Updates to BiocFileCache, AnnotationHub, and ExperimentHub default caching location

What changed?

Instead of using

```
Rappdirs::user_cache_dir
```

We are changing to use

```
tools::R_user_dir
```

What happens to my cache?

If you have an old cache location populated in Bioc 3.13 you will receive a deprecation warning and a URL pointing to a help section in the appropriate vignette

```
> bfc  = BiocFileCache()

Warning message:

In BiocFileCache() :

  DEPRECATION: As of BiocFileCache (>1.15.1), default caching location has changed.

  Problematic cache: /home/shepherd/.cache/BiocFileCache

  See
https://www.bioconductor.org/packages/devel/bioc/vignettes/BiocFileCache/inst/doc/BiocFileCache.html#default-caching-location-update
```

In Bioc 3.14, this warning will become an ERROR and not allow you to proceed.

Package specific caches are not affected!

This is only for the default BiocFileCache location. If you specified a package specific cache it will not be affect

```
> cache =  rappdirs::user_cache_dir(appname="biomaRt")
> BiocFileCache(cache)
class: BiocFileCache
bfccache: ~/.cache/biomaRt
bfccount: 14
For more information see: bfcinfo() or bfcquery()
```

If you use the designated system environment variables, this check is ignored!

Like AnnotationHub and ExperimentHub, BiocFileCache now has an environment variable that can control the default caching location. This can be set to any location, but if it is set to the old location, you will not get the deprecation warning and can continue using the old location.

BFC_CACHE

ANNOTATION_HUB_CACHE

EXPERIMENT_HUB_CACHE