

# snpMatrix 4-digit Series

Hin-Tak Leung

August 28, 2013

## 1 Introduction

The snpMatrix 4-digit series started with 1.2.2.1 (Mar 15 2008) and reaches 1.19.0.17 (Dec 10 2012<sup>1</sup>). It consists of changes, bug fixes or enhancements, some of which appeared in later 3-digit series, and also enhancements which never did, such that the functionality to natively read Illumina's and deCODE's binary file formats.

Version 1.4.0 (April 2008) to 1.18.0/1.19.0 (October 2011) were briefly bundled with Bioconductor.

## 2 Details

### 2.1 Current

**1.19.0.18, April 2013** New uncertain option to `read.snps.chiamo()` for generating uncertain genotypes, and new `read.snps.vcf()` routine. New "IO Suite" vignette (requiring 1000 Genome and HapMap data to run).

### 2.2 Between 1.19.0 and 1.19.0.17

The difference between snpMatrix 1.19.0 and 1.19.0.17 consists of 498 in-tree commits and 385+ out-of-tree commits.

The in-tree commits consists of the following:

- Fixing bugs introduced between 2008 and 2011, by re-analysing the 2007 WTCCC1 data. (see also the out-of-tree commits section). Also examples and internal checks to make sure that bugs are not re-added.
- As a side-effect of the bug fixing effort, a fair number of David Clayton's home-brewed (and some buggy) linear algebra routines were replaced with their R LAPACK and BLAS equivalents. There is a few percents in speed gain.
- Natively read Illumina's EGT, BPM, and CNV-related binary file formats, as well as some of deCODE's.
- Major under-the-hood changes related to link-loaders; A few percents in speed gain, more noticeable in PE (i.e. Windows), less so in ELF/MACH-O (Linux/Mac OS X).

---

<sup>1</sup>As of the first draft of this document.

The bottom of the in-tree commits is `81b60ada308bf1fe90a6f4e5e308cea2a28b118f`, Feb 14 2011. The in-tree commits have been rebased many times, and not necessarily in chronological order.

### 2.2.1 The out-of-tree commits

The out-of-tree commits (385 up to `snpMatrix 1.19.0.17`, December 2012) started on Aug 26 2011, with `73f134d96760f48aef836068a620bc556234a397`, which resurrect the 2007 infra-structure for analysing WTCCC1 data, to track down bugs introduced between 2008 and 2011.

The first version of this document is the 386th.

Many of the out-of-tree commits are out of tree because of special requirements. For example:

- The “China and Chinese Cities” vignette requires Tibetan and Arabic capabilities on the host platform, as well as a cairo-capable R.
- The “Algorithms and Thailand” vignette and the “China and Chinese Cities” vignette requires  $\text{\LaTeX}$  capable of Thai and Chinese respectively.
- The “Regression and Migration” vignette requires the WTCCC1 data.
- The “MHC Subset Preparation” vignette requires the UK AMD data.
- The “snpStats Bug” vignettes obviously requires loading other extra R packages.

## A snpStats 4-digit Series

The “less buggy” `snpStats` 4-digit Series consists of the follow bug fixes, none of which are in the 3-digit series:

6. (Aug 24 2013) first non-(internal)-bug-fix release - upgrade bundled `zlib` from 1.2.5 to 1.2.8 . Note that `snpMatrix` upgraded to `zlib 1.2.8` in May 2013, and to 1.2.7 in Dec 2012, and have additional performance and portability enhancements in the `zlib`-related code.
5. (Mar 28 2013) second bug in Input/Output and conversion of uncertain genotypes.
4. (Nov 19 2012) `ld` statistics from `ld()` (the older `+ld.snps()` in `snpMatrix` is not affected).
3. (Nov 6 2012) `cbind/rbind`
2. (Sep 1 2012) Input/Output and conversion of uncertain genotypes.
1. (Oct 16 2011) Statistical tests plus miscellaneous bugs accumulated between 2008 and 2011.

More details in the “`snpStats` Bug” vignette.