



# Flapjack

<https://ics.hutton.ac.uk/flapjack>

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**Hutton**  
**Institute**

# Software team



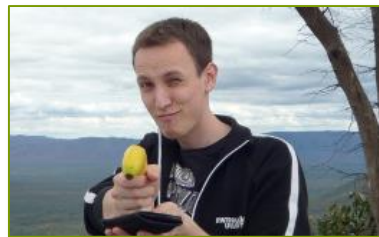
Iain Milne



Gordon Stephen



David Marshall



Sebastian Raubach



Paul Shaw



Linda Milne









# Flapjack

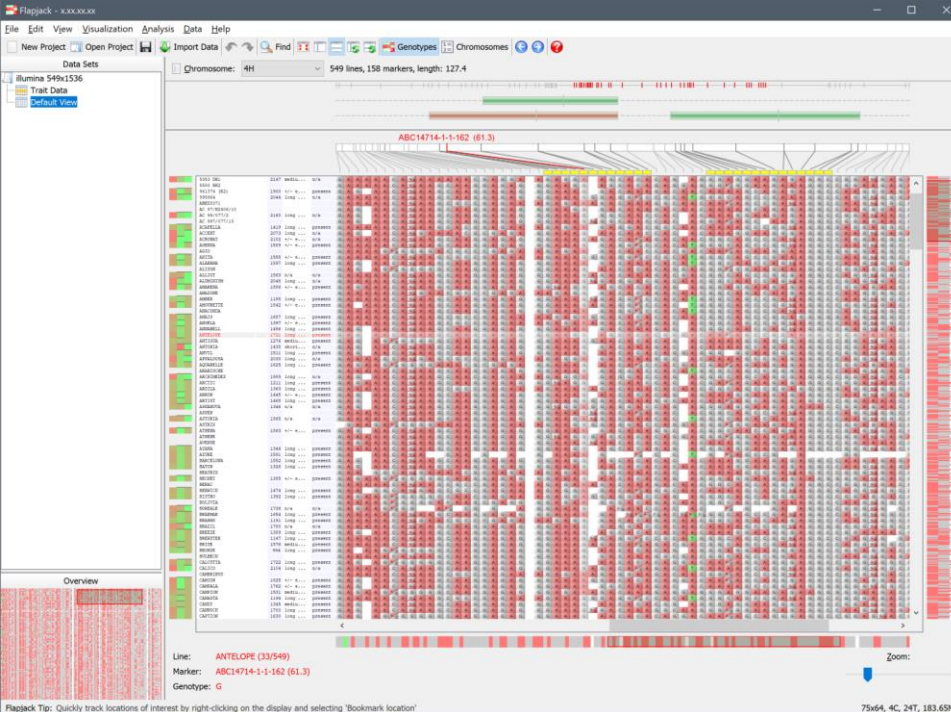
- Flapjack provides a high-performance visual interface into **graphical genotyping** applications in genetics and plant breeding
- Contains a range of **analysis modules**, such as PcOA and dendrogram generation, and statistics for MABC, pedigree verification of lines, and forward-breeding



# Other key features

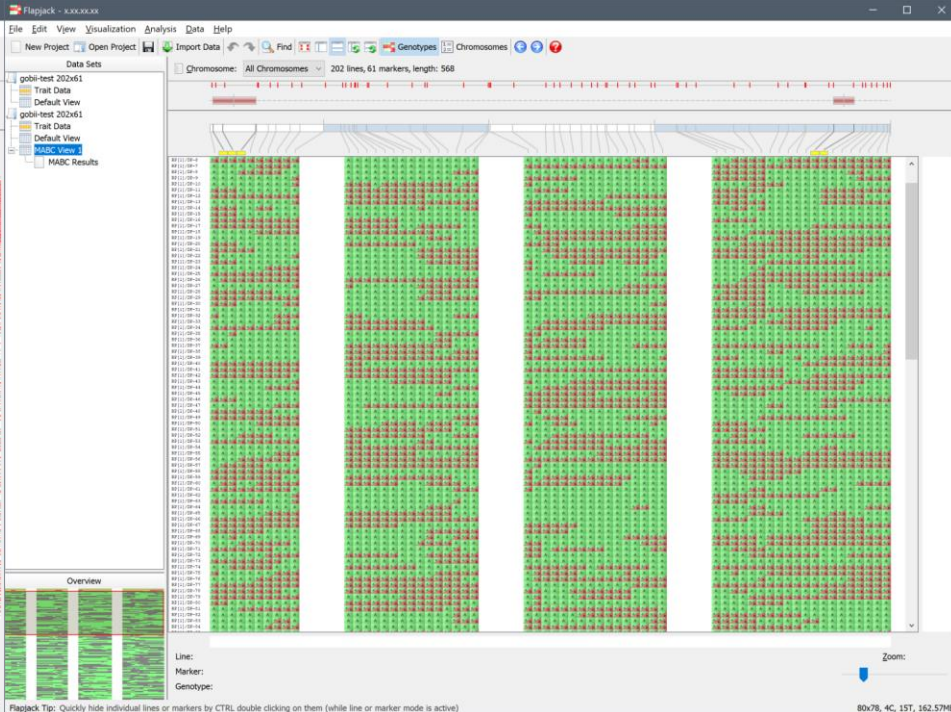
- Visually interact with marker data (mainly SNPs)
  - supports datasets from just a few markers to 10,000s+
- Allows lines and markers to be sorted, inserted, deleted, etc
  - sort manually, alphabetically, by genetic similarity (inc dendrogram order), by trait...
- Align map based info such as QTLs to the visual display to identify desired haplotypes
- Analyses modules can be run on single datasets or in batch mode across many at once
  - export results for downstream analysis in (eg) Excel
- BrAPI v2.0 compliant





Flagjack Tip: Quickly track locations of interest by right-clicking on the display and selecting 'Bookmark location'

75x64, 4C, 24T, 183.65MB



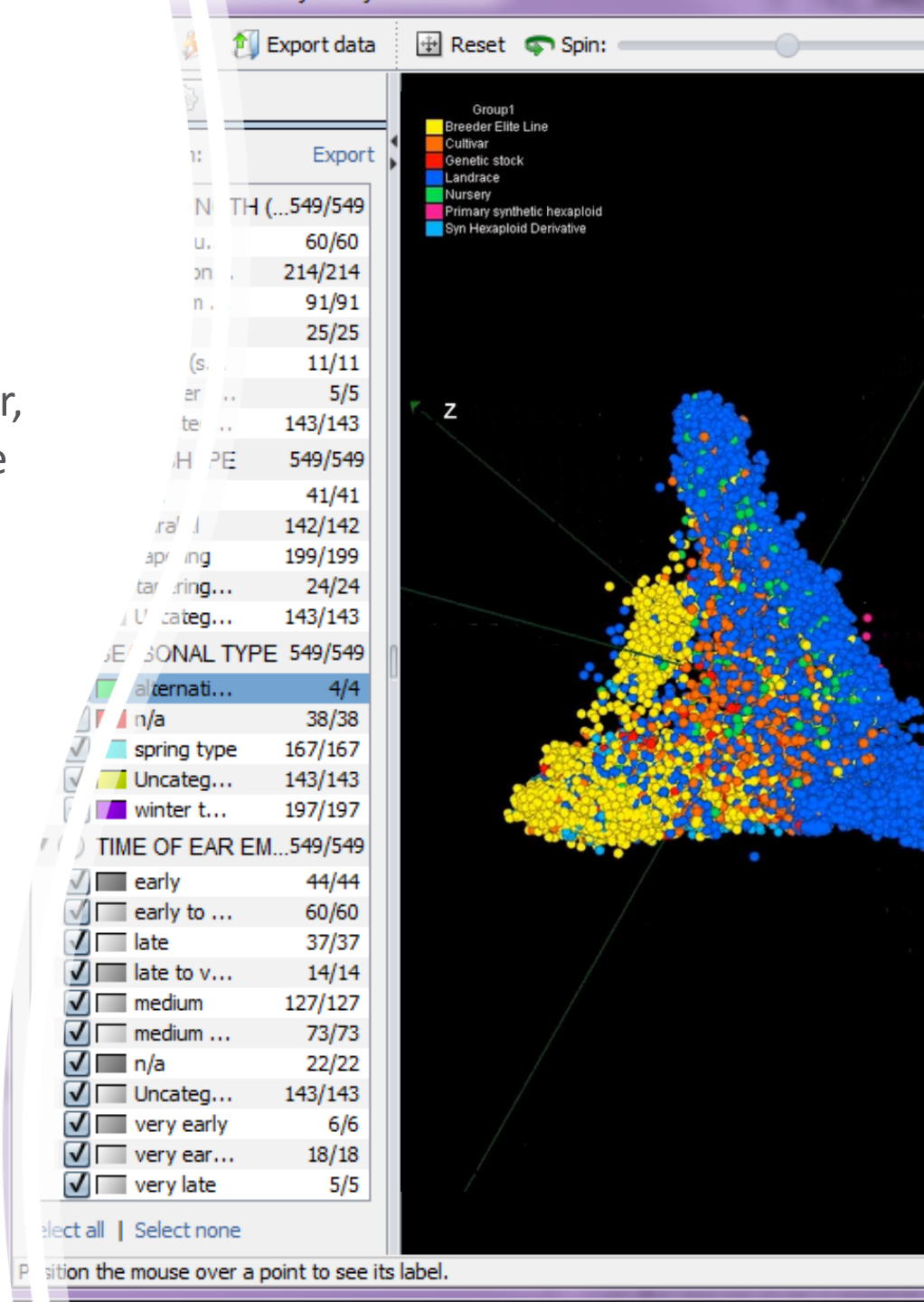
Flagjack Tip: Quickly hide individual lines or markers by CTRL double clicking on them (while line or marker mode is active)

80x78, 4C, 15T, 162.57MB

Line	Data ...	% Data	Het C...	% Het	RPP (1)	RPP (2)	RPP (3)	RPP (4)	RPP T...	RPP C...	LD (Q...	Status...	LD (Q...	Status...	QTL ...	Selected	Rank	Comm...	Don't...
BP	61	100	0	0	0	0	1	1	1	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	13	21.311	0.919	0.871	0.926	0.901	0.904	0.687	1	0	28	0	0	0	0	0	0
RP1 ...	61	100	36	59.016	0.669	1	0.5	0.686	0.7	0.687	37	0	46	0	0	0	0	0	0
RP1 ...	61	100	39	63.934	1	0.535	0.5	0.689	0.658	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	18	29.508	1	0.879	0.688	0.915	0.899	0.687	0	0	15	0	0	0	0	0	0
RP1 ...	61	100	28	45.902	0.5	1	0.935	0.626	0.771	0.687	62	1	54	1	2	0	0	0	0
RP1 ...	61	100	40	65.574	0.75	1	0.5	0.5	0.653	0.687	0	0	179	1	1	0	0	0	0
RP1 ...	61	100	16	26.23	0.735	0.906	1	0.766	0.856	0.687	29	0	0	0	0	0	0	0	0
RP1 ...	61	100	17	27.869	0.963	1	0.785	0.752	0.852	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	19	31.148	0.963	0.571	0.972	0.853	0.844	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	36	59.016	0.868	0.5	0.894	0.667	0.717	0.687	5	0	30	0	0	0	0	0	0
RP1 ...	61	100	39	63.934	0.5	0.724	0.812	0.775	0.726	0.687	62	1	19	0	1	0	0	0	0
RP1 ...	61	100	39	63.934	0.563	0.5	0.686	0.657	0.688	0.687	0	0	30	0	0	0	0	0	0
RP1 ...	61	100	2	3.277	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	1	1.638	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	2	3.277	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	3	4.916	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	4	6.554	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	5	8.193	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	6	9.832	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	7	11.471	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	8	13.110	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	9	14.749	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	10	16.388	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	11	18.027	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	12	19.666	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	13	21.305	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	14	22.944	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	15	24.583	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	16	26.222	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	17	27.861	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	18	29.500	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	19	31.139	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	20	32.778	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	21	34.417	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	22	36.056	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	23	37.695	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	24	39.334	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	25	40.973	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	26	42.612	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	27	44.251	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	28	45.890	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	29	47.529	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	30	49.168	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	31	50.807	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	32	52.446	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	33	54.085	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	34	55.724	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	35	57.363	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	36	59.002	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	37	60.641	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	38	62.280	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	39	63.919	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	40	65.558	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	41	67.197	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	42	68.836	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
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RP1 ...	61	100	44	72.114	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	45	73.753	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	46	75.392	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	47	77.031	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	48	78.670	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	49	80.309	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	50	81.948	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100	51	83.587	0.5	0.686	0.657	0.688	0.687	0.687	0	0	0	0	0	0	0	0	0
RP1 ...	61	100																	

# CurlyWhirly

- CurlyWhirly is a multidimensional data viewer, with a particular focus on the outputs of **Principle Coordinate Analysis** and **Principal Components Analysis**.
- Supports multiple categorization of data points allowing for different - category based - colouring schemes to be applied and for rich filtering of selected data points.



# Flapjack format

- The minimal input to Flapjack is a **genotype** file:
  - specifies the names of all lines and markers
  - and an allele score (in one of several supported formats) for each line/marker intersection
- Optionally, a **map** file can also be included:
  - specifies a chromosome name and position for each marker
- Other additional files include QTL (2 formats), traits, graph data, etc...



**# fjFile = MAP**

<b>ABC09402-1-2-275</b>	1H	4.3		
<b>3220-723</b>	1H	4.9		
<b>6195-2137</b>	1H	4.9		
<b>337-641</b>	1H	5.4		
<b>3101-111</b>	1H	7.6		
<b>7372-1253</b>	1H	13.2		
<b>6949-895</b>	1H	13.2		
<b>5494-316</b>	1H	25.3		
<b>4473-309</b>	1H	25.3		
<b>10922-503</b>	1H	26.5		
<b>2496-1916</b>	1H	26.5		
<b>1906-429</b>	1H	32.2		
<b>4226-570</b>	1H	32.2		
<b>5318-436</b>	1H	34.2		
<b>5194-1118</b>	1H	36.6		

**# fjFile = GENOTYPE**

	<b>1001-1187</b>	<b>10012-1239</b>	<b>10047-338</b>	<b>1007-651</b>	<b>10070-1435</b>
<b>12337 ZH (R2)</b>	G/A	A	T	G	A
<b>165</b>	A	A	T	G	A
<b>22746CO41</b>	G	G	A	G	A
<b>2808</b>	G	G	A	A/G	A
<b>404-65</b>	G	G	A	A/G	A
<b>410/3E</b>	A	G	A	G	G
<b>5353 DH1</b>	A	G	T	G	G
<b>5593 BH2</b>	A	A	T	G	G
<b>961374 (R2)</b>	A	A	T	A/G	G
<b>995964</b>	G	A	A	A/G	A
<b>ABED3371</b>	G	A	A	A/G	A
<b>AC 97/H2406/10</b>	A	G	A	A/G	G
<b>AC 99/077/2</b>	A	G	T	A/G	G
<b>AC 997/077/13</b>	A	G	T	A/G	A

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3129 <lines guid="3124" name="12337 ZH (R2)">
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3131 <loci>AgICAQQCBAIBBAIEAgUFAGQEBQMCAGQEAQIEBAICBAICBAAHBAIDAgICAgQHAgQCAGICBQQEAgICAgQCBQQCBQIEBAUCBQEGAgQCAgQFBQMEAgUEAgUEAAQEAgQEBQQCAGQCAGQCA
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3167 </genotypes>
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# CurlyWhirly (Diversity analysis of 80,000 wheat accessions)

- <https://www.nature.com/articles/s41467-020-18404-w>
- <https://ics.hutton.ac.uk/resources/curlywhirly/cw2.zip>