Knitr template

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2018-03-15

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Figure 1: A nice sample picture.

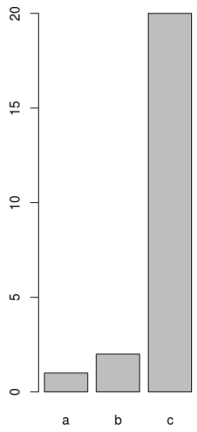

Table 1: **Nice table.** Check out booktabs for more inspiring table styles or the presentation of Markus Püschel small Guide to Making Nice Tables.

RIL7 (f7)	**exserta** (ex)	**axillaris** (ax)
plate 2 : 8 reads, data NA plate 3 : 94 reads plate 4 : 93 reads	plate 1 : 1 plate 3 : 1 plate 4 : 1	plate 1 : 2 plate 2 : 1
187 f7.platex.y.q30l50.sam f7.platex.y.jobnumber.out .err	3 ex.platex.y.q30l50.sam ex.platex.y.jobnumber.out .err	3 ax.platex.y.q30l50.sam ax.platex.y.jobnumber.out .err
TOTAL 193 samples reads at `/home/user/results`		

1 some examples

A path can be included like this : `home/user/knitr`
include a word from the glossary the first time *Petunia exserta* and the second time *P. exserta*.
`ls -l | grep 'useful'` to include an inline code.
code can be included like this as well : `listings`, but this does not allow for special symbols like _ . (Unless you escape them, of corse)

For references : see Figure 1.

2 another section

make nice paragraps : That works like this. By the way, referring to a table also works, see Table 1.

Citing a paper works like this: [1]

Do you need to have a colorful bar in your text? This todo can be seen at the end of the file again

Table 2: **minor allele frequencies** genolike_test.mafs.gz output file

chromo	position	major	minor	unknownEM	pu-EM	nInd
Peex113Ctg00003	28382	T	C	0.097175	0.0000001997185	6
Peex113Ctg00004	118715	A	G	0.003254	0.00000000004385381	181
Peex113Ctg00004	119009	A	G	0.333003	0	178
Peex113Ctg00016	11831	T	C	0.016492	0.0000000003690032	12
Peex113Ctg00016	11870	T	A	0.107668	0	4
Peex113Ctg00016	11878	A	G	0.147158	0	9
Peex113Ctg00016	11914	C	T	0.163204	0	9
Peex113Ctg00016	11924	G	T	0.147181	0	9
Peex113Ctg00016	11925	G	T	0.147206	0	9
Peex113Ctg00016	57577	A	G	0.094229	0	8
Peex113Ctg00016	57585	G	A	0.094234	0	8
Peex113Ctg00016	57587	T	G	0.094228	0	8

That's the default color for todonotes inline todos. Check out the todonotes package for more nice things.

```
# Ever heard about Phred quality score? No? This is how it works:
error = seq(0,1,0.01)
Qphred = -10*log10(error)
```

```
plot(error, Qphred, xlab='Error probability per base call')
```

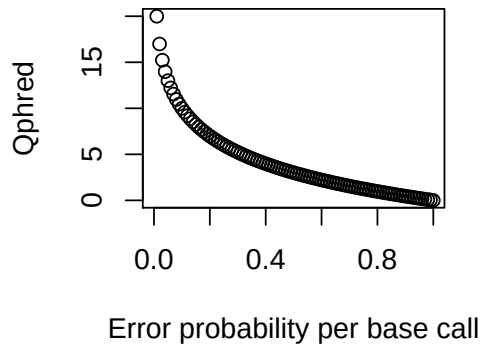

Figure 2: Phred quality score

See Figure 2 for phred. A knitr inline works like this : $0, 0.5, 1$

Listing 1: from single_ job.sh, running a program with some settings

```
#!/bin/sh
# -GL 2 : use GATK , -doGlf 2 : output beagle file

# note : Elapsed Time = 01:03:32 of 04:00:00
```

I can also include an output from the terminal as a listing. That looks like this:

Listing 2: beagle likelihood file

```
marker allele1 allele2 Ind0 Ind0 Ind0
1_14000202 2 0 0.000532 0.999468 0.000000
1_14000873 2 0 0.000000 0.030324 0.969676
1_14001018 3 1 0.000000 0.015429 0.984571
1_14001867 0 2 0.000056 0.333333 0.666611
1_14002342 1 3 0.941072 0.058928 0.000000
1_14002422 0 3 0.000000 0.111147 0.888853
1_14002474 3 1 0.969662 0.030338 0.000000
1_14003581 1 3 0.000000 0.200027 0.799973
1_14004623 3 1 0.000000 0.200035 0.799965
```

By the way, see listings 1 to show you how to refer to listings.

THEORY — **a topic** —
here I include some theory about a topic. Or use the box for any other purpose.

```
# wondering how to run a .Rnw document from terminal?
cd ~/wherethedocumentis/template_knitr.Rnw
Rscript -e "library(knitr); knit('template_knitr.Rnw')" # makes you a .tex file from the R code chunks.
pdflatex template_knitr.tex
pdflatex template_knitr.tex
biber template_knitr # to have references and bibliography correctly
pdflatex template_knitr
# if you use ubuntu, you can open the pdf with:
gnome-open template_knitr.pdf
```

3 Glossary

References

[1] Rasmus Nielsen et al. “Genotype and SNP calling from next-generation sequencing data”. In: *Nature Reviews Genetics* 12.6 (2011), p. 443.

Todo list