

## Common Equipment & Microscopes Scheduling



A new Electronic calendar version has been installed. New features include:

### ***Adding appointment to your Outlook calendar***

- Step 1.** Schedule an appointment.
- Step 2.** Return to View Calendar.
- Step 3.** Click on "Add to Outlook."
- Step 4.** Open icpop.ics file into Outlook calendar or Select Open.
- Step 5.** For multiple appointments for the same equipment calendar, "Cut & Paste" event into one calendar or Overlay Calendars (until another way to synchronize BrownBear iCal calendars in the Outlook Program is determined).

### ***Finding which calendars do not already have an event scheduled for a specified date and time***

- Step 1.** Open a calendar group (eg. Microscopy or PCR).
- Step 2.** Go to the bottom of the calendar.
- Step 3.** Click on "Time Slot" to search in selected calendars.
- Step 4.** Select calendars to compare.

***In the future, email reminders should be available once we understand how to code the BrownBear iCal program to interact with Outlook.***

## Epigenetics Solexa Sequencing Core

On the 9th floor, tucked away in S9.8229, is the Epigenetics Solexa Sequencing Core run by Louis Ramagli. It has been in operation for about a year. The core is based on Next-Gen Sequencing of large numbers of "short" fragments on an Illumina Genome Analyzer II. It can sequence your Chromatin Immunoprecipitates (ChIP) DNA, nucleosome DNA, methylated DNA, mRNA, or microRNA samples and align it to a genome of interest. This is a good complement or replacement of ChIP-CHIP or to other techniques.

The standard sequencing length is 36 bases, but the GA II can sequence up to 72 bases on single read or up to 104 bases using a paired-end sequencing approach. A normal 36 base single read sequencing run produces about 10 million tags or 140 million bases of align sequences. A paired-end run will produce about twice that amount. Human, mouse, yeast and *Drosophila* are currently supported and soon monkey will be as well. Don't see your species? If the genome is available, it can be obtained.

Contact Dr. Ramagli at [Iramagli@mdanderson.org](mailto:Iramagli@mdanderson.org) or 713-834-6299 if you have any questions, or go to the core's website for frequently asked questions:

<http://www.mdanderson.org/education-and-research/resources-for-professionals/scientific-resources/core-facilities-and-services/solexa-sequencing-core/index.html>