

# Submission guide for the GitHub web interface

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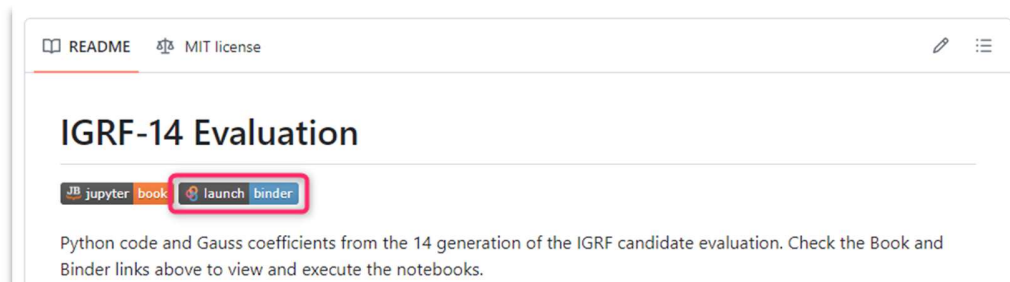
**Date:** 2024-03-13

**Version:** 2

## Validate candidate models with the notebooks (optional)

*The IGRF14eval repository contains simple validation and visualization notebooks that allow teams to compare their candidate models with the previous IGRF and candidate models already submitted by other teams. This way, teams can check the file format of the candidate models and detect possibly unintended features in the candidate models before the submission.*

1. Go to the IGRF14eval repository on the IAGA-VMOD GitHub organization at <https://github.com/IAGA-VMOD/IGRF14eval>.
2. There are two options for running the validation notebooks—local (a) and remote (b):
  - a. Download the repository and install the required Python packages using the instructions in the **Local development** section of the README. Candidate model files can now be added to `/data/coefficients/<model-type>` in the downloaded repository, and the notebooks in `/notebooks/` can be started on the local machine.
  - b. Click on **launch binder** to start a remote JupyterLab session of the repository on Binder.

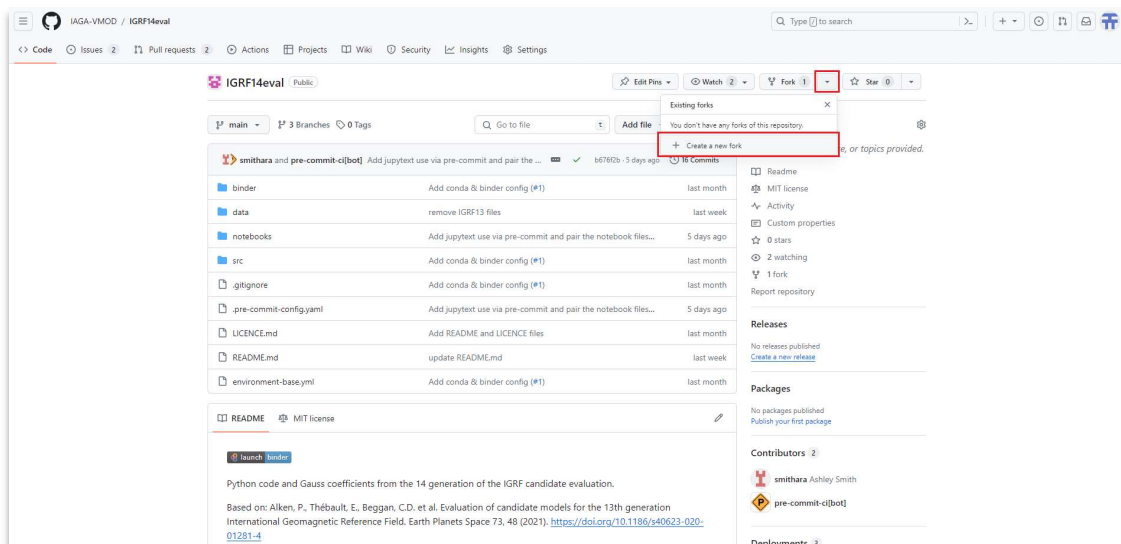


Within JupyterLab (it may take a few minutes to launch), candidate models can be uploaded to `/data/coefficients/<model-type>` and read into the validation notebooks in `/notebooks/`. Note that any changes only affect the image of the repository on Binder and will be discarded when the JupyterLab session is closed or terminated.

## Fork the IGRF14eval repository

A fork is a new repository in a personal GitHub account that shares code and visibility settings with the original repository. Forking allows to change the repository code, i.e., by uploading the coefficients files, without affecting the original repository.

1. Go to the IGRF14eval repository on the IAGA-VMOD GitHub organization at <https://github.com/IAGA-VMOD/IGRF14eval> and log in to GitHub.
2. Create a new fork for the IGRF14eval repository by clicking the black arrow next to **Fork** in the upper right corner and **Create a new fork**.



3. Ensure that the fork will be created in your personal account. There is no need to change any of the default settings. Click **Create fork**.

## Create a new fork

A *fork* is a copy of a repository. Forking a repository allows you to freely experiment with changes without affecting the original project. [View existing forks.](#)

Required fields are marked with an asterisk (\*).

Owner \*      Repository name \*

/

✔ IGRF14eval is available.

By default, forks are named the same as their upstream repository. You can customize the name to distinguish it further.

Description (optional)

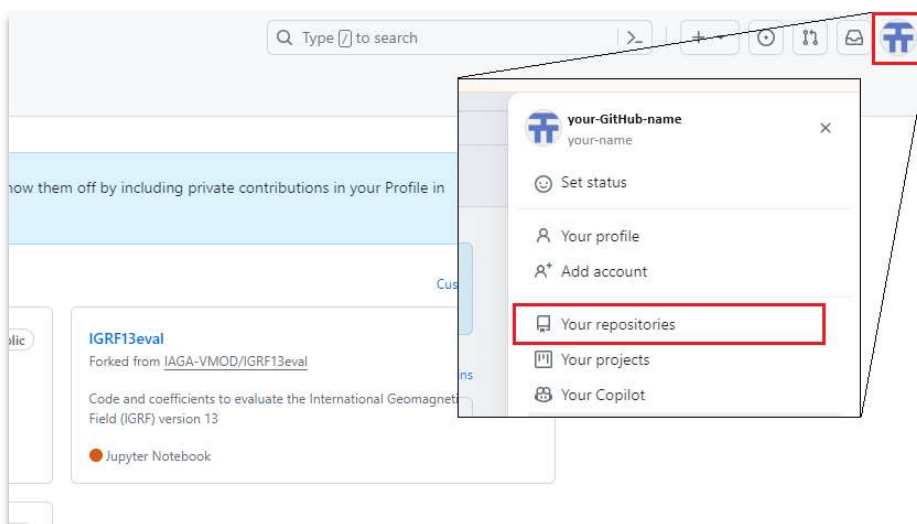
Copy the `main` branch only  
Contribute back to IAGA-VMOD/IGRF14eval by adding your own branch. [Learn more.](#)

ⓘ You are creating a fork in your personal account.

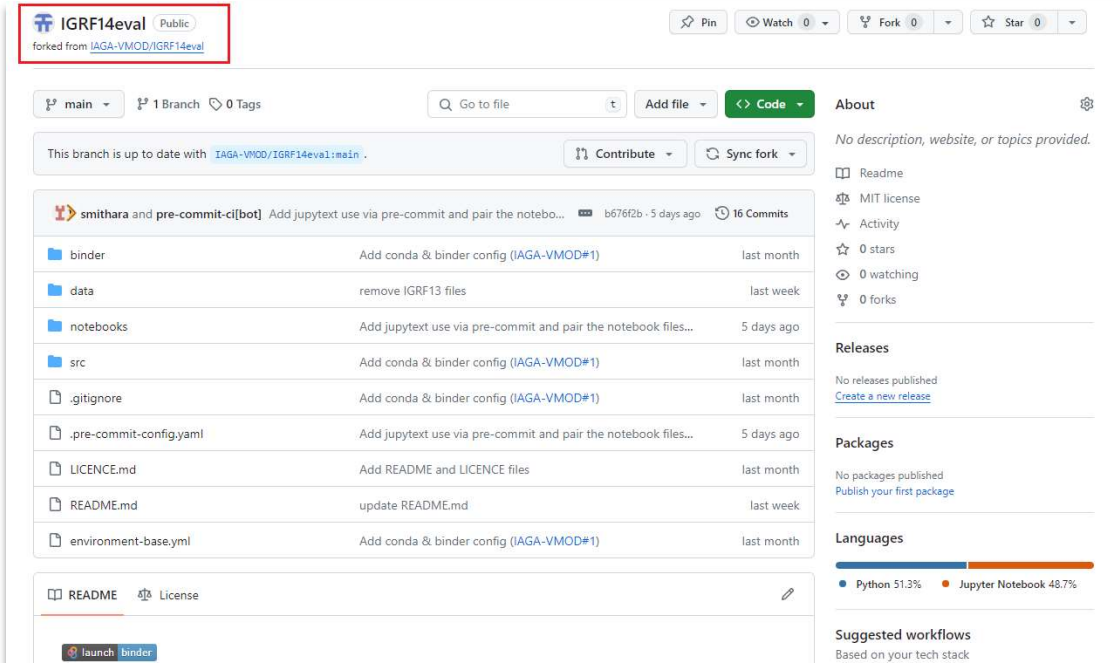
## Create a new branch and upload your files

*It is good practice to create new branches for modifications to the repository. Therefore, you should upload your submission files to a new branch instead of changing the main branch.*

4. Click on your profile logo in the top right corner and **Your repositories** to open the list of your repositories.



5. Find the forked IGRF14eval among the listed repositories and click to open. It should indicate in the upper left corner that it is a forked repository.

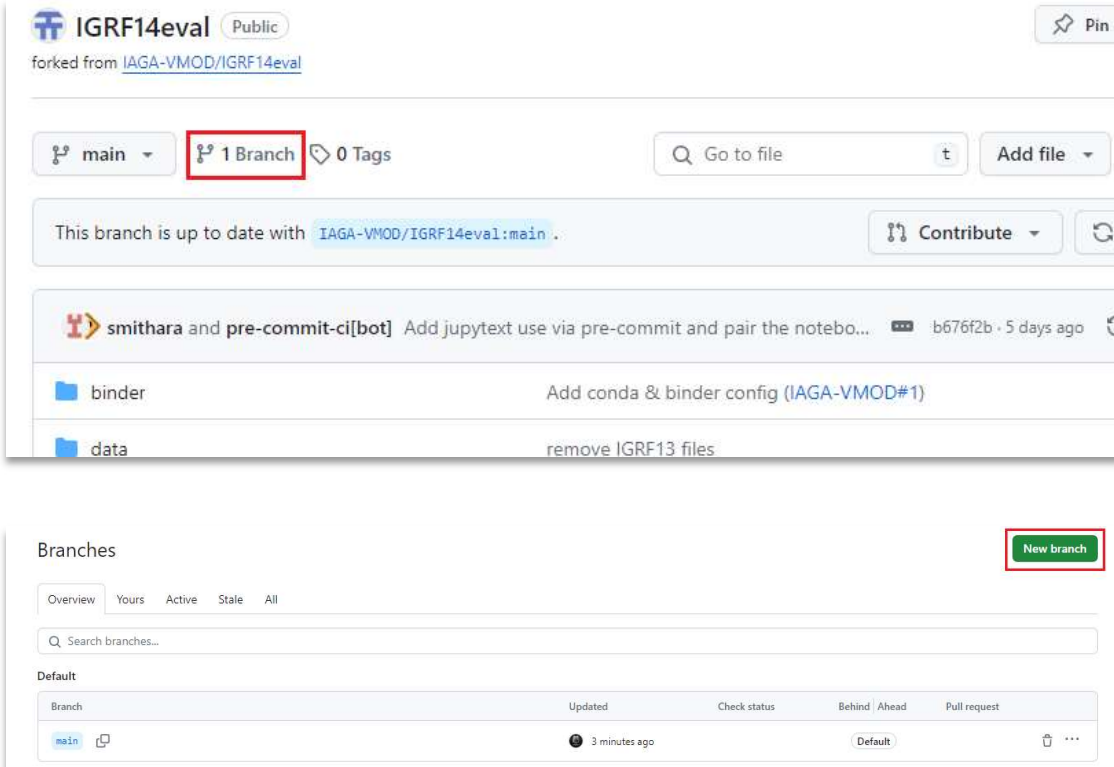


The screenshot shows the GitHub repository page for **IGRF14eval**. The repository is marked as "Public" and "forked from IAGA-VMOD/IGRF14eval". The upper left corner of the repository header is highlighted with a red box, showing the fork icon and the text "IGRF14eval" and "forked from IAGA-VMOD/IGRF14eval". The repository has 1 branch and 0 tags. The main branch is `main`. The repository is up to date with the parent repository. The repository contains 16 commits, with the most recent commit by `smithara` and `pre-commit-ci[bot]` 5 days ago. The repository contains the following files and folders:

File/Folder	Description	Last Commit
<code>binder</code>	Add conda & binder config (IAGA-VMOD#1)	last month
<code>data</code>	remove IGRF13 files	last week
<code>notebooks</code>	Add jupyter text use via pre-commit and pair the notebook files...	5 days ago
<code>src</code>	Add conda & binder config (IAGA-VMOD#1)	last month
<code>.gitignore</code>	Add conda & binder config (IAGA-VMOD#1)	last month
<code>.pre-commit-config.yaml</code>	Add jupyter text use via pre-commit and pair the notebook files...	5 days ago
<code>LICENCE.md</code>	Add README and LICENCE files	last month
<code>README.md</code>	update README.md	last week
<code>environment-base.yml</code>	Add conda & binder config (IAGA-VMOD#1)	last month

The repository also has a `README` and `License` section. The repository is also available on Binder. The right sidebar shows the repository's activity, including a Readme, MIT license, and 0 stars, 0 watching, and 0 forks. The repository also has a "Releases" section with no releases published and a "Packages" section with no packages published. The repository also has a "Languages" section showing Python (51.3%) and Jupyter Notebook (48.7%). The repository also has a "Suggested workflows" section based on the tech stack.

6. Create a new branch by clicking on **Branch** in the upper left corner of the IGRF14eval repository and then **Create branch** in the upper right corner.



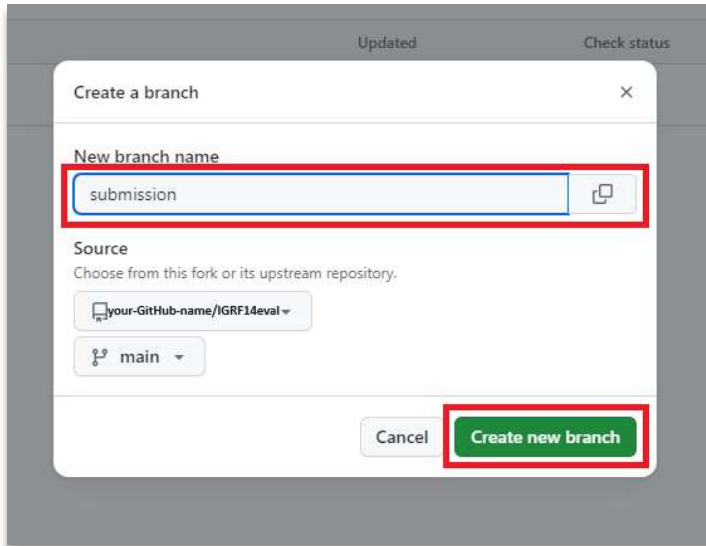
The screenshot shows the GitHub repository page for **IGRF14eval**. The repository is marked as "Public" and "forked from IAGA-VMOD/IGRF14eval". The upper left corner of the repository header is highlighted with a red box, showing the fork icon and the text "IGRF14eval" and "forked from IAGA-VMOD/IGRF14eval". The repository has 1 branch and 0 tags. The main branch is `main`. The repository is up to date with the parent repository. The repository contains 16 commits, with the most recent commit by `smithara` and `pre-commit-ci[bot]` 5 days ago. The repository contains the following files and folders:

File/Folder	Description
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<code>data</code>	remove IGRF13 files

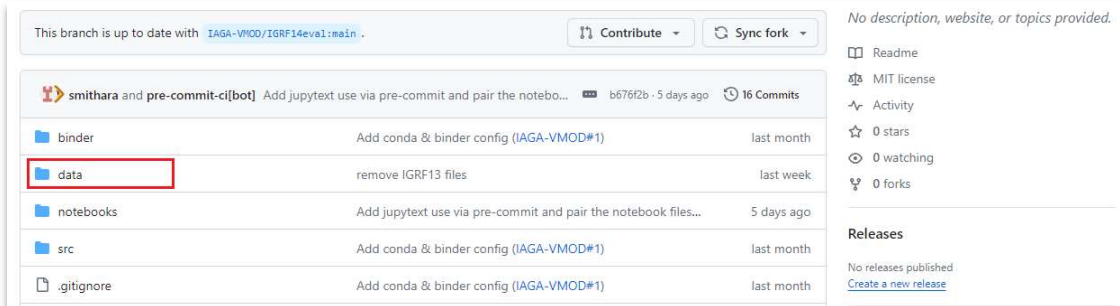
The repository also has a `README` and `License` section. The repository is also available on Binder. The right sidebar shows the repository's activity, including a Readme, MIT license, and 0 stars, 0 watching, and 0 forks. The repository also has a "Releases" section with no releases published and a "Packages" section with no packages published. The repository also has a "Languages" section showing Python (51.3%) and Jupyter Notebook (48.7%). The repository also has a "Suggested workflows" section based on the tech stack.

The screenshot also shows the "Branches" section of the repository. The "Branches" section is highlighted with a red box. The "Branches" section shows the "main" branch and a "New branch" button. The "New branch" button is highlighted with a red box.

- Call the new branch "submission- $\langle$ your-insitute $\rangle$ ," replacing " $\langle$ your-institute $\rangle$ " with the name of your institute, e.g., "submission-bgs,". Then, click **Create new branch**, which adds the submission branch to the list of branches.

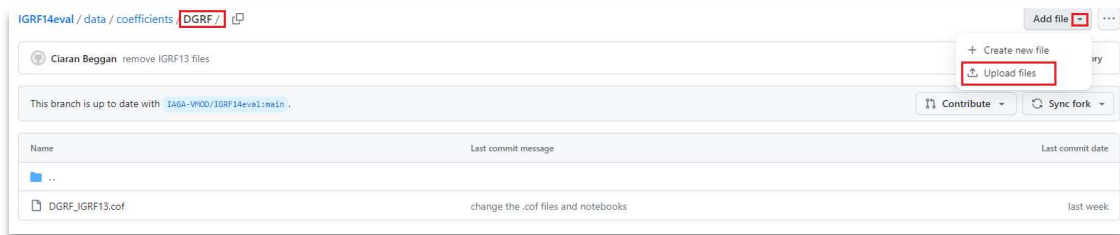


- Click on the newly created branch in your repository list to open it.
- Use the file tree to go to the "data/coefficients/" directory. There are three folders available: "DGRF", "IGRF" and "SV".

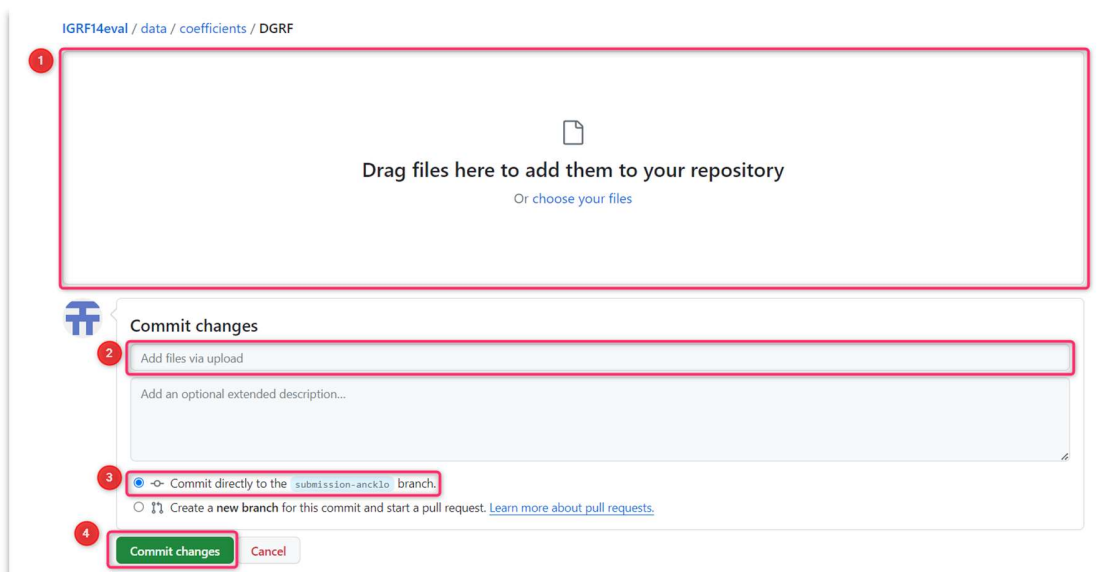


- Upload your candidate model files to the appropriate directories. For example, to upload your DGRF candidate model, open the "DGRF" directory and click on **Add file** and **Upload**

files.



11. (1) Follow the instructions for uploading a file; (2) add a commit message, e.g., "Adding DGRF candidate model."; (3) ensure you commit directly to your submission branch; and (4) click **Commit changes**.



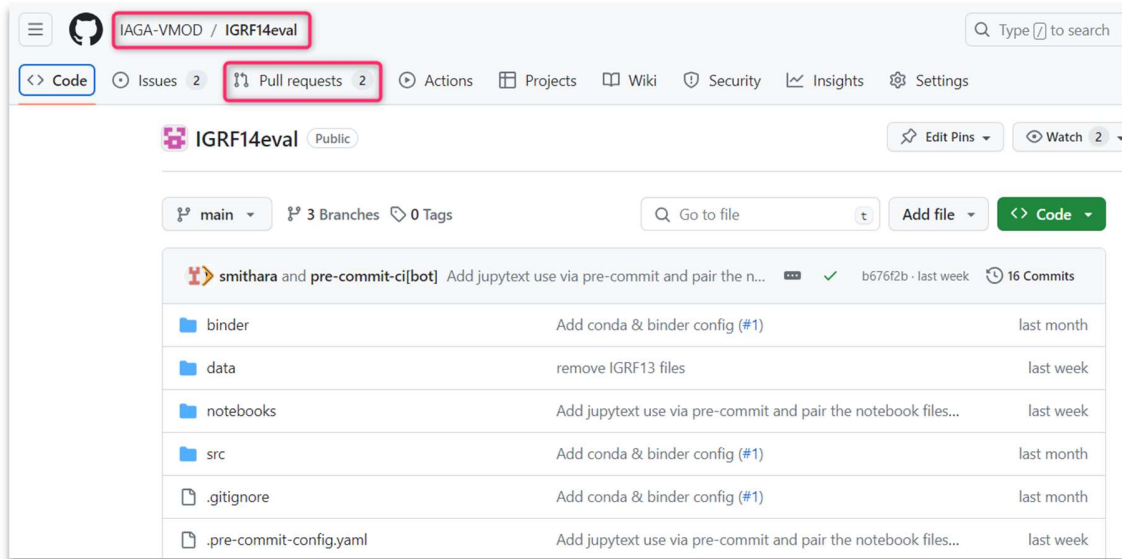
12. Repeat step 11 with the other candidate models you want to submit, making sure to use the correct directory for the model files. You can also change existing files by simply re-uploading modified versions of these files with an appropriate commit message, e.g., "Adding DGRF candidate model (version 2)."

## Create a pull request

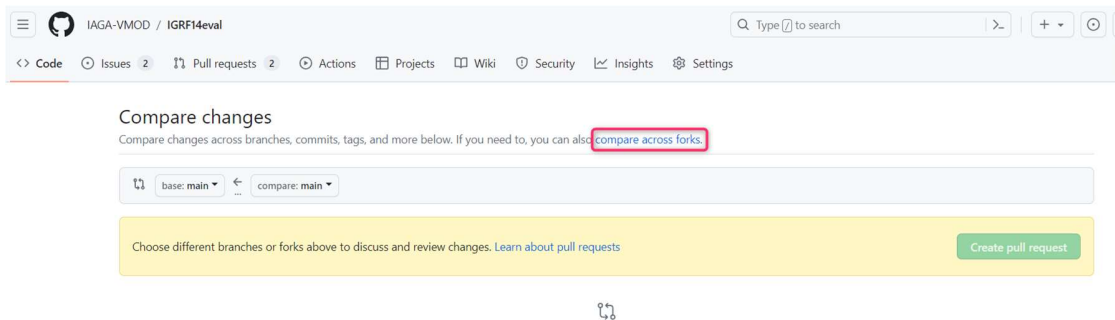
*All changes made so far have only affected your personal account. To make your changes visible to everyone, you must merge them into the public IGRF14eval repository by creating a pull request.*

13. Return to the IGRF14eval repository at <https://github.com/IAGA-VMOD/IGRF14eval>. Click **Pull requests** and **New pull request** to create a pull request. Ensure you are in the original

repository of the IAGA-VMOD GitHub organization, IAGA-VMOD/IGRF14eval.

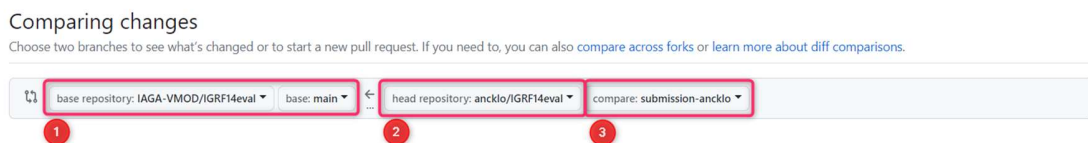


#### 14. Click **compare across forks**.



Compare and review just about anything

#### 15. Select (1) the "IAGA-VMOD/IGRF14eval" as base repository with base "main", then (2) your forked repository "<your-GitHub-name>/IGRF14eval, and (3) your submission branch.



#### 16. At the top, it should say that your submission branch can be merged with the main branch of IAGA-VMOD/IGRF14eval. Ensure you have only added the candidate models while

keeping the rest of the repository unchanged. Click **Create pull request**.

Comparing changes

Choose two branches to see what's changed or to start a new pull request. If you need to, you can also [compare across forks](#) or [learn more about diff comparisons](#).

base repository: IAGA-VMOD/IGRF14eval base: main head repository: ancklo/IGRF14eval compare: submission-ancklo

✓ Able to merge. These branches can be automatically merged.

Discuss and review the changes in this comparison with others. [Learn about pull requests](#)

Create pull request

2 commits 1 file changed 1 contributor

Commits on Feb 21, 2024

- Adding DGRF candidate model. Verified 3c41eec
- Updated DGRF candidate model (version 2). Verified 5906d85

17. Add the title and the description. Finally, click **Create pull request** to submit your changes.

Open a pull request

Create a new pull request by comparing changes across two branches. If you need to, you can also [compare across forks](#). [Learn more about diff comparisons here](#).

base repository: IAGA-VMOD/IGRF14eval base: main head repository: ancklo/IGRF14eval compare: submission-ancklo

✓ Able to merge. These branches can be automatically merged.

Add a title

Submission of DGRF

Add a description

Write Preview H B I  $\equiv$   $\lt$   $\gt$   $\ll$   $\gg$   $\oplus$   $\otimes$   $\@$   $\<$   $\>$   $\boxtimes$

Add your description here...

Reviewers: No reviews—at least 1 approving review is required.

Assignees: No one—assign yourself

Labels: None yet

Projects: None yet

Milestone: No milestone

Development: Use [Closing keywords](#) in the description to automatically close issues

Helpful resources

Allow edits by maintainers Create pull request

## What happens next

After creating the pull request, the IAGA-VMOD chair and co-chair will review the submission to ensure the files are in the correct format and can be loaded into the visualization notebooks (see Sect. 1 on validating your candidate models before submission). Once the review is completed, the pull request is approved, and the candidate models become part of the repository's main branch upon which they are publicly available.