinifera PN40024 assembly8x chromosome4	19293076
chr5 CU462742 Vitis vinifera PN40024 assembly8x chromosome5	23428299
chr6 CU462743 Vitis vinifera PN40024 assembly8x chromosome6	24148918
chr7 CU462744 Vitis vinifera PN40024 assembly8x chromosome7	15233747
chr7 _{random}	176143
chr8 CU462745 Vitis vinifera PN40024 assembly8x chromosome8	21557227
chr8 _{random}	12125
chr9 CU462746 Vitis vinifera PN40024 assembly8x chromosome9	16532244
chrUn _{random}	154883714
total	497508771

3.3.2 Reformat sequence headers for VITVI_PN40024_12x_v0_scaffolds_EMBL_r102

Launch script:

```
ln -s ../../data/urgi/VV_12X_embl_102_Scaffolds.fsa.gz .
echo "../../src/reformat_VV_12X_embl_102_Scaffolds.bash" \
| qsub -cwd -j y -V -N reformat_VV_12X_embl_102_Scaffolds -q normal.q
```

Check:

```
zcat VV_12X_embl_102_Scaffolds.fsa.gz | wc -l # 8091565
zcat VV_12X_embl_102_Scaffolds.fsa.gz | grep -c ">" # 2059
zcat VITVI_PN40024_12x_v0_scaffolds_EMBL_r102.fa.gz | wc -l # 8091565
zcat VITVI_PN40024_12x_v0_scaffolds_EMBL_r102.fa.gz | grep -c ">" # 2059
diff <(zcat VV_12X_embl_102_Scaffolds.fsa.gz) <(zcat
    VITVI_PN40024_12x_v0_scaffolds_EMBL_r102.fa.gz)
```

Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_12x_v0_scaffolds_EMBL_r102.fa.gz | md5sum # 4
    fa2432d7a66c019c7cb41ee4d0cb7bc
zcat VITVI_PN40024_12x_v0_scaffolds_EMBL_r102.fa.gz | grep -v ">" | md5sum #
    df5cdb0c6f73cb133261905374cdf2f2
```

3.3.3 Reformat sequence headers for VITVI_PN40024_12x_v0_chroms_URGI

Launch script:

```
ln -s ../../data/urgi/VV_chr12x.fsa.gz .
echo "../../src/reformat_VV_chr12x.bash" \
| qsub -cwd -j y -V -N reformat_VV_chr12x -q normal.q
```

Check:

```
zcat VV_chr12x.fsa.gz | wc -l # 8240706
zcat VV_chr12x.fsa.gz | grep -c ">" # 33
zcat VITVI_PN40024_12x_v0_chroms_URGI.fa.gz | wc -l # 8240706
zcat VITVI_PN40024_12x_v0_chroms_URGI.fa.gz | grep -c ">" # 33
diff <(zcat VV_chr12x.fsa.gz) <(zcat VITVI_PN40024_12x_v0_chroms_URGI.fa.gz)
```

Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_12x_v0_chroms_URGI.fa.gz | md5sum #  
    eff315994faf35333462b9595e10ce5
```

3.3.4 Reformat sequence headers for VITVI_PN40024_12x_v2_chroms_URGI

Launch script:

```
ln -s ../../data/urgi/12Xv2_grapevine_genome_assembly.fa.gz .  
echo "../../src/reformat_12Xv2_grapevine_genome_assembly.bash" \  
| qsub -cwd -j y -V -N reformat_12Xv2_grapevine_genome_assembly -q normal.q
```

Check:

```
zcat 12Xv2_grapevine_genome_assembly.fa.gz | wc -l # 8103449  
zcat 12Xv2_grapevine_genome_assembly.fa.gz | grep -c ">" # 20  
zcat VITVI_PN40024_12x_v2_chroms_URGI.fa.gz | wc -l # 8103449  
zcat VITVI_PN40024_12x_v2_chroms_URGI.fa.gz | grep -c ">" # 20  
diff <(zcat 12Xv2_grapevine_genome_assembly.fa.gz) <(zcat  
    VITVI_PN40024_12x_v2_chroms_URGI.fa.gz)
```

Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_12x_v2_chroms_URGI.fa.gz | md5sum # 4  
    e487c28eaf19ef59b0b6128b73935af
```

Length of each sequence:

```
zcat VITVI_PN40024_12x_v2_chroms_URGI.fa.gz \  
| awk 'BEGIN{RS=">"} {split($0,a,"\n");  
if(length(a)==0)next;  
sum=0; for(i=2;i<=length(a);++i){sum+=length(a[i])};  
print a[1]": "sum; sumTot+=sum} END{print sumTot}'
```

header	length (bp)
chr1 Vitis vinifera PN40024 assembly12x.2	24233538
chr2 Vitis vinifera PN40024 assembly12x.2	18891843
chr3 Vitis vinifera PN40024 assembly12x.2	20695524
chr4 Vitis vinifera PN40024 assembly12x.2	24711646
chr5 Vitis vinifera PN40024 assembly12x.2	25650743
chr6 Vitis vinifera PN40024 assembly12x.2	22645733
chr7 Vitis vinifera PN40024 assembly12x.2	27355740
chr8 Vitis vinifera PN40024 assembly12x.2	22550362
chr9 Vitis vinifera PN40024 assembly12x.2	23006712
chr10 Vitis vinifera PN40024 assembly12x.2	23503040
chr11 Vitis vinifera PN40024 assembly12x.2	20118820
chr12 Vitis vinifera PN40024 assembly12x.2	24269032
chr13 Vitis vinifera PN40024 assembly12x.2	29075116
chr14 Vitis vinifera PN40024 assembly12x.2	30274277
chr15 Vitis vinifera PN40024 assembly12x.2	20304914
chr16 Vitis vinifera PN40024 assembly12x.2	23572818
chr17 Vitis vinifera PN40024 assembly12x.2	18691847
chr18 Vitis vinifera PN40024 assembly12x.2	34568450
chr19 Vitis vinifera PN40024 assembly12x.2	24695667
chrUkn Vitis vinifera PN40024 assembly12x.2	27389308
total	486205130

3.3.5 Format VITVI_PN40024_8x_chroms_URGI for BLAST

Launch:

```
echo "../../../src/blast_format.bash VITVI_PN40024_8x_chroms_URGI.fa.gz" \
| qsub -cwd -j y -V -q normal.q -N blast_format_VITVI_PN40024_8x_v0_chroms_URGI
```

3.3.6 Format VITVI_PN40024_12x_v0_chroms_URGI for BLAST

Launch:

```
echo "../../../src/blast_format.bash VITVI_PN40024_12x_v0_chroms_URGI.fa.gz" \
| qsub -cwd -j y -V -q normal.q -N blast_format_VITVI_PN40024_12x_v0_chroms_URGI
```

3.3.7 Format VITVI_PN40024_12x_v2_chroms_URGI for BLAST

Launch:

```
echo "../../src/blast_format.bash VITVI_PN40024_12x_v2_chroms_URGI.fa.gz" \  
| qsub -cwd -j y -V -q normal.q -N blast_format_VITVI_PN40024_12x_v2_chroms_URGI
```

3.3.8 Index VITVI_PN40024_12x_v0_chroms_URGI for BWA

Launch:

```
echo "../../src/bwa_index_VITVI_PN40024_12x_v0_chroms_URGI.bash" \  
| qsub -cwd -j y -V -N bwa_index_VITVI_PN40024_12x_v0_chroms_URGI -q normal.q
```

3.3.9 Index VITVI_PN40024_12x_v2_chroms_URGI for BWA

Launch:

```
echo "../../src/bwa_index_VITVI_PN40024_12x_v2_chroms_URGI.bash" \  
| qsub -cwd -j y -V -N bwa_index_VITVI_PN40024_12x_v2_chroms_URGI -q normal.q
```

3.3.10 Prepare VITVI_PN40024_12x_v2_chroms_URGI for SAMtools and Picard

Make an index as well as a SAM header.

Launch:

```
echo "../../src/samtools-picard_prep_VITVI_PN40024_12x_v2_chroms_URGI.bash" \  
| qsub -cwd -j y -V -N samtools-picard_prep_VITVI_PN40024_12x_v2_chroms_URGI -q  
normal.q
```

3.3.11 Index VITVI_PN40024_12x_v0_chroms_URGI for Bowtie2

Launch:

```
echo "../../src/bowtie2_index_VITVI_PN40024_12x_v0_chroms_URGI.bash" \  
| qsub -cwd -j y -V -N bowtie2_build_VITVI_PN40024_12x_v0_chroms_URGI -q normal.q
```

3.3.12 Index VITVI_PN40024_12x_v2_chroms_URGI for Bowtie2

Launch:

```
echo "../../src/bowtie2_index_VITVI_PN40024_12x_v2_chroms_URGI.bash" \  
| qsub -cwd -j y -V -N bowtie2_build_VITVI_PN40024_12x_v2_chroms_URGI -q normal.q
```

3.3.13 Index VITVI_PN40024_12x_v2_chroms_URGI for Bowtie2 compatible with Tassel

Tassel requires numbers as chromosome identifiers.

Launch:

```
echo "../../src/bowtie2_index_VITVI_PN40024_12x_v2_chroms_URGI_for_Tassel.bash" \  
| qsub -cwd -j y -V -N bowtie2_build_VITVI_PN40024_12x_v2_chroms_URGI_for_Tassel -  
q normal.q
```

3.3.14 Translate CRIBI annotations from 12x.0 to 12x.2

Requirement: use or write a script taking as input the 12x.0 GFF3 file as well as the 12.0-12.2 AGP file, and returns as output the 12x.2 GFF3 file

The URGI provides the following AGP file: `golden_path_V2_111113_allChr.csv`. Unfortunately, after looking at the official specification of the AGP format, the URGI file doesn't seem to be valid, neither for version 1.1, nor 2.2. After contacting URGI, they told me they were working on it (October 2015).

TODO: look at the annotations from CRIBI on 12x.0 transposed to 12x.2 by URGI

Another script was developed by G. Sarah, but it suffers from several issues.

TODO: test CrossMap

3.3.15 Convert SNP data of the 18K Illumina array from xls to txt.gz

On the command-line, working with tabulated files is much easier, and they should be compressed (e.g. with `gzip`). The 18071 probe sequences also need to be saved in two fasta files, one for the 13562 "vinifera" SNPs and one for the 4509 "species" SNPs.

See the corresponding task in the script `src/vitisomics.R`.

Note that, as of January 2016, even though at least two articles were published which used this genotyping array, the data are not (yet?) part of dbSNP nor EVA, unfortunately. Therefore, no unambiguous SNP identifiers exist which can be used across studies and genome assemblies.

3.3.16 Align Illumina probes on PN40024 assemblies

Requires the VITVI_PN40024_12x_v0_chroms_URGI.fa.gz bank to be formatted for BLAST (see above).

```
echo "zcat GrapeReSeq_Illumina_18K_SNP_vinifera_probes.fa.gz | blastn -query - -task
      megablast -db VITVI_PN40024_12x_v0_chroms_URGI -out /dev/stdout -outfmt 6 |
      gzip > Ill118Kprobes-vinifera_12x0-chroms_megablast.txt.gz" | qsub -cwd -j y -V -
      q normal.q -N blastn-megablast_Ill118Kprobes-vinifera_12x0-chroms
```

The alignments are analyzed in the corresponding task in the script `src/vitisomics.R`.

Among the 13562 "vinifera" probes, 33 are not aligned on the 12x0 assembly of the PN40024 genome, 24 are aligned on different chromosomes than indicated (mostly plastid genomes), and all the others look fine.

3.4 Manipulations of files from NCBI

```
mkdir -p ncbi; cd ncbi/
```

3.4.1 Reformat sequence headers for VITVI_PN40024_8x_scaffolds_NCB1

Launch script:

```
ls ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr*.fa.gz | grep -v -E "Pltd" |
  while read f; do ln -s $f .; done
echo "../../src/reformat_scaffs_NCB1-8x.bash" \
  | qsub -cwd -j y -V -N reformat_scaffs_NCB1-8x -q normal.q
```

Check:

```
\ls vvi_ref_chr* | while read f; do zcat $f; done | wc -l # 6963886
\ls vvi_ref_chr* | while read f; do zcat $f; done | grep -c ">" # 3514
zcat VITVI_PN40024_8x_scaffolds_NCB1.fa.gz | wc -l # 6963886
zcat VITVI_PN40024_8x_scaffolds_NCB1.fa.gz | grep -c ">" # 3514
diff <(\ls -v vvi_ref_chr* | while read f; do zcat $f; done) <(zcat
  VITVI_PN40024_8x_scaffolds_NCB1.fa.gz)
```


Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_8x_scaffolds_NCBI.fa.gz | md5sum #  
a66f86ab2d89eb582935454ae3b7a49d
```

3.4.2 Reformat sequence headers for VITVI_PN40024_12x_v0_scaffolds_NCBI

Launch script:

```
ls ../../data/ncbi/CHRS/vvi_ref_12X_chr*.fa.gz | grep -v -E "Pltd|MT" | while read f  
; do ln -s $f .; done  
echo "../../src/reformat_scaffs_NCBI-12x.bash" \  
| qsub -cwd -j y -V -N reformat_scaffs_NCBI-12x -q normal.q
```

Check:

```
\ls vvi_ref_12X_chr* | while read f; do zcat $f; done | wc -l # 6934292  
\ls vvi_ref_12X_chr* | while read f; do zcat $f; done | grep -c ">" # 2059  
zcat VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz | wc -l # 6934292  
zcat VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz | grep -c ">" # 2059  
diff <(\ls -v vvi_ref_12X_chr* | while read f; do zcat $f; done) <(zcat  
VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz) | less
```

Only the headers differ, not the sequences, so everything is fine.

Basic stats:

```
zcat VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz | md5sum # 20  
fa822ed5679519a20fe768c422a701  
zcat VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz | grep -v ">" | md5sum # 9  
ddb5761fe0e4356c7ef73410011ccb
```

3.4.3 Format VITVI_PN40024_8x_scaffolds_NCBI for BLAST

Launch:

```
echo "../../src/blast_format.bash VITVI_PN40024_8x_scaffolds_NCBI.fa.gz" \  
| qsub -cwd -j y -V -N blast_format_VITVI_PN40024_8x_scaffolds_NCBI -q normal.q
```

3.4.4 Format VITVI_PN40024_12x_v0_scaffolds_NCBI for BLAST

Launch:

```
echo "../../../src/blast_format.bash VITVI_PN40024_12x_v0_scaffolds_NCBI.fa.gz" \  
| qsub -cwd -j y -V -N blast_format_VITVI_PN40024_12x_v0_scaffolds_NCBI -q normal.  
q
```

3.4.5 Convert gbs files to GFF3

Check that there is one LOCUS entry per scaffold:

```
ls ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr*.gbs.gz | grep -v "Pltd" |  
while read f; do zcat $f; done | grep -c "LOCUS" # 3514
```

Use the bp_{genbank2gff3}.pl script from BioPerl:

```
zcat ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr1.gbs.gz | bp_genbank2gff3  
.pl -in stdin -out stdout | gzip > vvi_ref_chr1.gff3.gz  
# Error::throw  
# Bio::Root::Root::throw /usr/local/share/perl5/Bio/Root/Root.pm:449  
# Bio::SeqFeature::Tools::Unflattener::unflatten_seq /usr/local/share/perl5/Bio/  
SeqFeature/Tools/Unflattener.pm:1636  
# main::unflatten_seq /usr/local/bin/bp_genbank2gff3.pl:1030  
# /usr/local/bin/bp_genbank2gff3.pl:504
```

Use the convert_{genbanktogff3}.py script from biocode:

```
zcat ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr1.gbs.gz > vvi_ref_8x_chr1.  
gbs  
convert_genbank_to_gff3.py -i vvi_ref_8x_chr1.gbs -o vvi_ref_8x_chr1.gff3 --no_fasta  
# File "convert_genbank_to_gff3.py", line 196, in <module> main()  
# File "convert_genbank_to_gff3.py", line 95, in main  
# locus_tag = feat.qualifiers['locus_tag'][0]  
# KeyError: 'locus_tag'
```

Additional remarks:

- it is written in Python;
- it uses Biopython, but also custom libraries;
- it is on GitHub;

- it doesn't handle gzipped file as input;
- it skips features not from type gene, mRNA, tRNA, rRNA and CDS.

Use the **GFF** library from BCBio (not yet integrated into Biopython) as explained here:

```
zcat ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr1.gbs.gz > vvi_ref_8x_chr1.gbs
genbank_to_gff.py vvi_ref_8x_chr1.gbs
```

Remarks:

- the **sequence-region** are interspersed in the output file;
- what does the first data line correspond to, with source **annotation**?
- the source is present in the output as a feature;
- why is **=feature =** added in the 2nd field?
- why is it written **db_xref** instead of **Dbxref** (from official specification)?
- same for **note** instead of **Note**?
- exons seem to have 2nd field as **feature mRNA**

TODO: Use gffutils (doc, code)

TODO: Use a custom script based on Biopython only:

```
genbank2gff3.py -i ../../data/ncbi/ARCHIVE/BUILD.1.1/CHRS/vvi_ref_chr1.gbs.gz -o
vvi_ref_8x_chr1.gff.gz -t 29760 -g "NCBI 1.1" -s Genbank
```

TODO: check for "pseudo" but empty

3.5 Creation of R/Bioconductor packages

- <http://www.bioconductor.org/>
- Huber, W. et al. Orchestrating high-throughput genomic analysis with bioconductor. Nature Methods 12, 115-121 (2015). URL <http://dx.doi.org/10.1038/nmeth.3252>.

TODO: see AnnotationHub

3.5.1 BSgenome IGGP12Xv2 package

<http://bioconductor.org/packages/release/bioc/html/BSgenome.html>

Retrieve the sequence data from URGI:

```
cd results/
mkdir -p make_BSgenome_IGGP12Xv2
cd make_BSgenome_IGGP12Xv2/
ln -s ../../data/urgi/12Xv2_grapevine_genome_assembly.fa.gz .
```

Split into one chromosome per file (in the headers, discard everything after the first space):

```
zcat 12Xv2_grapevine_genome_assembly.fa.gz | awk 'BEGIN{RS=">"} {if(NF==0)next;
  split($0,a,"\n"); split(a[1],b," "); print b[1]; print ">"b[1] > b[1]".fa"; for(
    i=2;i<length(a);++i){print a[i] >> b[1]".fa"}}'
gzip chr*.fa
```

Using the latest version of Bioconductor and its BSgenome package, prepare the seed file (IGGP12Xv2_seed.txt) by hand as indicated in the vignette as well as in the official R manual "Writing R extensions". Following this article, I chose the CC0 license (present in the R list of licenses in share/licenses/license.db). Following suggestions from Hervé Pagès (Bioconductor staff):

- the common_name field can be Grape;
- the organism_biocview field has to be Vitis_vinifera (see this link).

Forge the target package from the seed file:

```
echo "date; echo \"library(BSgenome); forgeBSgenomeDataPkg(\\\\"IGGP12Xv2_seed.txt\\\\"
  "); sessionInfo()\" | R --vanilla; date" | qsub -cwd -j y -V -N forge_BSgenome -
q normal.q
```

Build the package and check it:

```
echo "date; R CMD build BSgenome.Vvinifera.URGI.IGGP12Xv2; date" | qsub -cwd -j y -V
  -N build_BSgenome -q normal.q
echo "date; R CMD check BSgenome.Vvinifera.URGI.IGGP12Xv2_0.1.tar.gz; date" | qsub -
  cwd -j y -V -N check_BSgenome -q normal.q
```

The target package is now ready to be installed:

```
R CMD INSTALL BSgenome.Vvinifera.URGI.IGGP12Xv2_0.1.tar.gz
```

A.-F. Adam-Blondon (INRA, member of IGGP) and other colleagues also from INRA gave positive feedback. I hence sent the package to the Bioconductor team (Hervé Pagès, maintainer of the BSgenome generic package). The 12Xv2 package is now available here, and it also appears in this list.

3.5.2 BSgenome IGGP12Xv0 package

Similarly as for the 12Xv2 package, retrieve the sequence data from URGI:

```
cd results/
mkdir -p make_BSgenome_IGGP12Xv0
cd make_BSgenome_IGGP12Xv0/
ln -s ../../data/urgi/VV_chr12x.fsa.gz .
```

Split into one chromosome per file (headers as chr1, chr1_random, etc):

```
zcat VV_chr12x.fsa.gz | awk 'BEGIN{RS=">"} {if(NF==0)next; split($0,a,"\n"); split(a
    [1],b," "); print b[length(b)]; print ">"b[length(b)] > b[length(b)]".fa"; for(i
    =2;i<length(a);++i){print a[i] >> b[length(b)]".fa"}}'
gzip chr*.fa
```

Replace chrUn by chrUkn to be compatible with the 12Xv2:

```
zcat chrUn.fa.gz | sed 's/chrUn/chrUkn/' | gzip > chrUkn.fa.gz
diff <(zcat chrUn.fa.gz) <(zcat chrUkn.fa.gz) # check
rm chrUn.fa.gz
```

Prepare the seed file (IGGP12Xv0_seed.txt) using the one for IGGP12Xv2 as a template.

Forge the target package from the seed file:

```
echo "date; echo \"library(BSgenome); forgeBSgenomeDataPkg(\\\\"IGGP12Xv0_seed.txt\\\\"
    "); sessionInfo()\" | R --vanilla; date" | qsub -cwd -j y -V -N forge_BSgenome -
    q normal.q
```

Build the package and check it:

```
echo "date; R CMD build BSgenome.Vvinifera.URGI.IGGP12Xv0; date" | qsub -cwd -j y -V
    -N build_BSgenome -q normal.q
echo "date; R CMD check BSgenome.Vvinifera.URGI.IGGP12Xv0_0.1.tar.gz; date" | qsub -
    cwd -j y -V -N check_BSgenome -q normal.q
```

The target package is now ready to be installed:

```
R CMD INSTALL BSgenome.Vvinifera.URGI.IGGP12Xv0_0.1.tar.gz
```

The 12Xv0 package is now available here.

3.5.3 BSgenome IGGP8x package

Similarly as for the 12Xv2 and 12Xv0 package, retrieve the sequence data from URGI:

```
cd results/  
mkdir -p make_BSgenome_IGGP8X  
cd make_BSgenome_IGGP8X/  
ln -s ../../data/urgi/VV_chr8x.fsa.gz .
```

Split into one chromosome per file (headers as chr1, chr1_random, etc):

```
zcat VV_chr8x.fsa.gz | awk 'BEGIN{RS=">"} {if(NF==0)next; split($0,a,"\n"); split(a  
    [1],b," "); print b[length(b)]; print ">"b[length(b)] > b[length(b)]".fa"; for(i  
    =2;i<length(a);++i){print a[i] >> b[length(b)]".fa"}}'  
gzip chr*.fa
```

Prepare the seed file (IGGP8X_seed.txt) using the one for IGGP12Xv0 as a template:

```
cp ../make_BSgenome_IGGP12Xv0/IGGP12Xv0_seed.txt IGGP8X_seed.txt
```

Forge the target package from the seed file:

```
echo "date; echo \"library(BSgenome); forgeBSgenomeDataPkg(\\\\"IGGP8X_seed.txt\\");  
    sessionInfo()\" | R --vanilla; date" | qsub -cwd -j y -V -N forge_BSgenome -q  
    normal.q
```

Build the package and check it:

```
echo "date; R CMD build BSgenome.Vvinifera.URGI.IGGP8X; date" | qsub -cwd -j y -V -N  
    build_BSgenome -q normal.q  
echo "date; R CMD check BSgenome.Vvinifera.URGI.IGGP8X_0.1.tar.gz; date" | qsub -cwd  
    -j y -V -N check_BSgenome -q normal.q
```

The target package is now ready to be installed:

```
R CMD INSTALL BSgenome.Vvinifera.URGI.IGGP8X_0.1.tar.gz
```

TODO: package sent to Hervé Pagès; wait for agreement

The 8X package is now available here.

3.5.4 TxDb IGGP8X package from Genoscope annotations

<http://www.bioconductor.org/packages/release/bioc/html/GenomicFeatures.html>

TODO: use `makeTxDbFromGFF()`

3.5.5 TxDb IGGP12Xv0 package from NCBI annotations

TODO