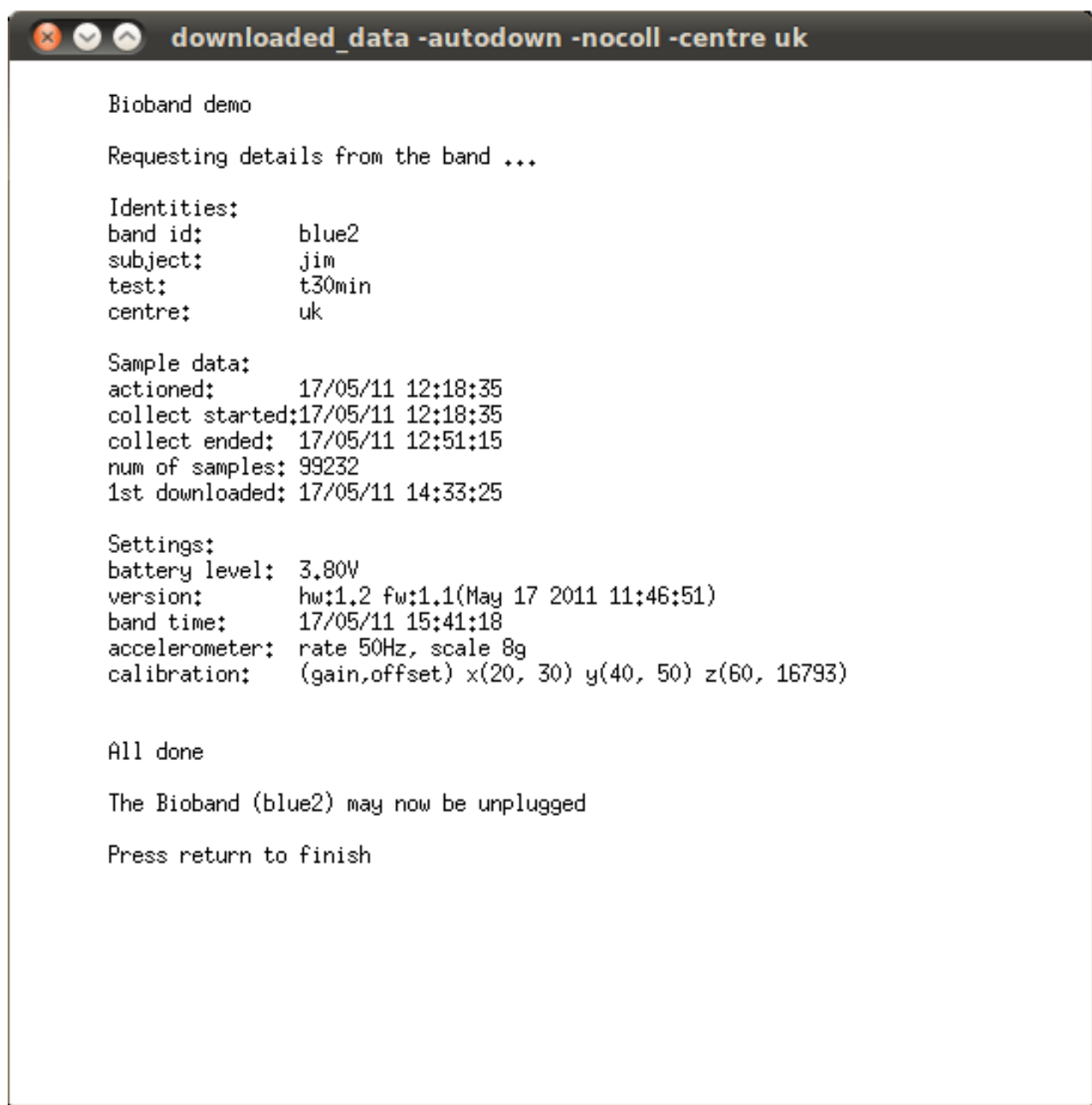# Quickstart Guide

Assuming a configured system (see Bioband_flashing_and_PC_setup_guide.pdf), there are two demonstration programs (demo, mrc) that can be used to access data on the Bioband. Both are located within the Bioband/PC directory tree of the installed code.

Demo

The demo program is designed to show how a simple workflow of data download and program for the next collection cycle might be encoded using the Bioband API methods

The following is example output from demo running in an xterm on Ubuntu (Linux):

```
downloaded_data -autodown -nocoll -centre uk

    Bioband demo

    Requesting details from the band ...

    Identities:
    band id:        blue2
    subject:        jim
    test:           t30min
    centre:         uk

    Sample data:
    actioned:       17/05/11 12:18:35
    collect started:17/05/11 12:18:35
    collect ended:  17/05/11 12:51:15
    num of samples: 99232
    1st downloaded: 17/05/11 14:33:25

    Settings:
    battery level:  3.80V
    version:        hw:1.2 fw:1.1(May 17 2011 11:46:51)
    band time:      17/05/11 15:41:18
    accelerometer:  rate 50Hz, scale 8g
    calibration:    (gain,offset) x(20, 30) y(40, 50) z(60, 16793)


    All done

    The Bioband (blue2) may now be unplugged

    Press return to finish
```

It has been invoked using the -autodown and -nocoll options

The demo code can be configured to manually question or automatically download a raw file from a band when it is connected (only if the raw file hasn't been downloaded before, given by the 1st downloaded time).

```
downloaded_data -autodown -nocoll -centre uk

        Requesting details from the band ...

        Identities:
        band id:        black1
        subject:        jim
        test:           t6hrs
        centre:         uk

        Sample data:
        actioned:       16/05/11 14:42:54
        collect started:16/05/11 14:42:54
        collect ended:  16/05/11 21:19:33
        num of samples: 1188045
        1st downloaded: not set

        Settings:
        battery level:  3.73V
        version:        hw:1.2 fw:1.1(May 16 2011 14:09:21)
        band time:      17/05/11 15:36:50
        accelerometer:  rate 50Hz, scale 8g
        calibration:    (gain,offset) x(10, 20) y(30, 40) z(50, 60)

        0%.........10%.........20%.........30%.........40%.........50%.........60%........
.70%.........80%.........90%.........100%

        num samples received:    1188044
        expected total:          1188044

        Successfully downloaded raw file: /home/mrc/bioband2/downloaded_data/black1_jim_t6
hrs_uk.raw

        All done

        The Bioband (black1) may now be unplugged

        Press return to finish
```
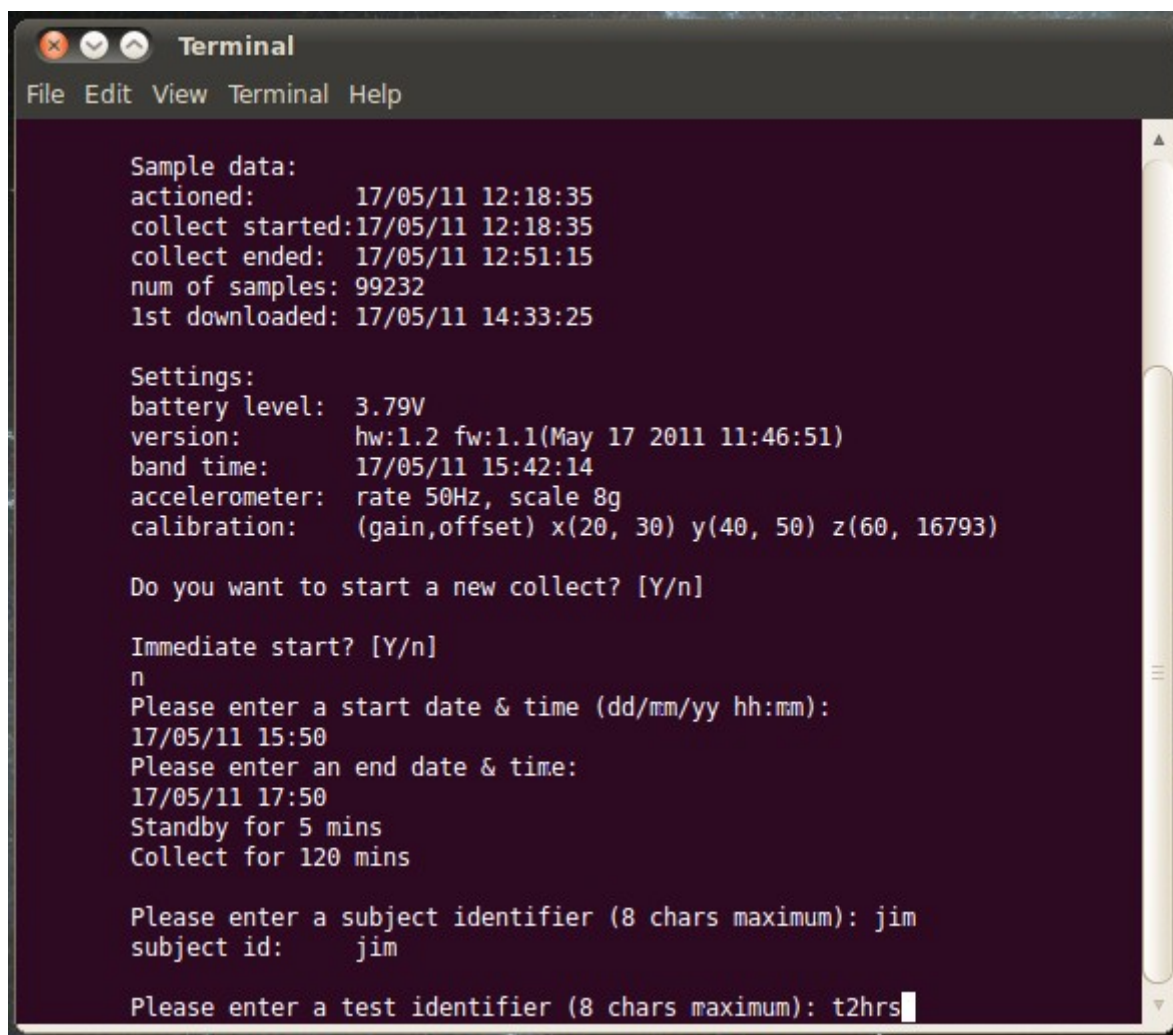
Example output showing the successful download of a short raw file from the Bioband, the automatic naming of the raw file and placing into a specified download directory.

The demo code can also be configured to ask questions relating to starting a new collection, in case a quick turnaround of the band is needed

```
    Terminal
File  Edit  View  Terminal  Help

    Sample data:
    actioned:        17/05/11 12:18:35
    collect started:17/05/11 12:18:35
    collect ended:   17/05/11 12:51:15
    num of samples: 99232
    1st downloaded: 17/05/11 14:33:25

    Settings:
    battery level:  3.79V
    version:        hw:1.2 fw:1.1(May 17 2011 11:46:51)
    band time:      17/05/11 15:42:14
    accelerometer:  rate 50Hz, scale 8g
    calibration:    (gain,offset) x(20, 30) y(40, 50) z(60, 16793)

    Do you want to start a new collect? [Y/n]

    Immediate start? [Y/n]
    n
    Please enter a start date & time (dd/mm/yy hh:mm):
    17/05/11 15:50
    Please enter an end date & time:
    17/05/11 17:50
    Standby for 5 mins
    Collect for 120 mins

    Please enter a subject identifier (8 chars maximum): jim
    subject id:     jim

    Please enter a test identifier (8 chars maximum): t2hrs
```

The example above, being manually run (./demo) in a normal terminal, shows a collection being configured not for an immediate start but for a point of time in the future. The user is asked to enter subject and test identifiers, also centre id if not specified already on the command line.

These demo program actions are configured by the optional command line parameters

-snum <serial number>	specific Bioband serial number to connect to
-autodown	always download if data not already downloaded
-downdir <dir_path>	directory to place the download files in
-nocoll	don't ask collect question
-centre <id>	set the centre id to use for any sample collection

MRC

The mrc program is the original code used for development and testing of the band, given its use it has grown to provide a range of requests, mainly for development, using the Bioband APIs to manipulate the device at a individual element level compared to Demo

The main useful commands are:

```
./mrc -p 5 -l 5 -sj jim -tst test1 -cen uk
```

This would start a collect for 5 minutes after a pause for 5 minutes, labelling the data with subject(jim), test(test1) and centre id(uk)

```
./mrc -uraw
```

This can be used to download the raw file from the band into the current directory, naming the file according to the band, subject, test and centre ids.

Alternatively if a specific filename is required

```
./mrc -raw collection2.raw
```

The raw options can be used with rsum, rbl, rtl & rcsv options if wish to produce particular detail files at the time of download from the Bioband.

```
./mrc -rsum -rbl black1_battery -raw collection2.raw
```

Offline working

The mrc program can also be used, when not connected to a band, to extract details from a raw file

For example

```
./mrc -rsum -rbl black1_battery -rtl black1_battery -rcsv black1_battery -fraw
black1_jim_t6hrs_uk.raw
```

The above command will output a summary, showing what is in raw file black1_jim_t6hrs_uk.raw. It will also output battery, temperature and csv file details into separate files as named.

Note the -fraw, -raw or -uraw commands must come at the end of the command line since the invocation of the command causes the processing of the raw file

The full set of mrc commands are shown below:

./mrc ?
MRC
Version: May 16 2011 14:37:28

Cmd line params & default values:
Raw file command options
     -raw [filename] read raw image of data from band to file or screen
     -uraw read raw image from band and produce a uniquely named raw file
     -fraw <filename> read raw image of band data from file
     -rbl <filename> store raw battery levels to file
     -rtl <filename> store raw temperature levels to file
     -rdbg <filename> store raw debug to file
     -rcsv <filename> store csv output to file
     -uall create uniquely named files for bl,tl,dbg & csv from band
Band sampling command options
     -l collection time (in mins)
     -p standby time (in mins)
     -z set mode (0 = real, 1 = debug)
     -sj set subject id (max 8 chars)
     -tst set test id (max 8 chars)
     -cen set centre id (max 2 chars)
Other band commands
     -id set band id (max 8 chars)
     -bl read all the stored battery level measurements
     -tl read all the stored temperature level measurements
     -gdt current device time
     -gfdt get first download time
     -ef erase flash (remember this wipes id and subject as well)
     -gi get band id
     -gsj get subject id
     -gt get test id
     -gcen get centre id
     -gsb get stored samples size in bytes
     -gsp get stored samples size in pages
     -rp <page number (between 1 and value given by -gsp)> read page number
     -gbl get current battery level
     -gv get the versions
     -sac <rate 50,100,400,1000> <scale 2,4,8> set accelerometer config
     -rac read current accelerometer data rate and g scale
     -raf read accelerometer data rate and g scale for previous run
     -scal set calibration data, 2 * unsigned values (gain & offset) for each axis
     -gts go to sleep
Diag commands
     -bb read bad block info
     -nobkp reset bkp domain on band
     -bug read dbg info from band