

PyQt

- Was ist Qt?
- Was ist PyQt?
- Installation/Einrichtung
- Grundlegende Konzepte
- Anwendung in Pipeline
- Forderung der GUI
- Quellen

Was ist Qt?

- Framework zur Erstellung von Anwendungen.
- Entwickelt von Qt Company (ex. Trolltech) (Finnland)
- Unterstützt GUI, Netzwerk, Datenbanken,...
- C++
- Plattformübergreifend (Linux, Windows, MacOS, Android, iOS...)

The Qt logo is displayed on a green, three-dimensional rectangular block. The letters 'Q' and 't' are white and rendered in a bold, sans-serif font. The 'Q' is significantly larger than the 't'. The block has a slight shadow on its right side, giving it a 3D appearance. The background is a dark blue gradient.



Was ist PyQt?

- Python-Bindung für Qt-Framework
- Ermöglicht die Nutzung der Qt-Bibliothek in Python.
- Entwickelt von Riverbank Computing.
- Unterstützt alle Funktionen von Qt, einschließlich GUI-Entwicklung.

Installation

- Qt Designer kann von der Qt-Website heruntergeladen und installiert werden
- PyQt selber mit Befehl:

```
pip install PyQt5
```

Anleitung:

https://github.com/lostcolor6/NGS_PyQt

Setup

Download the latest version for Windows Download Python 3.12.3 under <https://www.python.org/downloads/>

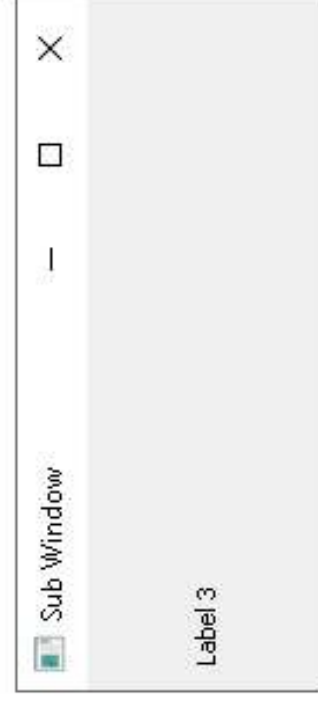
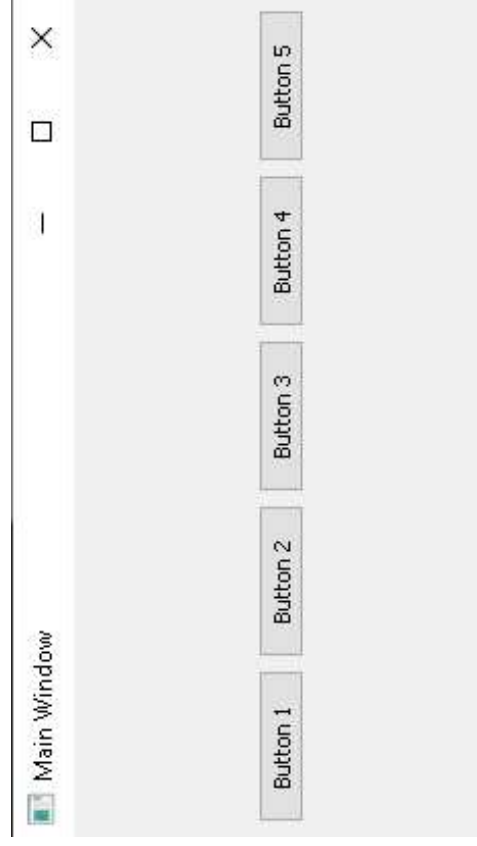
- paste and run in command prompt: "pip install PyQt5" (<https://pypi.org/project/PyQt5/>)

(It seems like the pip command is not recognized in your command prompt? This typically happens when Python is not added to your system's PATH environment variable during installation.

To fix this issue, you can follow these steps:

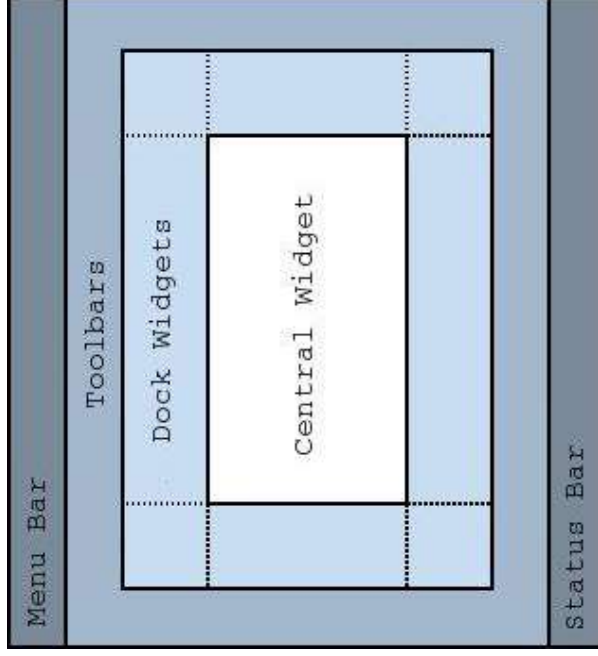
- Find the Path to Python Scripts: First, find out where Python is installed on your system. You can usually find it in

Widgets



- Buttons (Knöpfe)
- Labels (Beschriftungen)
- Textfelder
- Checkboxes

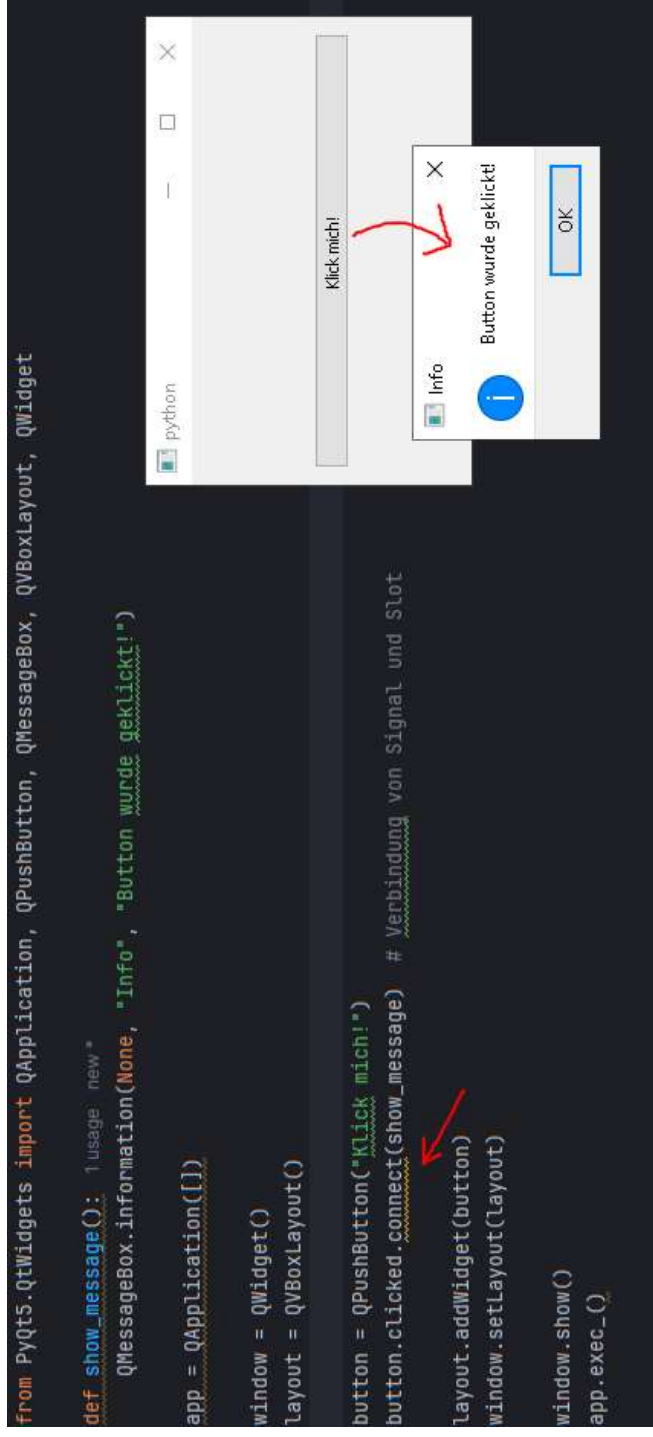
- QHBoxLayout
- QVBoxLayout
- QGridLayout



PyQt Gui Layout



Layouts

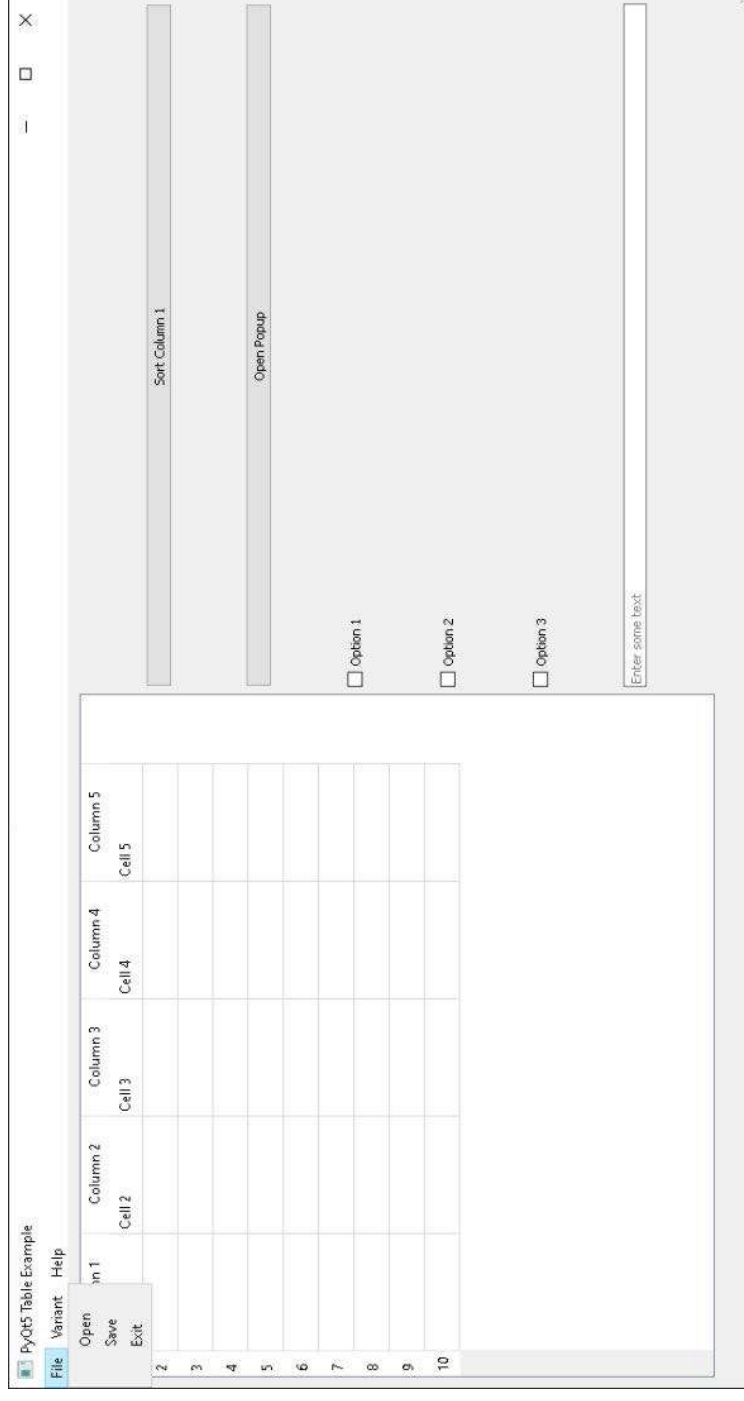
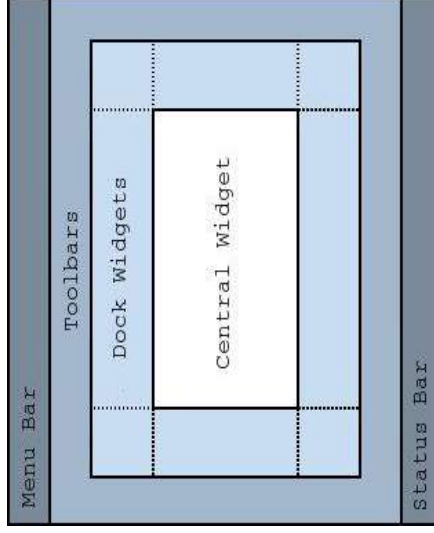


- Interaktivität/Kommunikation zwischen Widgets

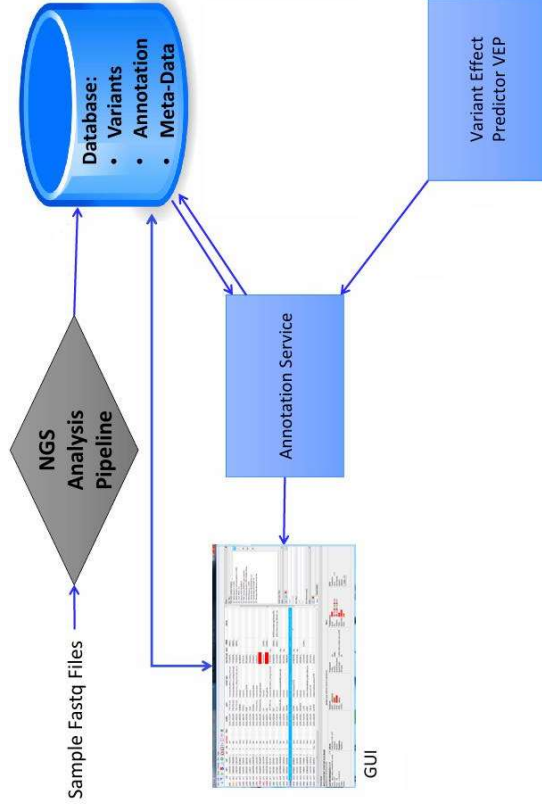
Signale und Slots

MainWindow

- Menüleisten
- Werkzeugleisten
- Statusleisten
- Zentrale Widgets



Pipeline



```

##fileformat=VCFv4.3
##fileDate=20090805
##source=MyImputationProgramV3.1
##referenceFile:///seq/References/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a60cf379d618ff66b28a,species="Homo sapiens",taxonomy=>
##phasingPartial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=1,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality Below 10">
##FILTER=<ID=q50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=DQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO
20 14370 rs604257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2
20 17330 . rs6040355 T A 3 Q10 NS=3;DP=11;AF=0.017
20 111696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333;0.667;AA=T;DB
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T
20 1234667 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G
  
```

- Schnittstelle für user
- Input und output: Variant Call Format (VCF)
- Alle Funktionen müssen über die GUI nutzbar sein
- Primär Kommunikation über Server (Http)

Konkret

- Varianten anzeigen (VCF wird als Tabelle angezeigt)
- Annotation anzeigen (zusätzliche Informationen)
- Priorisierung/Filterung von Varianten
- Links zu zusätzlichen Datenquellen (externen Datenbanken/Tools/Webseiten)
- Abspeichern der Userinputs (Parameter, Profile, etc.)

GSvar - W:\projects\test\KontrollIDNAConell\Sample_NA12878_03\NA12878_03.GSvar

File Edit Tools Variants IGV Help

chr	start	end	ref	obs	genotype	filter	quality	gene
17	131925483	131925483	G	C	het	pred_pathogenic;anno_omim	QUAL=814,DP=67,AF=0.49,MQM=...	RAD50
12	98232224	98232224	A	-	het	anno_omim	QUAL=263,DP=59,AF=0.54,MQM=...	PTCH1
19	7572996	7572996	G	T	het	anno_omim	QUAL=41,DP=216,AF=0.32,MQM=...	TP53

Filters: Target ref: none, Gene: none, Region: none, Breast cnc: Main filters: AF (over), AF (sub), impact, hdb, remove, keep da, keep da, pLL, rthetaz, genotyp, genotyp, Filter column: 1GV referer: none

Select HPO terms

Phenotype browser (double-click to select)

phenotype search

Selected phenotypes (double-click to remove)

HP:0003002 - Breast carcinoma

HP:0025318 - Ovarian carcinoma

OK Cancel

variant details

rs5:131925483-131925483 G>C (het)

me(s): RAD50 (chr=17, pL=0.00)

Quality: QUAL=814,DP=67,AF=0.49,MQM=60

Filters: pred_pathogenic_anno_omim

Databases		Frequencies		Pathogenicity	
dbSNP	rs55653181	1000g	0.0002	phyloP	6.3310
ClinVar	216618	gnomad	0.0000	Sift	T,T,T
HOVD		ExAC	0.0001	MetaLR	T
OMIM	604040	ExAC (sub)	0.0000,0.0000,0.0000,0.0000	PolyPhen2	B
cosmic		ExAC (sub)	0.0000,0.0000,0.0000,0.0000	FATHMM	T,T,T

Quellen

- [https://de.wikipedia.org/wiki/Variant_Call_Format#:~:text=Das%20Variant%20Call%20Format%20\(VCF,%2DGenome%2DProjekt%2C%20entwickelt.](https://de.wikipedia.org/wiki/Variant_Call_Format#:~:text=Das%20Variant%20Call%20Format%20(VCF,%2DGenome%2DProjekt%2C%20entwickelt.)
- <https://www.guru99.com/de/pyqt-tutorial.html>
- https://github.com/lostcolor6/NGS_PyQt
- https://wiki.qt.io/Einstieg_in_die_Programmierung_mit_Qt
- <https://wiki.python.org/moin/PyQt>
- https://youtube.com/playlist?list=PL3JVwFmb_BnRpvOelh_To4YSiebiggyXS&si=lnU8jtRXNGWGRJ5f

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