

QuartPAC: Identifying mutational clusters while utilizing protein quaternary structural data

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Abstract

The **QuartPAC** package is designed to identify mutated amino acid hotspots while accounting for protein quaternary structure. It is meant to work in conjunction with the **iPAC** [Ryslik and Zhao, 2012b], **GraphPAC** [Ryslik and Zhao, 2012a] and **SpacePAC** [Ryslik and Zhao, 2013] packages already available through Bioconductor. Specifically, the package takes as input the quaternary protein structure as well as the mutational data for each subunit of the assembly. It then maps the mutational data onto the protein and performs the algorithms described in **iPAC**, **GraphPAC** and **SpacePAC** to report the statistically significant clusters. By integrating the quaternary structure, **QuartPAC** may identify additional clusters that only become apparent when the different protein subunits are considered together.

1 Introduction

Recent advances in oncogenic pharmacology [Croce, 2008] have led to the creation of a variety of methods that attempt to identify mutational hotspots as these hotspots are often indicative of driver mutations [Wagner, 2007, Zhou et al., 2008, Ye et al., 2010]. Three recent methods, **iPAC**, **GraphPAC** and **SpacePAC** provide approaches to identify such hotspots while accounting for protein tertiary structure. While it has been shown that these mutations provide an improvement over linear clustering methods, [Ryslik et al., 2013, 2014b,a], they nevertheless consider only tertiary structure. **QuartPAC**, preprocesses the entire assembly structure in order to be able to accurately run these approaches

on the quaternary protein unit. This allows for the identification of additional mutational clusters that may otherwise be missed if only one protein subunit is considered at a time.

In order to run **QuartPAC**, four sources of data are required:

- The amino acid sequence of the protein which is obtained from the UniProt database (uniprot.org in FASTA format).
- The protein tertiary subunit information which is obtained from the .pdb file from PDB.org
- The quaternary structural information for the entire assembly which is obtained from the .pdb1 file from PDB.org
- The somatic mutation data which is obtained from the Catalogue of Somatic Mutations in Cancer (<http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>).

In order to map the mutations onto the protein quaternary structure, an alignment must be performed. For each uniprot within the assembly, mutational data must be provided. The data is in the format of $m \times n$ matrices for every subunit. A “1” in the (i, j) element indicates that residue j for individual i has a mutation while a “0” indicates no mutation. To be compatible with this software, please ensure that your mutation matrices have R column headings of $V1, V2, \dots, Vn$. Only missense mutations are currently supported, indels in the amino acid sequence are not. Sample mutational data are included in this package as textfiles in the *extdata* folder.

It is worth noting that there does not exist any one individual source to obtain mutational data. One common resource is the COSMIC database <http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>. The easiest way to obtain mutational data for many proteins is to load the COSMIC database on a local sql server and then query the database for the protein of interest. It is important to restrict your query to whole gene screens or whole genome studies to prevent specific mutations from being selectively chosen (and thus violating the uniformity assumption that **iPAC**, **GraphPAC**, and **SpacePAC** rely upon).

Should you find a bug, or wish to contribute to the code base, please contact the author.

2 Identifying Clusters and Viewing the Remapping

The general principle of **QuartPAC** is that we preprocess the data into a format that can be recognized by **iPAC**, **GraphPAC** and **SpacePAC**. Most of this is automated and all that is needed is to point the algorithm to the mutational and structural data. **QuartPAC** will then reorganize the data, execute the cluster finding algorithms and report the results. The clusters are reported by serial number. As each serial number is unique in the assembly, the user can then map each serial number to the exact atom of interest in the structure.

Below we run the algorithm with no multiple comparison adjustment. We do this to ensure that some clusters are found for each method. We also note that for **iPAC** and **GraphPAC**, if a multiple comparison adjustment is used and no clusters are found significant, the methods will show a null value. For **SpacePAC**, as there is no multiple comparison adjustment needed, the most significant clusters are always shown, regardless of the p-value. This behavior follows the functionality of the previous three packages, so users familiar with the tertiary algorithms will find the results directly comparable.

For more information on the output, please see the **iPAC**, **GraphPAC**, and **SpacePAC** packages as the output is similar. The main difference is that the amino acid numbers now refer to the serial numbers within the *.pdb1 file.

Code Example 1: Running QuartPAC.

```
> library(QuartPAC)
> #read the mutational data
> mutation_files <- list(
+ system.file("extdata", "HFE_Q30201_MutationOutput.txt", package = "QuartPAC"),
+ system.file("extdata", "B2M_P61769_MutationOutput.txt", package = "QuartPAC")
+ )
> uniprots <- list("Q30201", "P61769")
> mutation.data <- getMutations(mutation_files = mutation_files, uniprots = uniprots)
> #read the pdb file
> pdb.location <- "https://files.rcsb.org/view/1A6Z.pdb"
> assembly.location <- "https://files.rcsb.org/download/1A6Z.pdb1"
> structural.data <- makeAlignedSuperStructure(pdb.location, assembly.location)
> #Perform Analysis
> #We use a very high alpha level here with no multiple comparison adjustment
> #to make sure that each method provides shows a result.
> #Lower alpha cut offs are typically used.
> quart_results <- quartCluster(mutation.data, structural.data, perform.ipac = "Y",
+                               perform.graphpac = "Y", perform.spacepac = "Y",
+                               create.map = "Y", alpha = .3, MultComp = "None",
+                               Graph.Title = "MDS Mapping to 1D Space",
+                               radii.vector = c(1:3))
```

We observe that the MDS remapping plot provided by **QuartPAC** is done automatically if the *create.map* parameter is set to “Y”. The plot is shown in Figure 1 below.

For the **GraphPAC** approach, the linear “Jump Plot” (see the **GraphPAC** package for more details and interpretation) has been implemented and is shown in Figure 2 below. Feel free to contact the author if you want to assist in porting other graphing functionality.

With regards to **SpacePAC**, as there is no remapping from 3D to 1D space, a plotting option that shows the protein in its folded state is presented in Section 4.

Code Example 2: Plotting the GraphPAC candidate path.

MDS Mapping to 1D Space

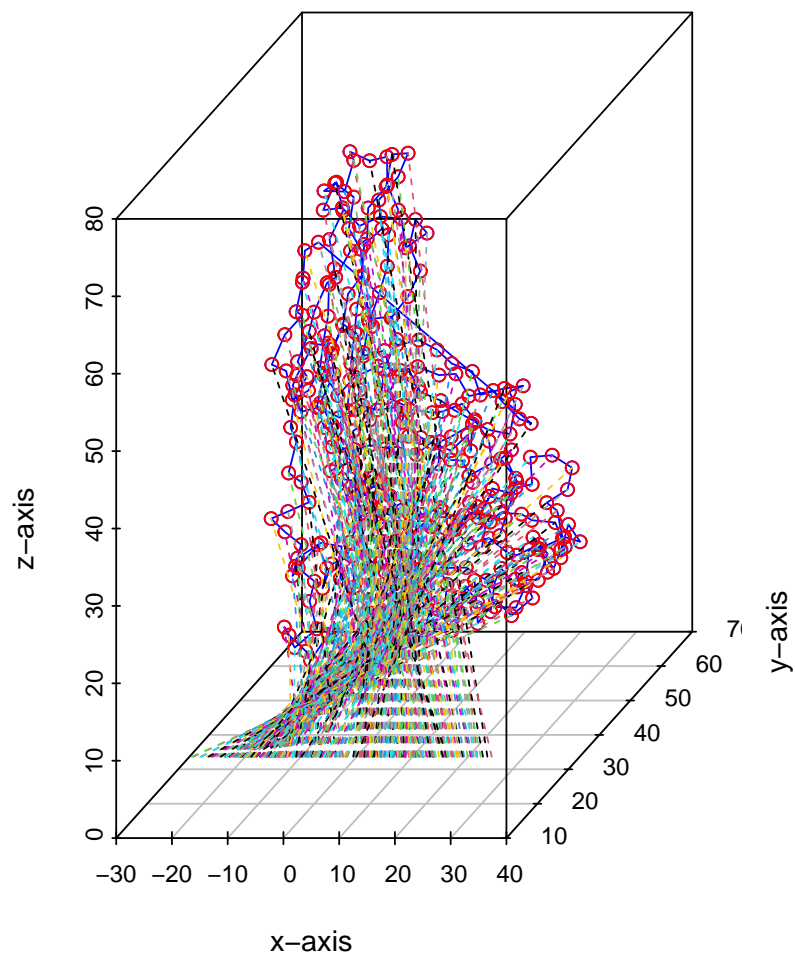


Figure 1: Remapping performed by iPAC.

```
> Plot.Protein.Linear(quart_results$graphpac$candidate.path, colCount = 10,  
+                      title = "Protein Reordering to 1D Space via GraphPAC")
```

Protein Reordering to 1D Space via GraphPAC

2	13	19	29	35	43	53	65	73	84
92	96	101	107	116	121	129	137	141	149
155	163	174	183	188	196	200	212	219	227
235	244	252	263	270	281	293	301	311	316
322	333	344	351	360	367	378	385	392	406
411	416	421	426	431	437	443	452	460	474
479	488	496	501	510	516	524	533	537	551
559	569	577	588	595	602	610	621	635	642
650	658	667	675	685	693	703	709	718	727
733	743	750	758	767	774	782	790	794	800
809	817	826	831	839	847	853	860	869	873
885	899	908	920	924	936	944	948	957	965
975	983	992	1003	1009	1016	1024	1031	1039	1047
1061	1072	1077	1082	1091	1098	1109	1114	1128	1135
1142	1151	1159	1168	1182	1191	1202	1212	1221	1229
1240	1245	1256	1265	1273	1284	1289	1301	1309	1318
1329	1337	1343	1350	1355	1364	1372	1381	1390	1398
1406	1415	1423	1427	1432	1436	1443	1451	1459	1468
1477	1484	1491	1498	1506	1513	1522	1529	1536	1546
1556	1563	1570	1576	1582	1589	1596	1603	1611	1622
1628	1639	1644	1652	1660	1672	1684	1691	1700	1708
1716	1723	1731	1740	1754	1762	1771	1779	1788	1797
1804	1812	1820	1825	1834	1843	1854	1863	1870	1879
1887	1894	1902	1909	1917	1921	1929	1933	1940	1952
1961	1965	1979	1987	1994	2002	2007	2014	2021	2028
2032	2041	2050	2059	2070	2082	2089	2095	2104	2111
2120	2130	2137	2141	2149	2157	2166	2173	2181	2189
2196	2204	2220	2228	2237	2248	2255	2262	2271	2279
2288	2295	2307	2313	2324	2334	2341	2346	2355	2363
2367	2376	2382	2390	2401	2409	2417	2423	2435	2442
2448	2452	2463	2473	2480	2486	2494	2502	2511	2518
2526	2534	2542	2551	2559	2563	2572	2583	2591	2600
2605	2612	2621	2631	2637	2645	2653	2659	2670	2676
2685	2693	2707	2713	2724	2736	2744	2752	2764	2776
2783	2792	2803	2810	2817	2824	2833	2838	2846	2855
2867	2872	2878	2889	2896	2904	2914	2921	2928	2936
2942	2951	2958	2967	2975	2982	2991	3005	3013	3024
3032									

Figure 2: Remapping performed by **GraphPAC**.

3 Using the Output

Now that we have the results, suppose that we wanted to visualize what the clusters are. For example, we see that the first cluster under the **SpacePAC** method for the optimal combination has two spheres. One sphere is centered at the atom with serial number 1265 and one sphere is centered at the atom with serial number 367.

To see where this matches we can query the *structural.data* list.

Code Example 3: Finding the residue of interest using the SpacePAC method.

```
> #look at the results for the optimal sphere combinations under the SpacePAC approach
> #For clarity we only look at columns 3 - 8 which show the sphere centers.
> quart_results$spacepac$optimal.sphere[,3:8]
```

	Center1	Center2	Start1	End1	Start2	End2
1	1265	367	1265	1265	367	367
2	2166	367	2166	2166	367	367
3	2295	367	2295	2295	367	367
4	2166	1265	2166	2166	1265	1265
5	2401	367	2401	2401	367	367
6	2295	1265	2295	2295	1265	1265
7	2583	367	2583	2583	367	367
8	2401	1265	2401	2401	1265	1265
9	2295	2166	2295	2295	2166	2166
10	2659	367	2659	2659	367	367
11	2583	1265	2583	2583	1265	1265
12	2401	2166	2401	2401	2166	2166
13	2846	367	2846	2846	367	367
14	2659	1265	2659	2659	1265	1265
15	2583	2166	2583	2583	2166	2166
16	2401	2295	2401	2401	2295	2295
17	2846	1265	2846	2846	1265	1265
18	2659	2166	2659	2659	2166	2166
19	2583	2295	2583	2583	2295	2295
20	2846	2166	2846	2846	2166	2166
21	2659	2295	2659	2659	2295	2295
22	2583	2401	2583	2583	2401	2401
23	2846	2295	2846	2846	2295	2295
24	2659	2401	2659	2659	2401	2401
25	2846	2401	2846	2846	2401	2401
26	2659	2583	2659	2659	2583	2583
27	2846	2583	2846	2846	2583	2583
28	2846	2659	2846	2846	2659	2659

```
> #Find the atom with serial number 1265
> required.row <- which(structural.data$aligned_structure$serial == 1265)
> #show the information for that atom
> structural.data$aligned_structure[required.row,]
```

	recordName	serial	atom	altLoc	resName	chainID	resSeq	iCode	xCoord	yCoord
1:	ATOM	1265	CA		ASN	A	157		5.743	52.485

```

      zCoord occupancy tempFactor element charge      UNP dbref protomer absPos
1: 13.919      1      42.28      C      Q30201      1      1      154
      canonical_pos
1:      179
>

```

Similarly, suppose you wanted to look at the **iPAC** results. The first cluster goes from serial 2583 and ends at 2846. To get all the residue information for that block, we can do the following:

Code Example 4: Finding the residue of interest using the iPAC method.

```

> #look at the results for the first cluster shown by the ipac method
> quart_results$ipac

      AA_in_Cluster serial_start serial_end number      p_value
V254           32      2583      2846      3 0.03093808
V172           22      2659      2846      2 0.04285346
V274           55      2401      2846      4 0.05244236
V254           52      2166      2583      4 0.07721776
V274           14      2295      2401      2 0.08306777
V254           37      2295      2583      3 0.09028823
V172           62      2166      2659      5 0.10970551
V274           29      2166      2401      3 0.12480796
V180          304       367      2846      8 0.12630378
V172          283       367      2659      7 0.16003397
V172           47      2295      2659      4 0.16898693
V278           68      2295      2846      5 0.19414336
V303           83      2166      2846      6 0.24825087
V180          222       367      2166      3 0.25497859

> #Find the atoms with serial numbers within the range of 2583 to 2846
> required.rows <- which(structural.data$aligned_structure$serial %in% (2583:2846))
> #show the information for those atoms
> structural.data$aligned_structure[required.rows,]

      recordName serial atom altLoc resName chainID resSeq iCode xCoord yCoord
1:      ATOM      2583  CA          ILE      B      46      12.885 19.924
2:      ATOM      2591  CA          GLU      B      47      12.538 18.636
3:      ATOM      2600  CA          LYS      B      48       9.370 18.878
4:      ATOM      2605  CA          VAL      B      49       9.120 22.638
5:      ATOM      2612  CA          GLU      B      50       7.189 24.889
6:      ATOM      2621  CA          HIS      B      51       7.867 28.493
7:      ATOM      2631  CA          SER      B      52       5.976 31.273
8:      ATOM      2637  CA          ASP      B      53       7.479 32.937
9:      ATOM      2645  CA          LEU      B      54      10.283 35.432
10:     ATOM      2653  CA          SER      B      55       8.837 38.923
11:     ATOM      2659  CA          PHE      B      56       9.783 42.469
12:     ATOM      2670  CA          SER      B      57       8.257 45.640
13:     ATOM      2676  CA          LYS      B      58       8.243 49.331
14:     ATOM      2685  CA          ASP      B      59      11.745 49.858

```

15:	ATOM	2693	CA	TRP	B	60	13.026	47.034
16:	ATOM	2707	CA	SER	B	61	13.661	44.800
17:	ATOM	2713	CA	PHE	B	62	12.750	41.139
18:	ATOM	2724	CA	TYR	B	63	10.369	38.996
19:	ATOM	2736	CA	LEU	B	64	9.841	35.241
20:	ATOM	2744	CA	LEU	B	65	7.561	33.020
21:	ATOM	2752	CA	TYR	B	66	8.522	29.543
22:	ATOM	2764	CA	TYR	B	67	5.960	27.185
23:	ATOM	2776	CA	THR	B	68	5.265	23.560
24:	ATOM	2783	CA	GLU	B	69	2.275	21.616
25:	ATOM	2792	CA	PHE	B	70	3.018	20.246
26:	ATOM	2803	CA	THR	B	71	1.565	19.125
27:	ATOM	2810	CA	PRO	B	72	3.166	20.559
28:	ATOM	2817	CA	THR	B	73	3.655	18.871
29:	ATOM	2824	CA	GLU	B	74	5.166	19.946
30:	ATOM	2833	CA	LYS	B	75	8.589	18.374
31:	ATOM	2838	CA	ASP	B	76	8.895	19.872
32:	ATOM	2846	CA	GLU	B	77	10.881	23.063

	recordName	serial	atom	altLoc	resName	chainID	resSeq	iCode	xCoord	yCoord	zCoord	occupancy	tempFactor	element	charge	UNP	dbref	protomer	absPos
1:		45.964	1		59.61	C	P61769	2	1	318									
2:		42.427	1		75.66	C	P61769	2	1	319									
3:		40.348	1		82.60	C	P61769	2	1	320									
4:		40.986	1		72.00	C	P61769	2	1	321									
5:		38.587	1		65.40	C	P61769	2	1	322									
6:		37.552	1		59.43	C	P61769	2	1	323									
7:		35.791	1		54.96	C	P61769	2	1	324									
8:		32.724	1		54.99	C	P61769	2	1	325									
9:		33.143	1		43.17	C	P61769	2	1	326									
10:		32.873	1		43.06	C	P61769	2	1	327									
11:		33.932	1		36.56	C	P61769	2	1	328									
12:		35.371	1		40.60	C	P61769	2	1	329									
13:		34.385	1		42.56	C	P61769	2	1	330									
14:		35.795	1		41.40	C	P61769	2	1	331									
15:		33.576	1		34.49	C	P61769	2	1	332									
16:		36.581	1		35.68	C	P61769	2	1	333									
17:		36.218	1		33.38	C	P61769	2	1	334									
18:		38.234	1		42.58	C	P61769	2	1	335									
19:		38.323	1		36.62	C	P61769	2	1	336									
20:		40.370	1		38.86	C	P61769	2	1	337									
21:		41.587	1		49.21	C	P61769	2	1	338									
22:		43.115	1		54.28	C	P61769	2	1	339									
23:		44.155	1		59.26	C	P61769	2	1	340									
24:		45.397	1		66.25	C	P61769	2	1	341									
25:		48.852	1		59.77	C	P61769	2	1	342									
26:		52.163	1		67.36	C	P61769	2	1	343									
27:		55.294	1		68.86	C	P61769	2	1	344									
28:		58.669	1		73.63	C	P61769	2	1	345									
29:		61.984	1		84.25	C	P61769	2	1	346									
30:		61.405	1		87.62	C	P61769	2	1	347									


```

31: 57.911      1      77.81      C      P61769      2      1      348
32: 57.189      1      68.89      C      P61769      2      1      349
      zCoord occupancy tempFactor element charge      UNP dbref protomer absPos
      canonical_pos
1:      66
2:      67
3:      68
4:      69
5:      70
6:      71
7:      72
8:      73
9:      74
10:     75
11:     76
12:     77
13:     78
14:     79
15:     80
16:     81
17:     82
18:     83
19:     84
20:     85
21:     86
22:     87
23:     88
24:     89
25:     90
26:     91
27:     92
28:     93
29:     94
30:     95
31:     96
32:     97
      canonical_pos

```

As the **GraphPAC** results are in the same format as the **iPAC** results, the approach for identifying clusters in those atoms is identical as in the example above.

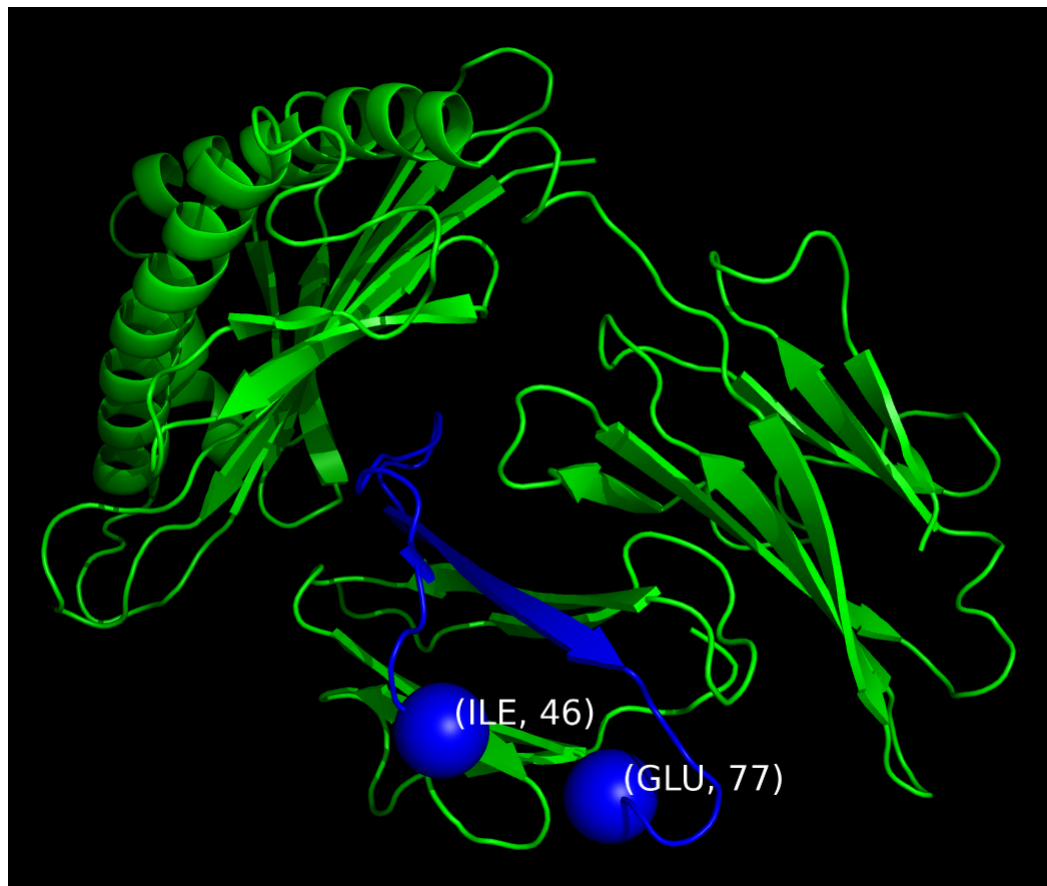
4 Visualizing the Results

Once you have the serial numbers of interest, you can then view the results in any pdb visualization application of your choice. One common option is to use the *PyMOL* software package [Schrödinger, LLC, 2010]. While it is not the purpose of this vignette to teach the reader *PyMOL* syntax, we present the following simplistic example and the resulting figure for reference. It will color

the first cluster outputted by the **iPAC** method, residues with serial numbers 2583-2846 in blue. The chain and resSeq information provided in Example 4 is used as below.

Code Example 5: PyMOL sample code

```
-----  
hide all  
show cartoon,  
show spheres, ///b/46/ca  
show spheres, ///b/77/ca  
color blue, ///b/46-77  
  
label c. B and n. CA and i. 46, "(%s, %s)" % (resn, resi)  
label c. B and n. CA and i. 77, "(%s, %s)" % (resn, resi)  
set label_position, (3,2,10)
```



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