FAQ:

**Q1**. I have successfully created the *bicseq* object using the function *BICseq*, but I got a segmentation fault during the *getBICseg* run.

**A1**. This happens for the BICseq R package prior to version 1.2.0. The reason is that some chromosomes in the *bicseq* object have no read available in the specified BAM files. After removing such chromosomes in your *bicseq* object, the *getBICseg* function should run smoothly. In versions after 1.2.0, an error message will be reported if there are such chromosomes in your *bicseq* object.

**Q2**. I have successfully created the *bicseq* object using the function *BICseq*, but R reported an error message when I call the function *getBICseg*. The error message is like the following

“*… Failed to scan BAM. In addition: Warning message: …. space '1' not in BAM header…*”.

**A2.** This happens because some chromosomes in the *bicseq* object are not in the BAM header. In BICseq after version 1.2.0, an error message will be reported while creating the *bicseq* object if some chromosomes are not in the BAM header. In some cases, this can be due to a mis-specified seqNames parameter: for example, if the BAM header specifies chromosomes named ‘chr1’, ‘chr2’, and so on, then the seqNames vector must also be a text vector of ‘chr1’, ‘chr2’, … and *not* ‘1’, ‘2’, … .

**Q3.** The BICseq package requires the case and control have the same bias. What if my data does not satisfy this condition?

**A3.** We have developed a new version of BICseq which does not require such a condition. This will be available soon to the public.

**Q4.** Which bin size should I use for CNV detection?

**A4.** BIC-seq does not care too much about the bin size. Larger bin size just makes the computation faster. You may just use our default value (100 bp). If you want to increase the detection resolution, you may use smaller bin sizes (e.g. 10 bp or smaller).

**Q5.** I got a loading error.

**A5.** This happens when you load BICseq in newer version of R (e.g. 2.15.1). This bug is fixed in BICseq version 1.2.0.