APIs:

* Can’t input the variable
  + ???
* Description of the API call is in the wrong place (not in the box)
  + OK 🡪 also give some example/format of the input
* The “Try it out” autofill button doesn’t autofill
  + ???

Overall:

* Search engines should allow also partial searches (eg: “Park” in disease should return all Parkinsons)
  + We have autocomplete
  + Need to add, also for multiple search
* Search engines should allow multiple entries
  + How? Can not see similar things in GPCRdb
* The preselected tables in each search page are not clear what they represent, why are there and what was the query behind them
  + Just random rows as sample
  + 🡪 should have description of the output
* The structure and design of the statistics pages is not clear, clean or user friendly. I would reconsider making it more simple to use, showing the data structure beforehand and then having plots appear
  + We can discuss
* Icons in the menu bar have a white background when you click on the menu item (Disease, Drugs, etc). Remove the white background for the icons
  + Done
* There are two “About” sections, one that points to external resource, the other that creates a modal pop up
  + Done
* Remove the possibility to click on empty plot (eg: "Biologic / phase 2")
  + OK 🡪 statistics pages should be discussed🡪 to do list
* Remove the pop-up (plots pages)
  + ??? 🡪 to do list
* As David mentioned, the homepage is very difficult to interpret
  + To be discussed
* The pie charts in the homepage have different functionalities (the last one for example)
  + To be discussed
* Citing PGx link doesn’t work
  + We will add new one later

Drugs:

* Put a link to the external reference for ATC codes
  + We don’t have such links 🡪 <https://www.who.int/tools/atc-ddd-toolkit/atc-classification>
  + Done
* Going from ATC code to page highlighting interactions seems a bit slow, maybe caching issues? (eg <https://pgx-db.org/atc_detail_view/?group_id=A&detail=A10AB03>)
  + Why slow for 7 letter? Where leads to this page?

A screenshot of a computer

Description automatically generated

* The Drug search page has no explanation at all
  + To be discussed (We have documentation) 🡪 should add “Read More”?
  + Search by related fields that are listed in the results
* Macrocategories has to be cached otherwise it takes WAY too much time to load the network visualization (Antithrombotic Agents B01)
  + We have improved it

Targets:

* The Target search page has no exp[1]lanation at all
  + (We have documentation) 🡪 should add “Read More”?
* Why the “interacting drugs” link points to a pretty print and not a webpage? What’s the logic behind it?
  + Error , fix later
* In the gene details page (/gene/gene\_detail) would it be possible to highlight multiple amino acids in the 3D visual?
  + Yes, done
* Ensembl Gene ID and UniProt ID should be links to respective external pages
  + Not clear
  + Add the link A close-up of a card

    Description automatically generated
  + Done

Disease:

* Disease search page is slow to load compared to other search pages
  + It should be fast as the underlying data are not as much
  + Decrease the number of examples
* Why there are different entries for the same disease? (eg Parkinson that has Parkinson’s Disease, Parkinson’s Disease 1 and Secondary Parkinson Disease). Maybe arrange disease subtypes in the same entry?
  + Nice suggestion. I should consult Zia

Variants:

* Links in the header of chromosome mapper ([*UCSC*](https://pgx-db.org/chromosome_mapper/), [*Ensembl*](https://pgx-db.org/chromosome_mapper/), [*Gencode*](https://pgx-db.org/chromosome_mapper/), [*RefSeq*](https://pgx-db.org/chromosome_mapper/) and [*NCBI*](https://pgx-db.org/chromosome_mapper/)) points to the same page but various comparisons. I would expect to go to the external sites
  + Add the refs to the links
  + Done
* Search has no autofill and no partial selection
  + To do list
* Search by Gene Symbol doesn’t work (eg PTPN1)
  + Works on localhost 🡪 should improved on live server
  + Should be rearranged
* Mismatch in input info in the page:
  + Enter a genename, gene Ensembl ID or variant in Ensembl format
  + Input format: Chromosome\_Coordinate\_Reference/Alternative allele. Examples: 20\_50581449\_C/G

🡪 Done