

Version Control with Git & GitHub

UBC

6 August 2014

Kim Gilbert

What is Git?

Version control software



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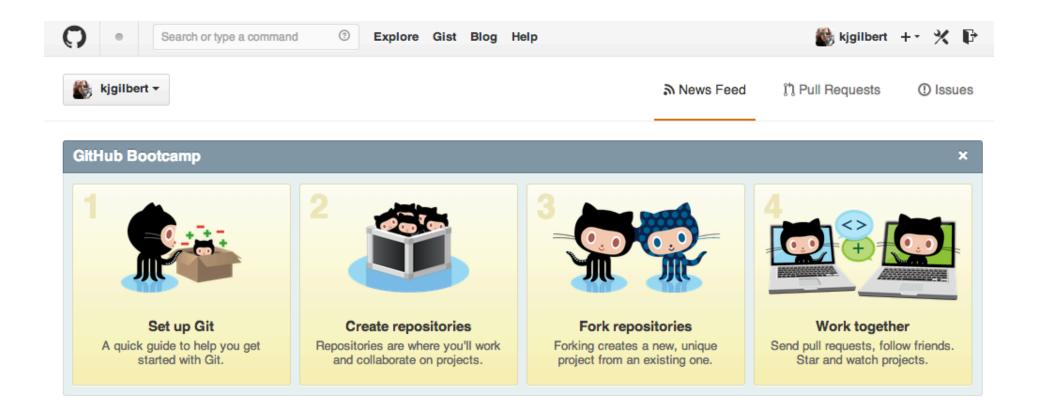
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a latifolia_ABC_ms_12132011.docx	Dec 12, 2011, 11:54 PM	2 MB	Microsument
atifolia_ABC_ms_12132011_PDF.docx	Dec 12, 2011, 11:55 PM	2 MB	Microsument
a latifolia_ABC_ms_12122011_SRK.docx	Dec 13, 2011, 8:41 AM	1.4 MB	Microsument
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a latifolia_ABC_ms_12132011_KJG.docx	Dec 13, 2011, 10:03 PM	1.7 MB	Microsument
atifolia_ABC_ms_12142011_KJG.docx	Dec 14, 2011, 10:40 AM	1.6 MB	Microsument

Better version control

- GitHub is an online repository-based server
 - Collaborate
 - Review/manage code
 - Open source/private projects

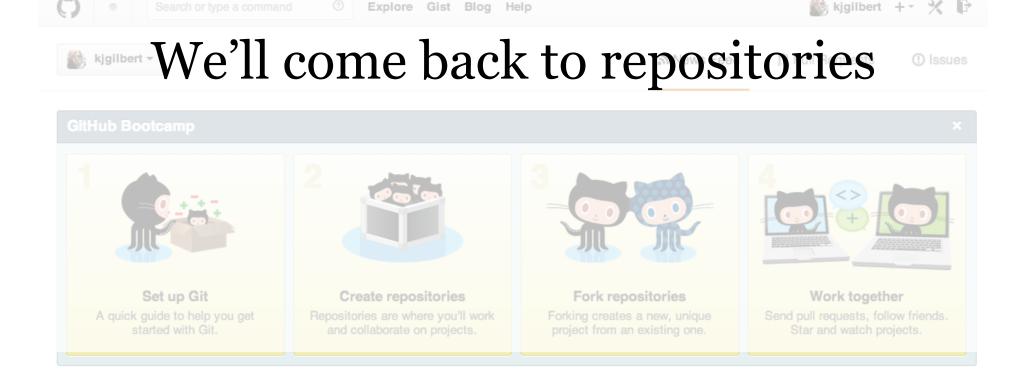
Better version control

GitHub is an online repository-based server



Better version control

• GitHub is an online repository-based server



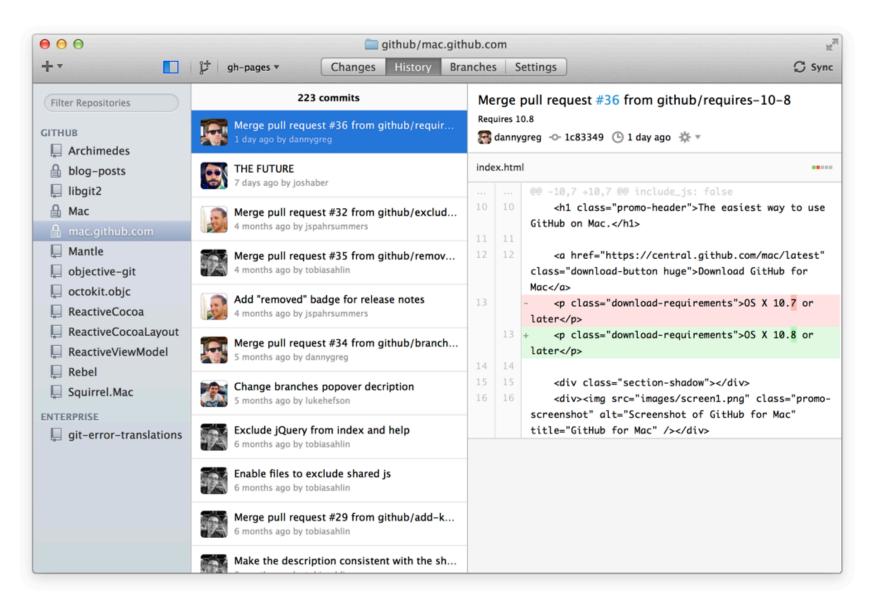
Git & GitHub

- Git is a command line tool
- But if you prefer a GUI, there is one

The easiest way to use GitHub on Mac



Requires OS X 10.8 or later. Learn more

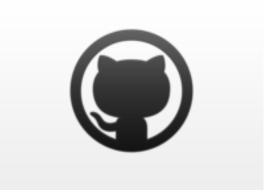


Git & GitHub

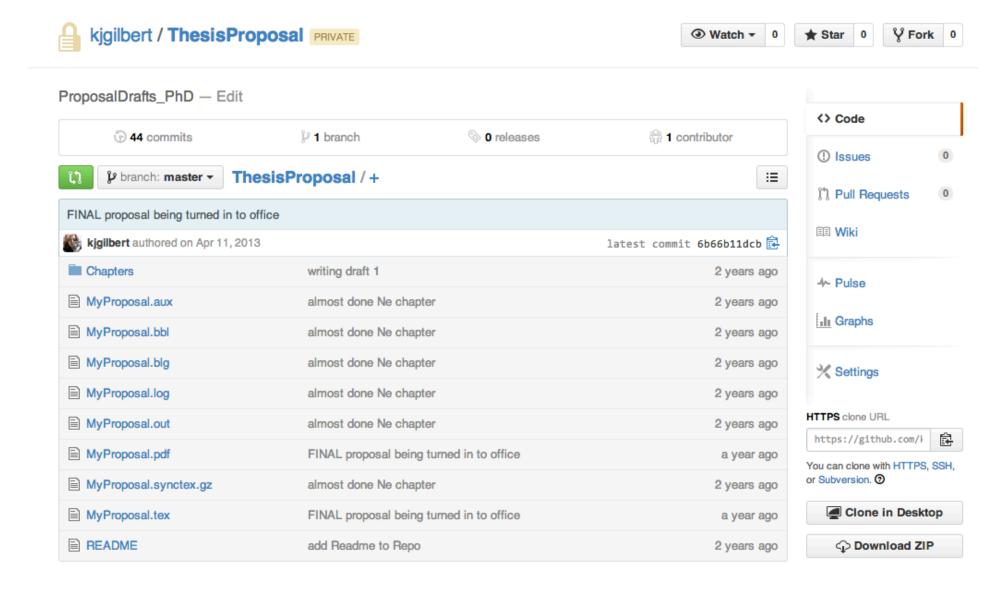
- Git is a command line tool
- GitHub is the online server
 - There are other online repositories you could use
 - e.g. Bitbucket
- Git lets you 'link' your local files with those stored online

How?

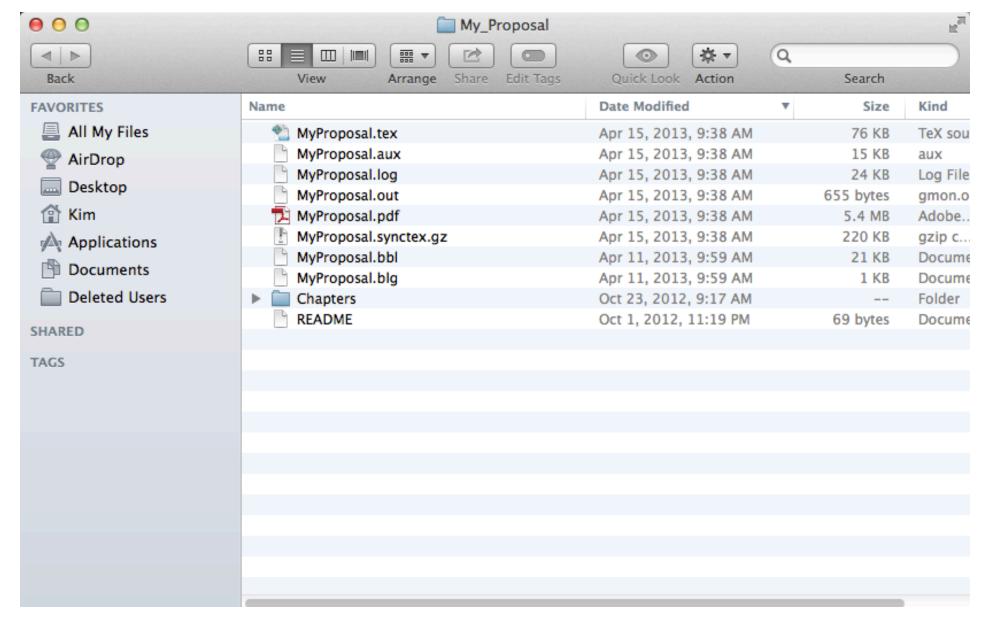
- Local directory
 - Have all your files here
 - Edit them, add/delete them
- Online repository
 - Mirrors local directory
 - Stores history of changes you've made to local
 - Allows sharing/collaborating with others

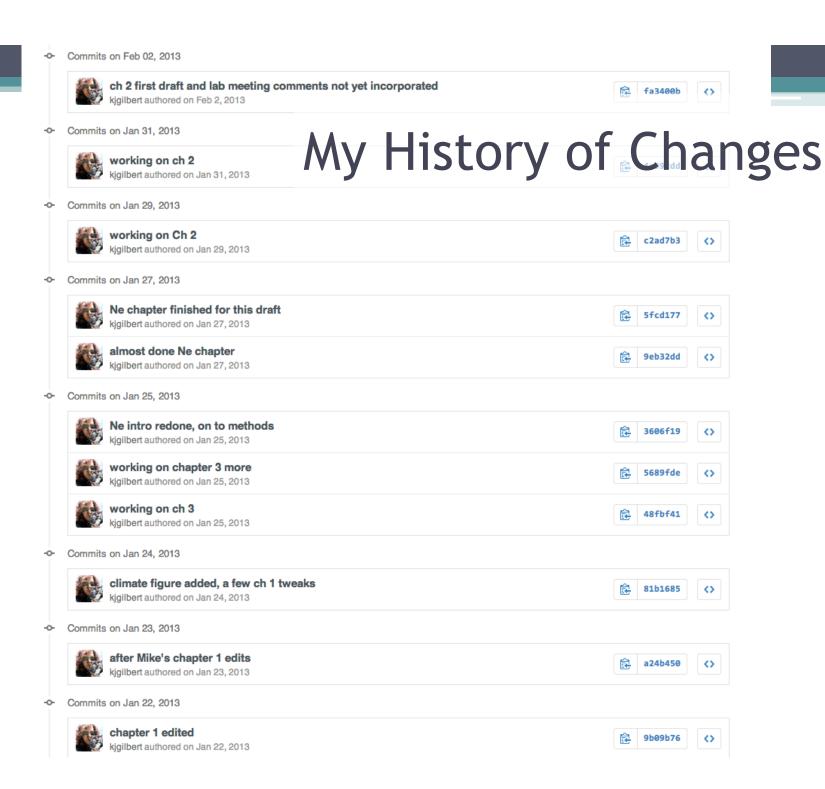


The Online Repository



My Local Directory





102	100	
103		-Though it is well-known that lodgepole pine exhibits local adaptation \citep{Illingworth:1981tp,Ying:1985vk}, the
		genetic basis of this ability is not well understood. How can such a long-lived organism (life spans average a
		century but can range up to 300 years, \citealt{Knowles:1983vl}) with high gene flow (wind-dispersed pollen) be
		capable of such fine scale adaptation? This question is of scientific interest, but also in application, as the lodgepole pine is a major timber resource of the Pacific northwest. Choosing trees that will be best adapted to
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105		 -A current project in the department of forestry at UBC, \textsc{AdapTree}, aims to uncover SNP markers conferring adaptation to different climatic conditions in terms of temperature and precipitation for just this purpose:
		choosing genetically well-adapted trees for reforestation. By sequencing and phenotyping seedlings collected from
		across the range of the species and grown in different climate conditions, genome-wise association studies (GWAS)
		are being conducted to identify outlier SNPs as candidates for predicting local adaptation. My aim is to ground-
		truth these findings and establish if such putatively adaptive SNPs truly associate with higher fitness. If
		confirmed as adaptive, my results would support further application of these identification methods in other scenarios. However, there are several reasons that merit this confirmation.
	103	+A current project in the department of forestry at UBC, \textsc{AdapTree}, aims to uncover SNP markers conferring
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		further application of these identification methods in other scenarios. By sequencing and phenotyping seedlings collected from across the range of the species and grown in different climate conditions, \textsc{AdapTree} is
		conducting genome-wise association studies (GWAS) to identify outlier SNPs as candidates for predicting local
		adaptation. These loci are classified as outliers when \emph{F}\$_{ST}\$ is calculated at loci across the genome, and
		some loci show values significantly greater than other locations. This uncovers SNP loci that have differentiated
		among populations geographically, therefore indicating genes that have either been selceted for, or drifted to fixation. There are thus several reasons that these procedures merit confirmation.
106	104	Tracton. There are that several reasons that these procedures ment to third matton.
107		-First, is that measuring fitness in long-lived organisms is difficult. Lodgepole pine has a long lifespan over which
		many phenotypic changes may occur, of which only some may be predicted from younger age. The GWAS study
		\textsc{AdapTree} is conducting compares first and second year phenotypes to genome scans to identify SNPs of
		interest. Seedling phenotypes may not correlate to adult phenotypes for the traits of interest in climate
	105	adaptation, resulting in incorrect associations being made between genotype and phenotype. +First, is that measuring fitness in long-lived organisms is difficult. Lodgepole pine has a long lifespan over which
	100	many phenotypic changes may occur, of which only some may be predicted from younger age. The GWAS study
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		interest. There is the potential that seedling phenotypes may not correlate to adult phenotypes for the traits of
100	106	interest in climate adaptation, resulting in incorrect associations being made between genotype and phenotype.
108	106	Second, outlier SNPs can exist for different biological reasons, and their selection can be done in several ways.
103	107	This may result in incorrect identification of SNPs believed to convey adaptation, termed false positives. Neutral
		demographic processes, such as allele surfing (Klopfstein et al. 2006) %% % Klopfstein S, Currat M, Excoffier L
		(2006). The fate of mutations surfing on the wave of a range expansion. Mol Biol Evol 23: 4820490.
	108	+%%CITATION
110	109	can result in clines of allele frequency change that are equally characteristic of selection when they occur across

Browse code

Show diff stats

1 parent d7fa533 commit e57258a3377e36f7a6239224e5b375f0f18fe5dc

<>

(1)

kjgilbert authored on Jun 1

Showing 1 changed file with 11 additions and 9 deletions.

```
20 R/QstFstComp.R
                                                                                                                           View
   盘
           @@ -51,6 +51,8 @@
 51
      51
                           which works for either balanced or unbalanced sampling designs
 53
      53
            #'
           +#' @param dam.offspring.relatedness
 54
      56
            #' @param output whether to output full or concise results, see details below
 55
      57
      58
            #' @return
 56
   盘
           @@ -102,7 +104,7 @@
102 104
103
     105
104
     106
           -QstFstComp <- function(fst.dat, qst.dat, numpops, nsim=1000, AFLP=FALSE, breeding.design, output="concise")
     107
           +QstFstComp <- function(fst.dat, qst.dat, numpops, nsim=1000, AFLP=FALSE, breeding.design, dam.offspring.relatedness=0.
     108
106
              if(missing(fst.dat)) stop("Genotypic data must be provided.")
     109
107
     110
              if(missing(qst.dat)) stop("Phenotypic data must be provided.")
108
           @@ -123,7 +125,7 @@ OstFstComp <- function(fst.dat, qst.dat, numpops, nsim=1000, AFLP=FALSE, breedin
123 125
                           qst.MS <- MeanSq.unbalanced.dam(qst.dat)</pre>
124
     126
                           qst.obs <- QSTfromDamModel(qst.MS$MSpops,qst.MS$MSdams,qst.MS$MSwithin,qst.MS$n0prime,qst.MS$n0,qst.MS$
                           mean.trait.value <- mean(qst.dat[,3], na.rm=TRUE) # this takes the mean of all trait values across all
125
     127
                           Va <- 4*(gst.MS$MSdams-gst.MS$MSwithin)/gst.MS$n0
     128
                           Va <- 1/dam.offspring.relatedness*(qst.MS$MSdams-qst.MS$MSwithin)/qst.MS$n0
                                                   # if Va includes negative values, the distribution is truncated to zero
127
     129
                           if(Va < 0){Va <- 0}
                   CVa <- sgrt(Va)/mean.trait.value * 100
128
     130
129
     131
```

Contributions



မှ Unfollow



Rich FitzJohn richfitz

Sydney, NSW

Doined on Mar 20, 2012

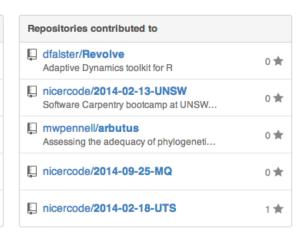
30 28 17
Followers Starred Following

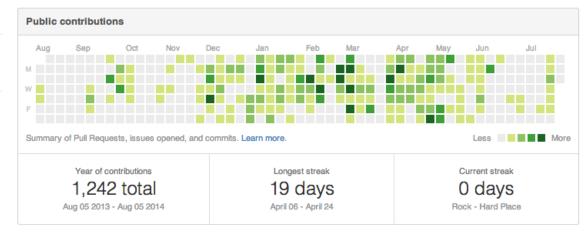
Popular repositories

☐ diversitree diversitree: comparative phylogenetic a...
☐ forest
New Phylogenetics Data Structures in R
☐ wood
How much of the world is woody?
☐ rodeint
Interface to boost's odeint-v2
☐ sowsear
Frictionless literate programming: gener...

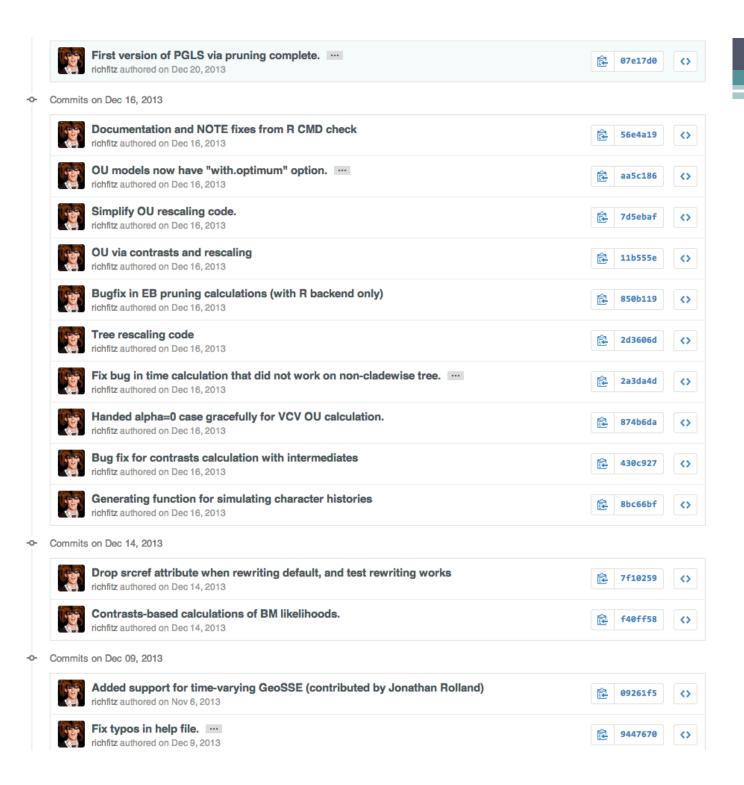
15 ★

Repositories



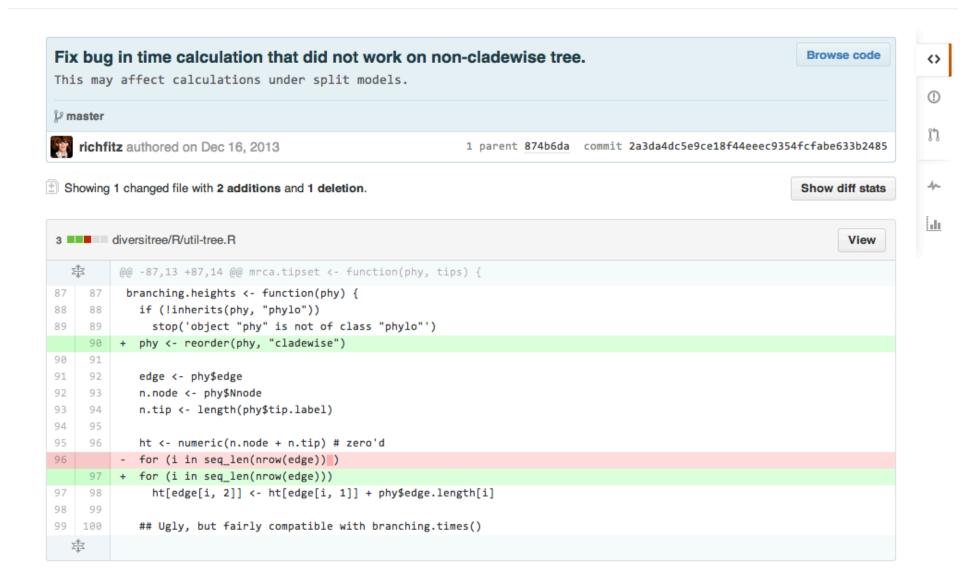












Hands-on

Recap

- Making a repository
- Pulling/pushing
- Forking
- .gitignore file

Recap - Making a repository

- On GitHub: create a new Repo
- Locally:
 - Create your directory and cd into it
 - git init
 - touch README
 - git add README
 - □ git commit −m "first commit"
 - git status (just to check, can be done at any time)
 - git remote add origin https://github.com/username/ repository_name.git (done only the first time)
 - git push -u origin master (or just git push)

Recap - Pushing & Pulling

- After making some edits locally in your directory:
 - *git add filename* (or *git add* . –*A* to add everything)
 - git commit -m "message to yourself about file"
 - You can do git status to see the status of your files ready for pushing
 - git push
 - If you're collaborating:
 - *git pull* will bring any changes made by others in the repo into your local directory
 - · This is where some errors occur if there are merge difficulties

Recap - Forking

- Someone else has a repo you want to use or contribute to
- You can fork it into your own account to make a copy
 - Do this online in github by going to the repo you want and clicking Fork in top tight corner
 - Clone it locally onto your computer
 - See https://help.github.com/articles/fork-a-repo for all of the details
 - Update your copy to match original with *git fetch* upstream

Recap - .gitignore file

- Dot in the name means it is an invisible file, i.e. you cannot see it in your Finder window
- The files listed within the .gitignore file are ignored and never pushed online to the GitHub repository
 - Create with touch .gitignore
 - □ Open with open −e .gitignore
 - Then add in the files you want ignored