GWAS and GS Are as Easy as Clicking and Dragging with iPat

World Congress On Genetics Applied to Livestock Production (WCGALP, 11th)

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WASHINGTON STATE UNIVERSITY

The Challenges of Biologists

Programming skills
Big data
Formatting
Modeling
…

iPat makes it easier for biologists to analyze data and stay focused on biology

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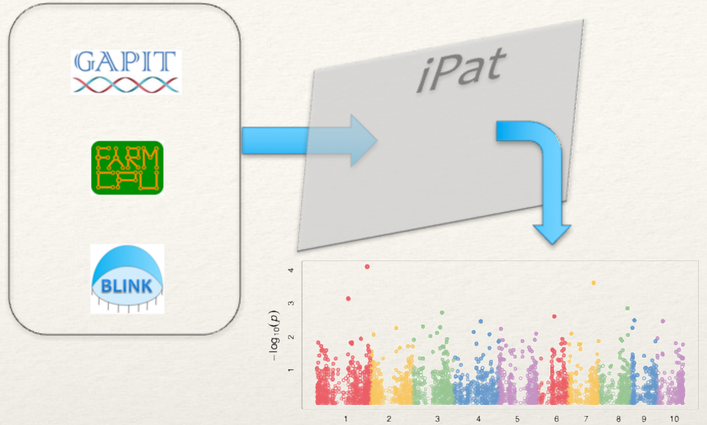
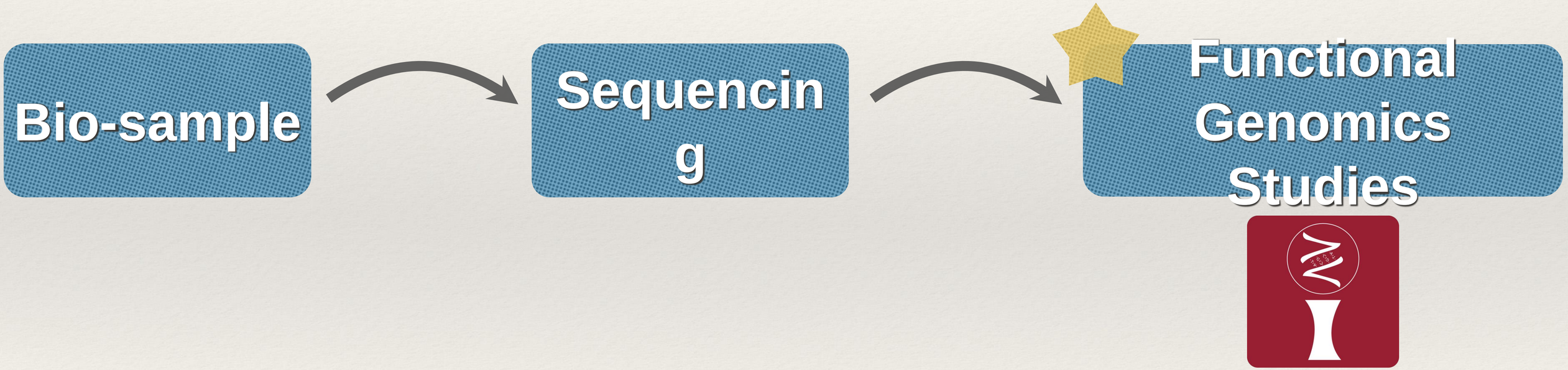


iPat

iPat makes it easier for biologists to analyze data and stay focused on biology

The Focus of iPat



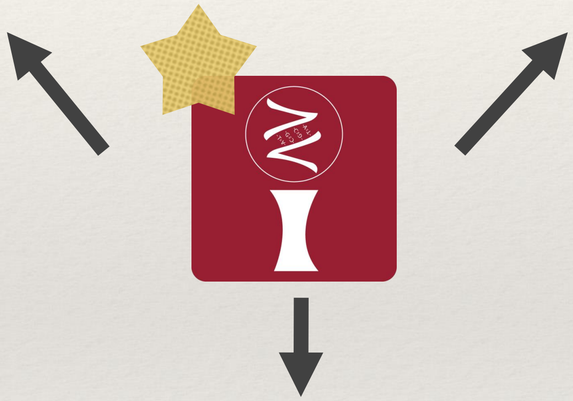
The Focus of iPat

Finding Associated Genes

Genome-Wide Association Studies

Genomic Selection

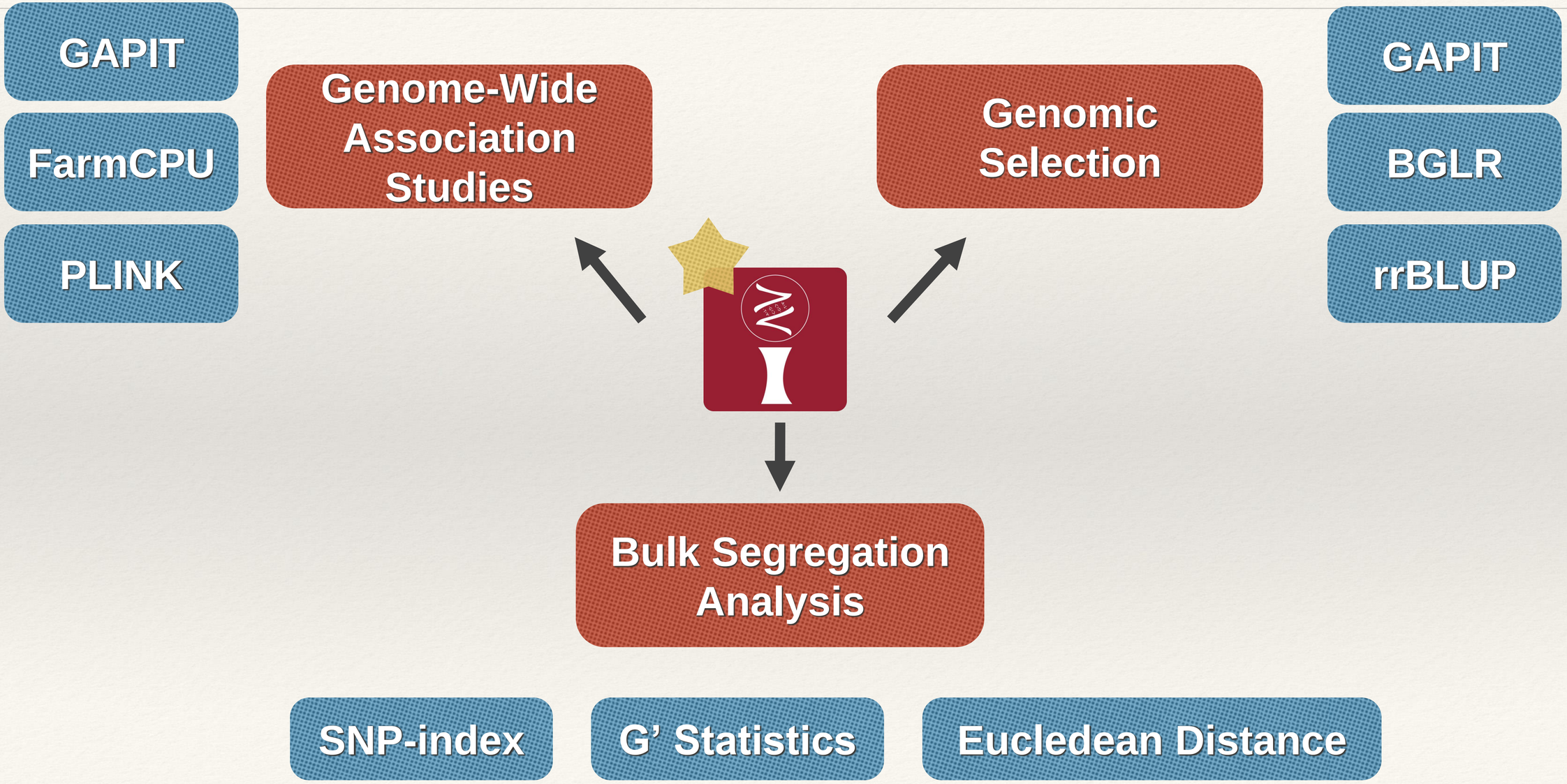
Predict Phenotype



Bulk Segregation Analysis

Finding Associated Genes by Pool Sequencing

Embedded Tools in One Place!



Unfortunately… not all formats work on them

Tool	Supported Format	
GAPIT	Numeric	Hapmap
FarmCPU	Numeric	
BGLR	Numeric	
rrBLUP	Numeric	
PLINK	PLINK	Binary

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rrBLUP	Numeric	
PLINK	PLINK	Binary

?

VCF

Inspect the format

Hapmap

```
rs  alleles chrom pos strand  assembly  center  protLSID  assayLSID panel QCcode  33-16 38-11 4
CML157Q CML158Q CML218  CML220  CML228  CML238  CML247  CML254  CML258  CML261  CML264  CML277
KI43  KI44  KY21  KY226 KY228 L317  L578  M14 M162W M37W  MEF156-55-2 MO17  MO18W MO1W  MO24W M
PA880 PA91  R109B R168  R177  R229  R4  SA24  SC213R  SC357 SC55  SD40  SD44  SG1533  SG18  T23
PZB00859.1  A/C 1 157104  + AGPv1 Panzea  NA  NA  maize282  NA  CC  CC  CC  CC  AA  CC  AA  AA
CC  CC  CC  CC  CC  AA  CC  AA  NN  AA  CC  CC  CC  CC  CC  AA  CC  CC  CC  CC  AA  CC  CC  AA
CC  CC  CC  CC  CC  CC  AA  CC  CC  AA  CC  CC  AA  AA  AA  AA  CC  CC  CC  CC  CC  CC  CC  CC
PZA01271.1  C/G 1 1947984 + AGPv1 Panzea  NA  NA  maize282  NA  CC  GG  CC  GG  CC  CC  CC  CC
GG  GG  NN  GG  GG  GG  GG  CC  CC  GG  CC  GG  GG  CC  GG  CC  CC  CC  CC  GG  CC  CC  CC  CC
GG  GG  NN  GG  GG  CC  GG  CC  GG  GG  GG  NN  CC  CC  CC  GG  GG  GG  GG  GG  GG  CC  CC  CC
```

PLINK

```
abc1  abc1  0 0 1 1 T T T T T T A A A A C C T T G G C C T T G G A
A A G G T T G G C C A A C C G G A A T T T T C C A A C C G A T T G
A A T T C C C C A A A A T T C C C C T T C C A A G T A A C C C C C
A A T T C C G T C C G G A A C C A A C C C C G G A A T C C A C C C
A A C C G G T T G G G A A A G G C A A A G G A A C C C T C C T T C
T T A A G G T T T T G G T T T T C T C C C C T T G G C C C C G G G
C C G G T T A A C C C C C C C C C A A G G C C C C G G G G G G T T A
```

VCF

```
#CHROM  POS ID  REF ALT QUAL  FILTER  INFO  FORMAT  33-16 38-11 4226  4722  A188  A214N A239  A272  A441-5  A554  A556  A6  A619  A6
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L317  L578  M14 M162W M37W  MEF156-55-2 MO17  MO18W MO1W  MO24W MO44  MO45  MO46  MO47  MOG MP339 MS1334  MS153 MS71  MT42  N192  N2
R229  R4  SA24  SC213R  SC357 SC55  SD40  SD44  SG1533  SG18  T232  T234  T8  TX303 TX601 TZI10 TZI11 TZI16 TZI18 TZI25 TZI8  TZI9
1 157104  PZB00859.1  C A . PASS  . GT  0/0 0/0 0/0 0/0 1/1 0/0 1/1 1/1 0/0 0/0 0/0 1/1 0/0 0/0 0/0 0/0 1/1 ./. 1/1 0/0 0/0 0/0 0/0
0/0 1/1 ./. 1/1 0/0 0/0 0/0 0/0 0/0 1/1 0/0 0/0 0/0 0/0 1/1 0/0 0/0 1/1 1/1 0/0 1/1 0/0 1/1 1/1 1/1 0/0 0/0 1/1 1/1 0/0 1/1 0/0 0/0
1/1 0/0 0/0 1/1 0/0 0/0 1/1 1/1 1/1 1/1 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 1/1 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0
1 1947984 PZA01271.1  G C . PASS  . GT  1/1 0/0 1/1 0/0 1/1 1/1 1/1 1/1 1/1 0/0 1/1 1/1 0/0 1/1 1/1 1/1 1/1 0/0 0/0 0/0 1/1 1/1 1/1
0/0 1/1 1/1 0/0 1/1 0/0 0/0 1/1 0/0 1/1 1/1 1/1 1/1 0/0 1/1 1/1 1/1 1/1 0/0 0/0 0/0 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1
0/0 1/1 0/0 0/0 0/0 ./. 1/1 1/1 1/1 0/0 0/0 0/0 0/0 0/0 0/0 1/1 1/1 1/1 1/1 0/0 0/0 1/1 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 1/1 0/0
1 2914066 PZA03613.2  T G . PASS  . GT  1/1 1/1 1/1 1/1 1/1 0/0 0/0 0/0 1/1 0/0 1/1 0/0 1/1 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0
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0/0 0/0 1/1 0/0 0/0 ./. 1/1 ./. 0/0 0/0 1/1 0/0 0/0 0/0 1/1 0/0 0/0 0/0 0/0 1/1 0/0 0/0 0/0 0/0 0/0 0/0 ./. 0/0 0/0 0/0 1/1 0/0 1/1
```
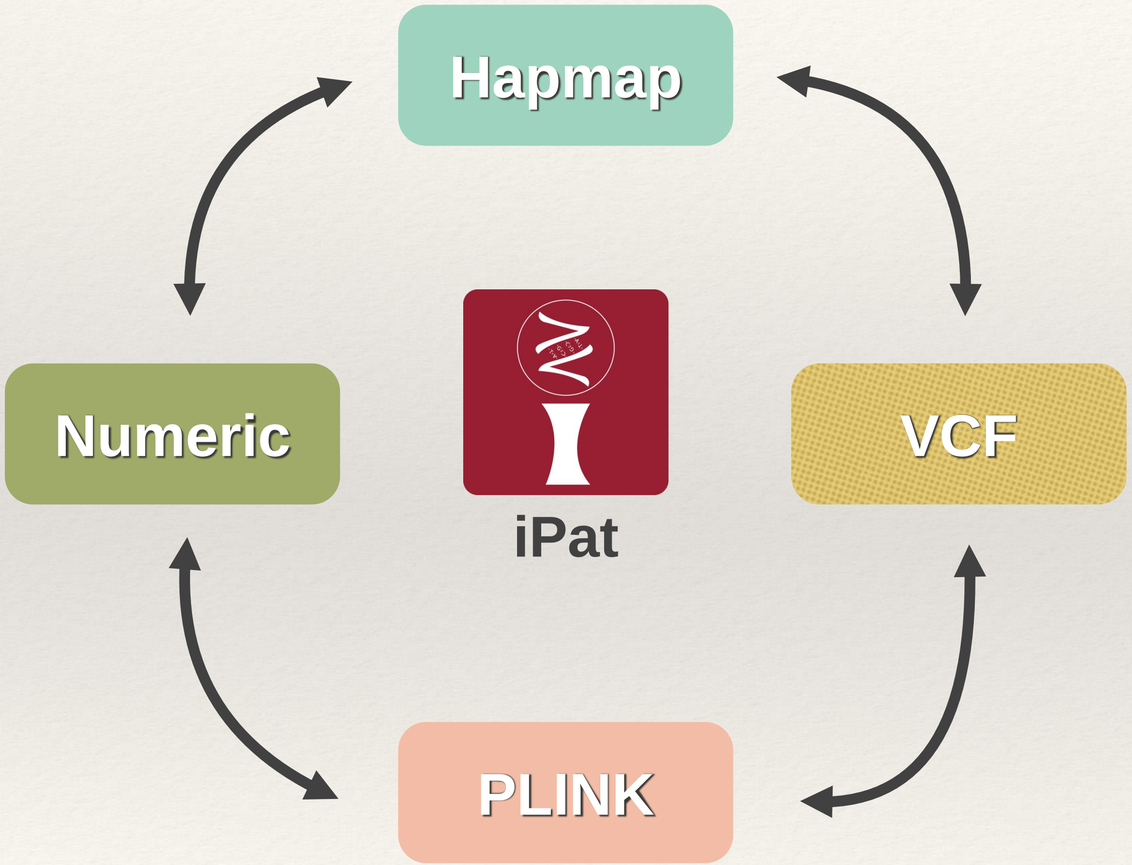

Format Free



No need to spend effort on format conversion

Let’s work with iPat step by step!

Task : GWAS

Import Data → **Quality Control** → **Define a Method** → **Inspect Results**

Import Data

```
genotype = read.table("data.hmp", header = T, sep = "\t")
phenotype = read.table("data.txt", header = T, sep = "\t")
```

Import Data

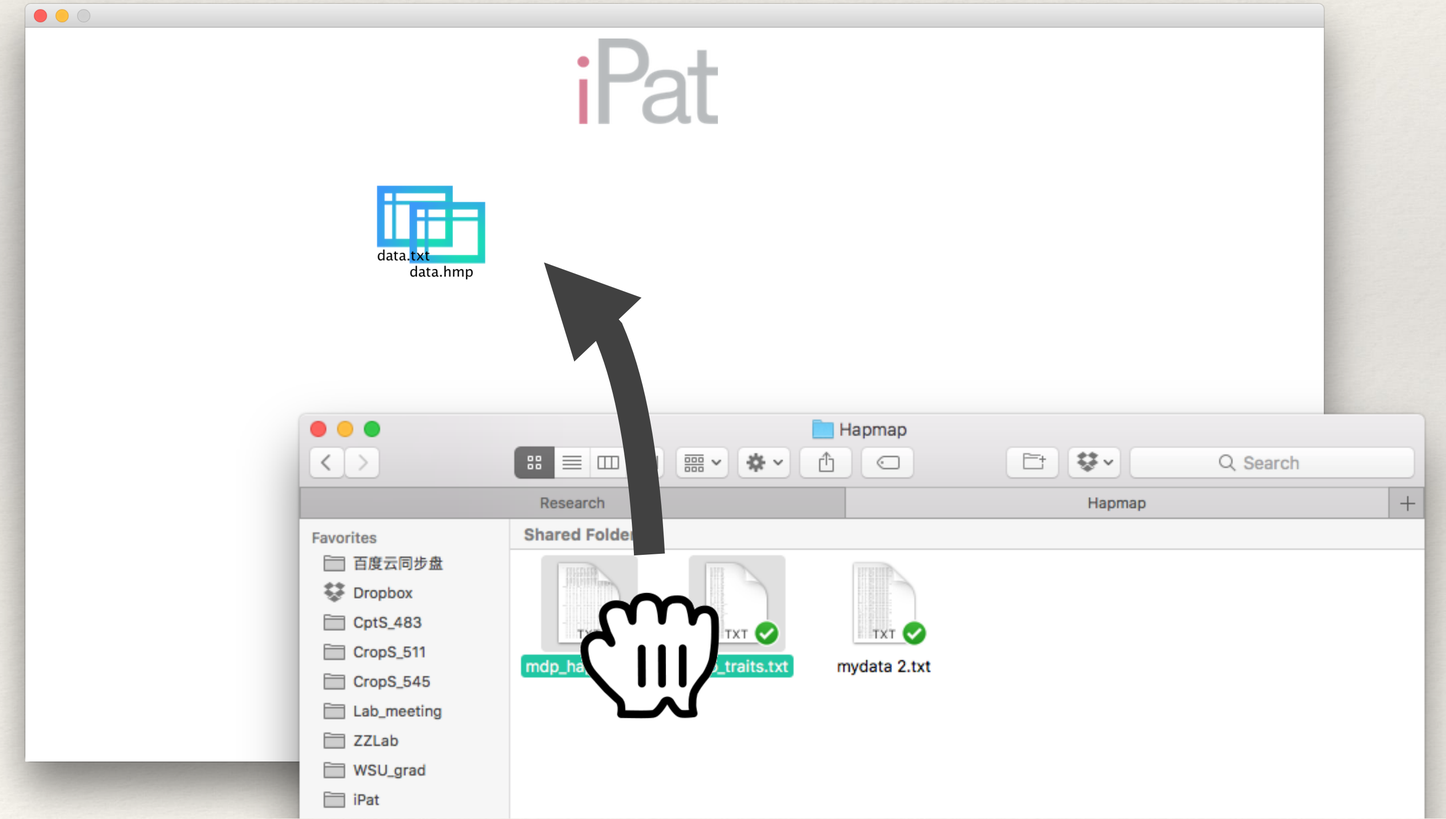
```
genotype = read.table("data.hmp", header = T, sep = "\t")
phenotype = read.table("data.txt", header = T, sep = "\t")
```

Does data contain a header?

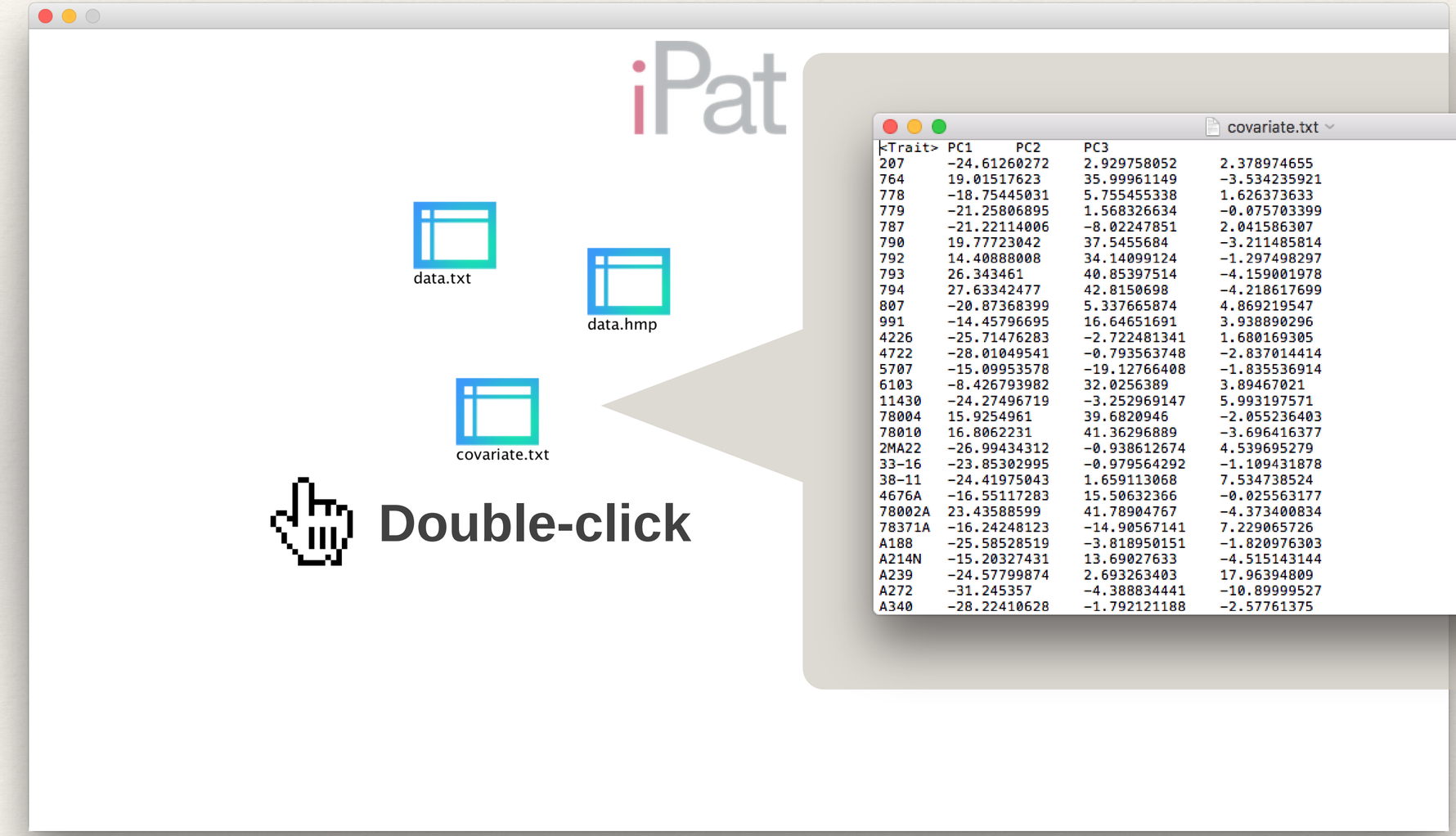
What's the delimiter? Tab? Comma? Space?

Drag and Drop To Import

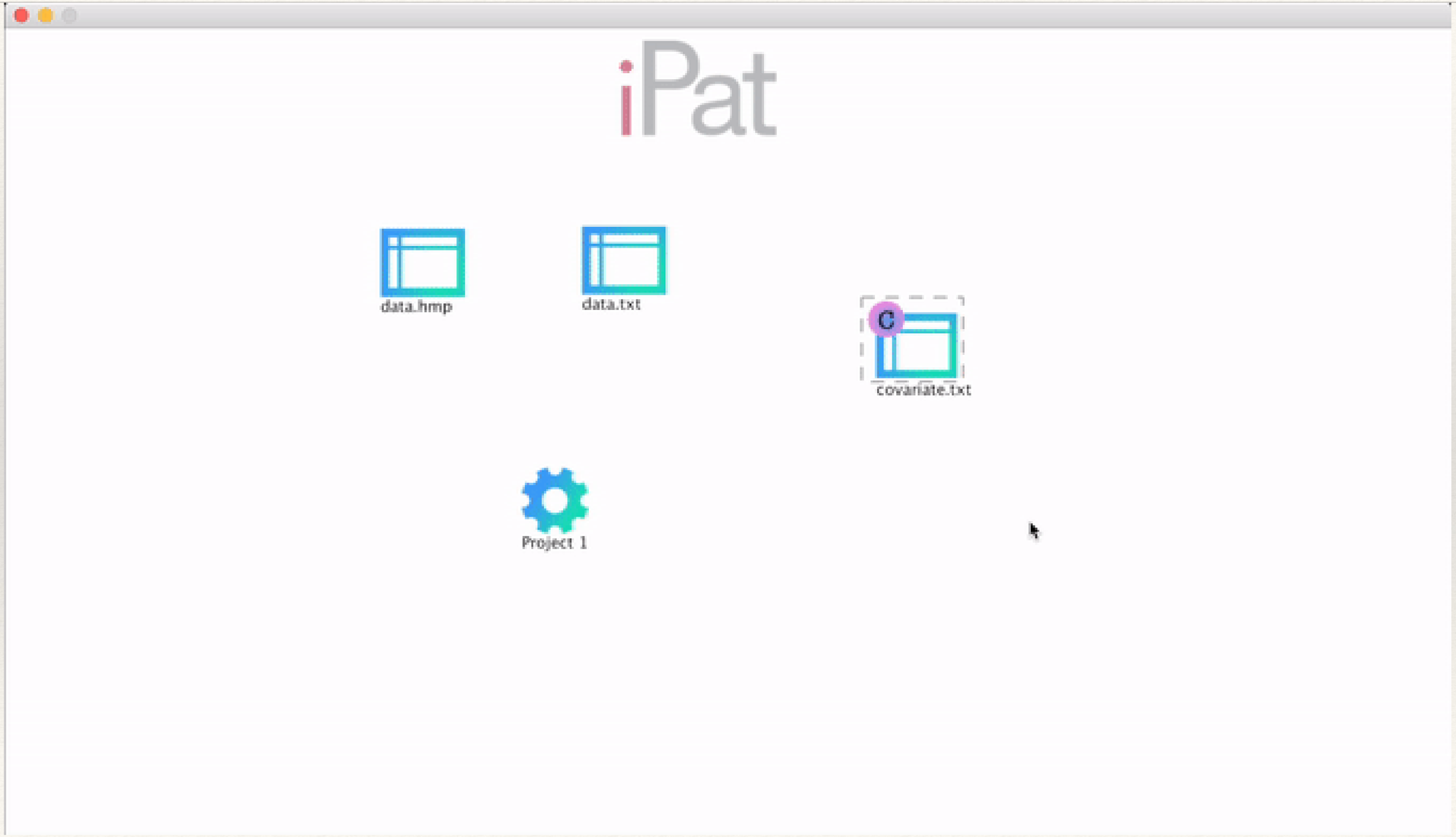
Detect the header and delimiter automatically



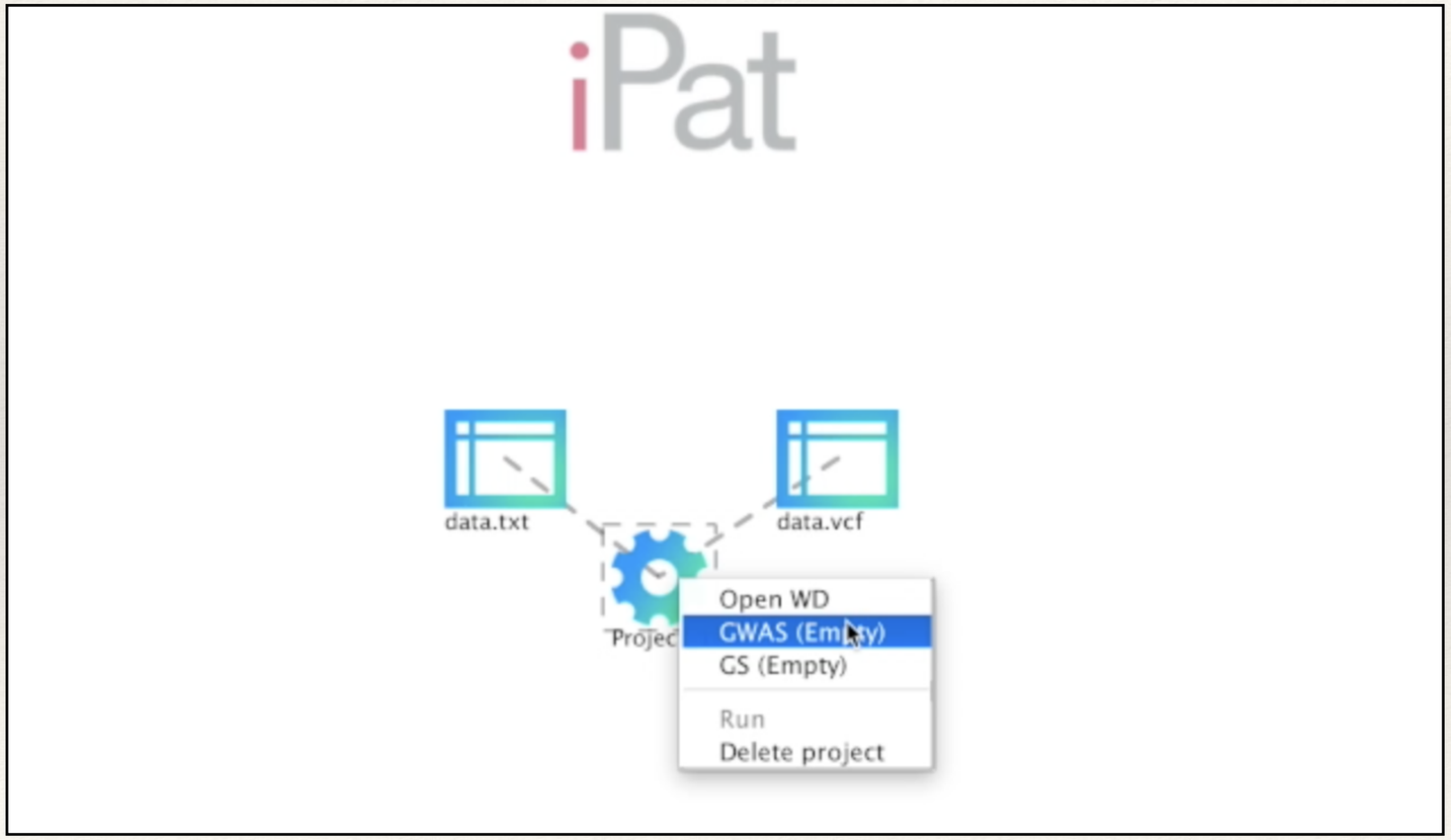
Inspect

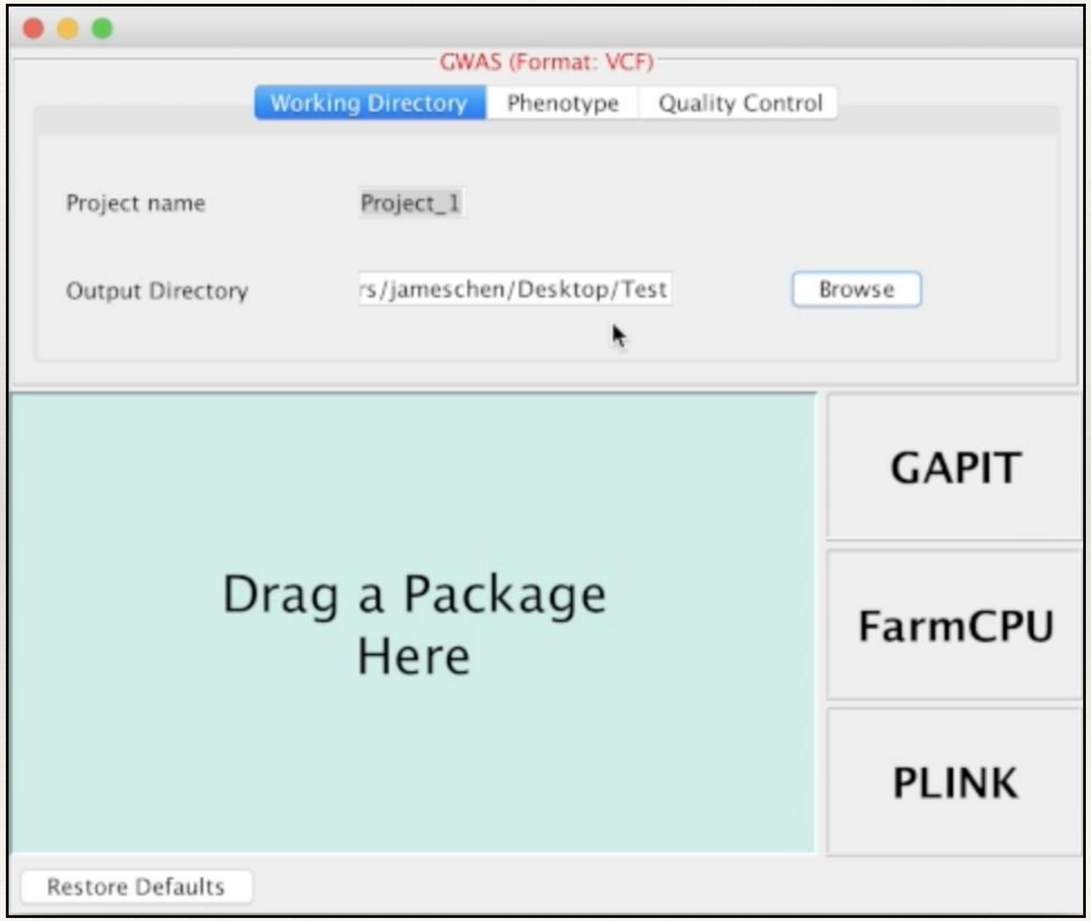

iPat
data.txt
data.hmp
covariate.txt
Double-click
covariate.txt
<Trait> PC1 PC2 PC3
207 -24.61260272 2.929758052 2.378974655
764 19.01517623 35.99961149 -3.534235921
778 -18.75445031 5.755455338 1.626373633
779 -21.25806895 1.568326634 -0.075703399
787 -21.22114006 -8.02247851 2.041586307
790 19.77723042 37.5455684 -3.211485814
792 14.40888008 34.14099124 -1.297498297
793 26.343461 40.85397514 -4.159001978
794 27.63342477 42.8150698 -4.218617699
807 -20.87368399 5.337665874 4.869219547
991 -14.45796695 16.64651691 3.938890296
4226 -25.71476283 -2.722481341 1.680169305
4722 -28.01049541 -0.793563748 -2.837014414
5707 -15.09953578 -19.12766408 -1.835536914
6103 -8.426793982 32.0256389 3.89467021
11430 -24.27496719 -3.252969147 5.993197571
78004 15.9254961 39.6820946 -2.055236403
78010 16.8062231 41.36296889 -3.696416377
2MA22 -26.99434312 -0.938612674 4.539695279
33-16 -23.85302995 -0.979564292 -1.109431878
38-11 -24.41975043 1.659113068 7.534738524
4676A -16.55117283 15.50632366 -0.025563177
78002A 23.43588599 41.78904767 -4.373400834
78371A -16.24248123 -14.90567141 7.229065726
A188 -25.58528519 -3.818950151 -1.820976303
A214N -15.20327431 13.69027633 -4.515143144
A239 -24.57799874 2.693263403 17.96394809
A272 -31.245357 -4.388834441 -10.89999527
A340 -28.22410628 -1.792121188 -2.57761375

Build a Module



Define Your Analysis

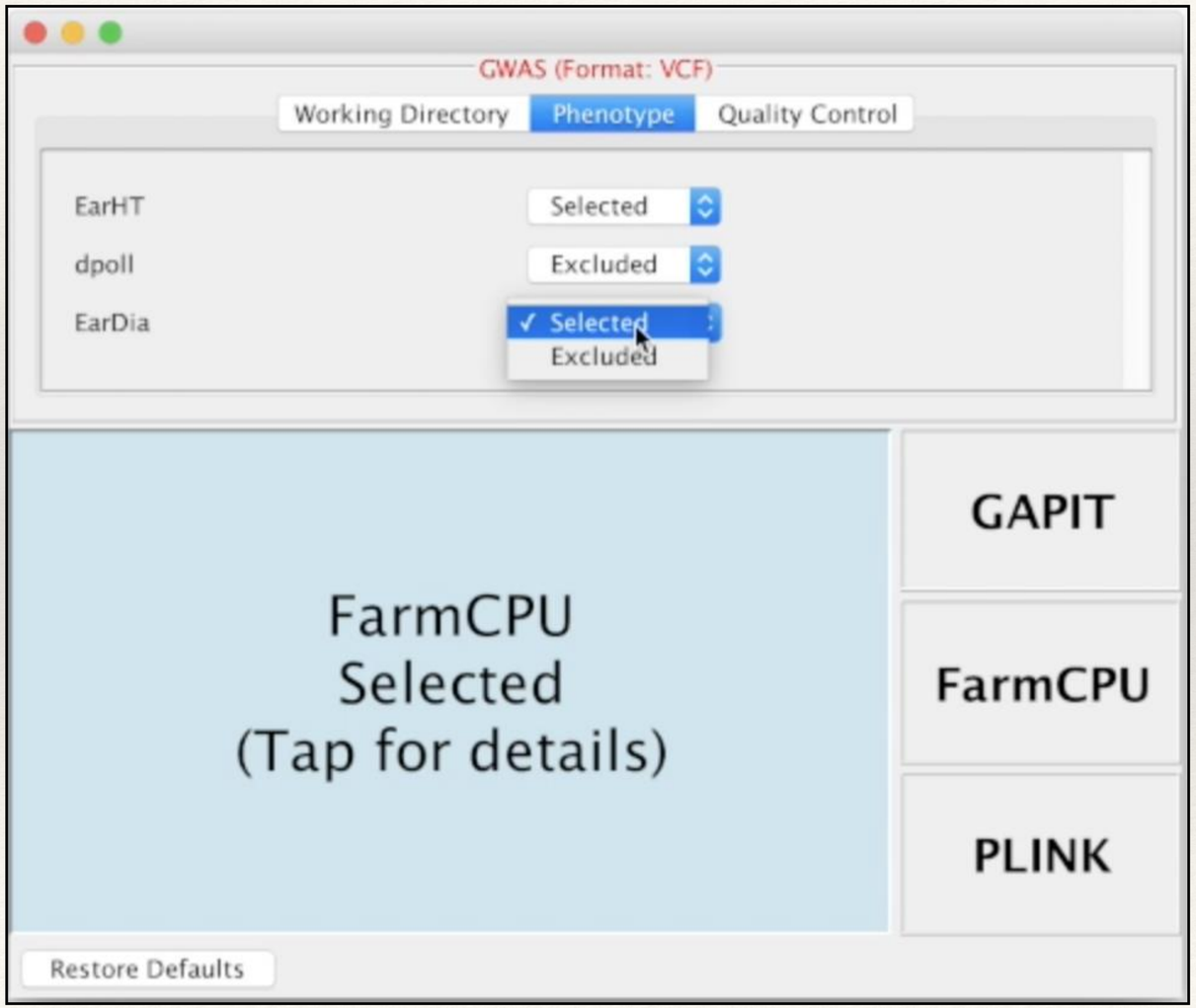


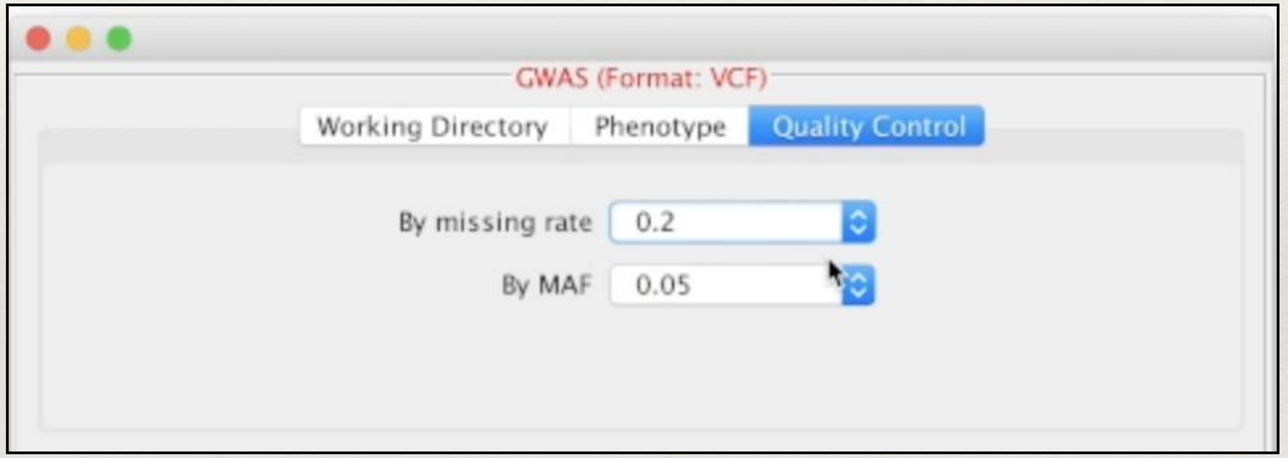


Missing Rate? Minor Allele Frequency?

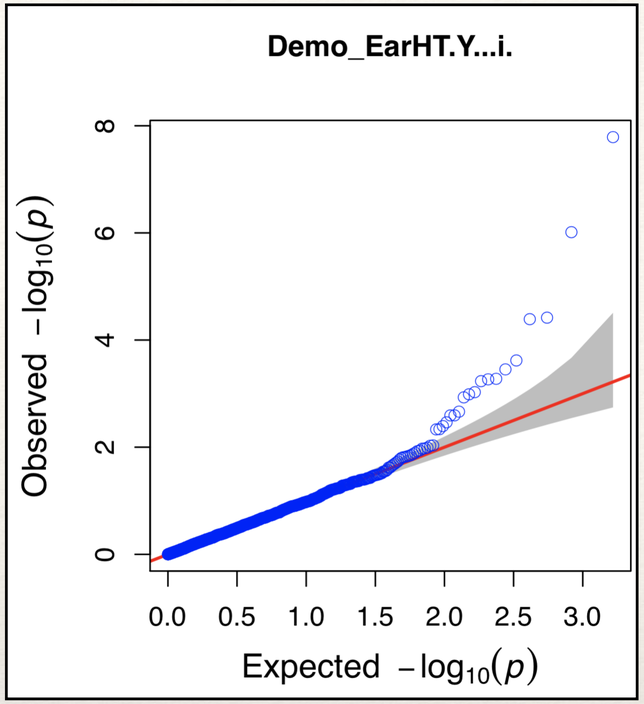
```
phenotype = phtnoeyp[,c(2, 3)]
MS = is.na(genotype) %>%
      apply(2, function(x) sum(x)/length(x))
MAF = apply(genotype, 2, mean) %>%
       as.matrix() %>%
       apply(1, function(x) min(1 - x/2, x/2))
```

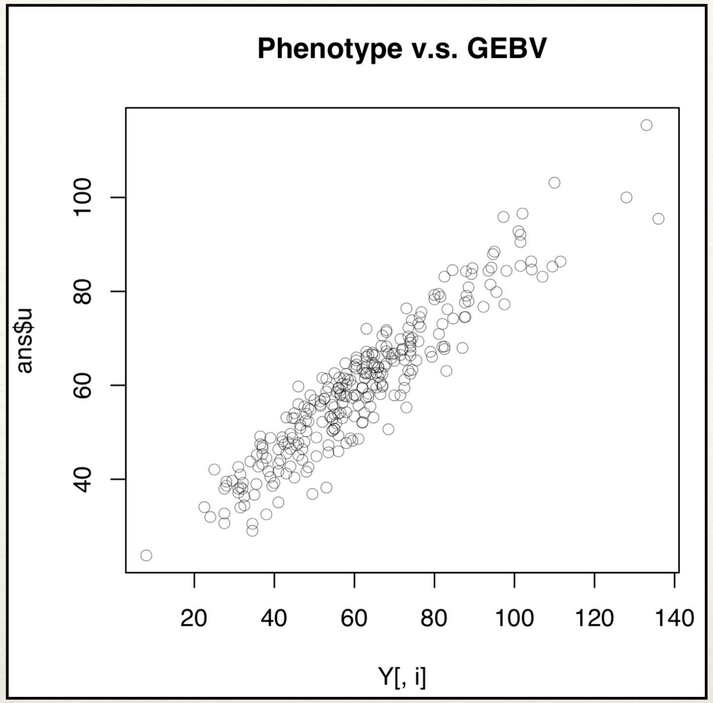
iPat Got You Back!

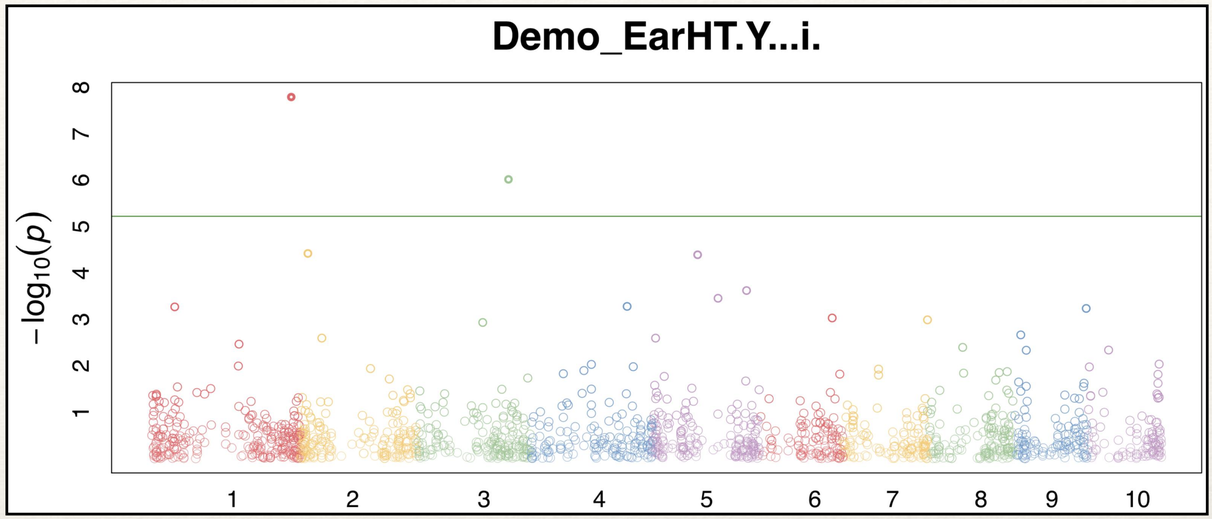




iPat







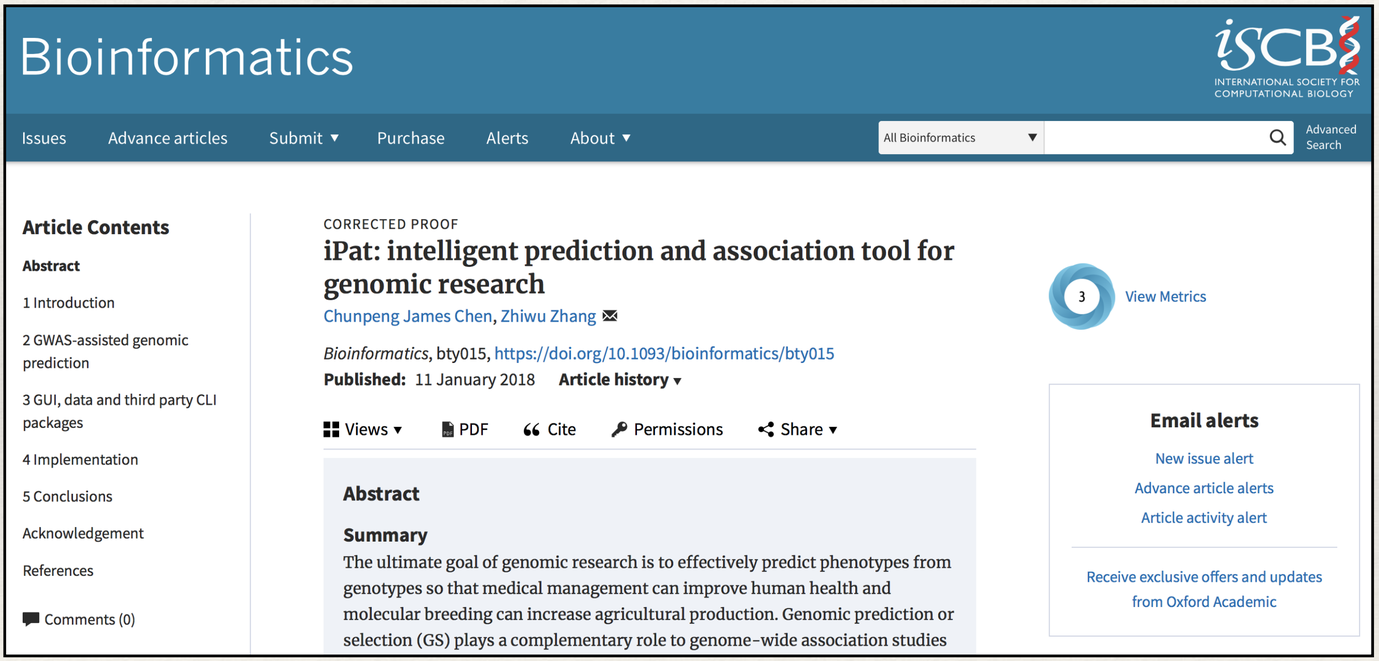
Breeding value

taxa	u	u.SE
33-16	53.1213677206192	8.05706131458929
38-11	76.7092223273507	8.11027035267517
4226	62.6168677588951	7.92749161327708
4722	70.9413420726807	7.37336167756384
A188	30.6209637249398	7.97636416276851
A214N	63.8441664303389	7.40571054863867
A239	52.4632605177171	8.3795399083574
A272	45.2143214735658	8.38647699841112
A441-5	59.5710810597331	8.45442977368395
A554	41.7105684119449	7.7820324109983
A556	39.477390280773	8.11221141057064
A6	85.3066022321695	8.17941245867077
A619	42.6893547823443	6.96544922422308
A632	53.4090273261965	6.43925558329717
A634	53.3302784522467	7.06167844955625

P value of association test

SNP	Chromosom	Position	P.value	MAF	
PZB00859.1	1	157104	0.315789212723918		0.240213523131673
PZA01271.1	1	1947984	0.0436995168679747		0.48932384341637
PZA03613.2	1	2914066	0.16552837227778		0.290035587188612
PZA03613.1	1	2914171	0.598855533795033		0.250889679715303
PZA03614.2	1	2915078	0.0678701534537391		0.469750889679715
PZA03614.1	1	2915242	0.240188905155287		0.469750889679715
PZA00258.3	1	2973508	0.118528522798418		0.284697508896797
PZA02129.1	1	3706018	0.856262621133709		0.480427046263345
PZA00393.1	1	4175293	0.80813438581583		0.247330960854093
PZA02869.4	1	4429927	0.0974914108116822		0.215302491103203
PZA02869.2	1	4430055	0.559008736584389		0.231316725978648
PZB00919.1	1	5353319	0.998059668362255		0.227758007117438
PZA03093.10	1	8075572	0.485393283284251		0.491103202846975
PZA00181.2	1	8366411	0.262385243401303		0.302491103202847
PZA00528.1	1	8367944	0.74639129220144		0.250889679715303
PZA00175.2	1	8510027	0.0459860426759082		0.414590747330961
PZA00447.6	1	9023947	0.223056121959639		0.494661921708185

Availability



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http://zzlab.net/iPat/

Acknowledgement : Z.Z. Lab

Zhiwu Zhang Laboratory for Statistical Genomics

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