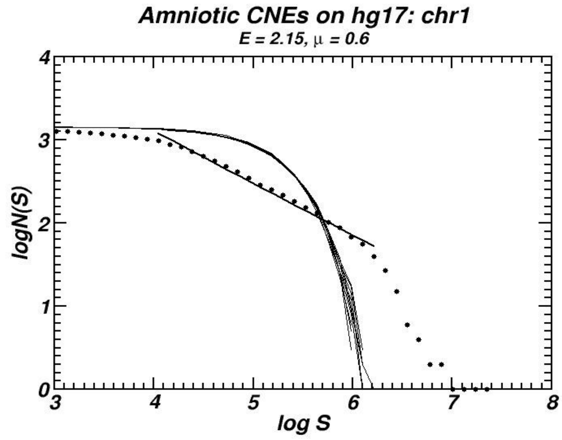
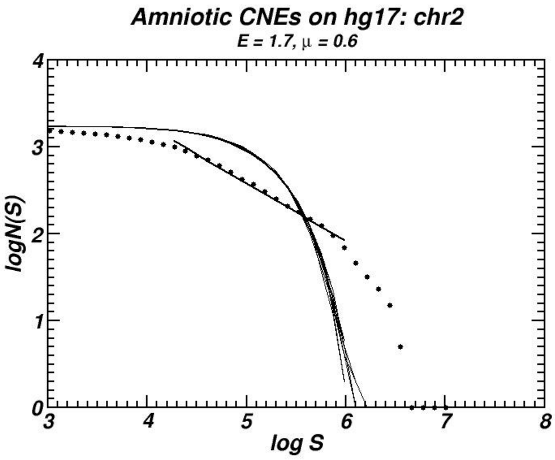
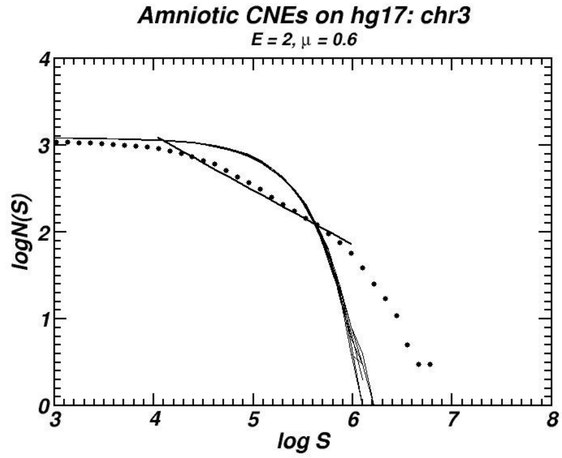
Amniotic CNEs (Dataset iib)


Amniotic CNEs on hg17: chr1

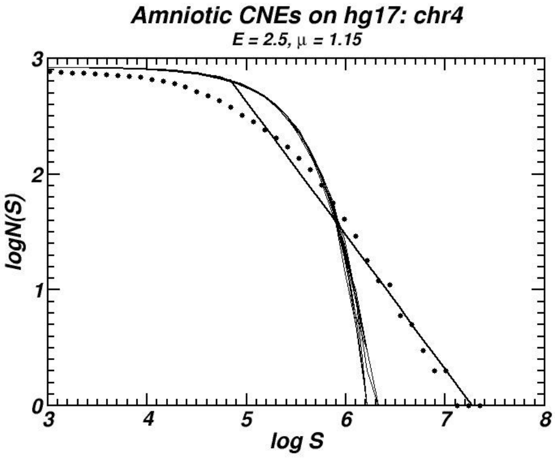
E = 2.15, μ = 0.6


Amniotic CNEs on hg17: chr2

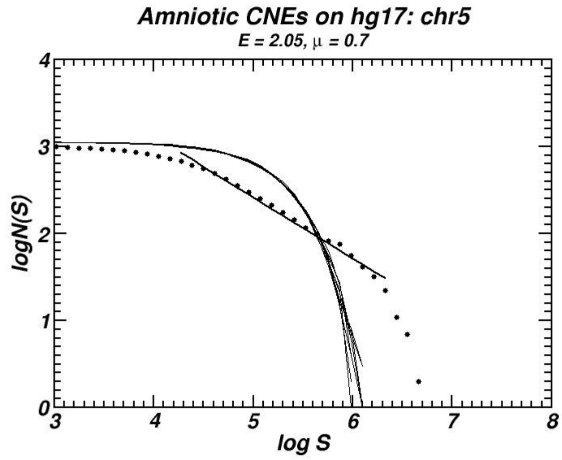
E = 1.7, μ = 0.6


Amniotic CNEs on hg17: chr3

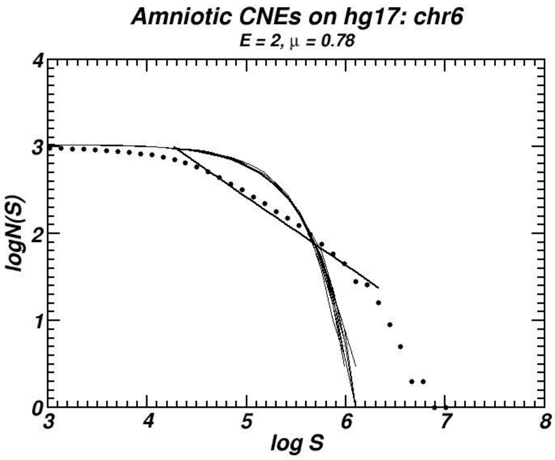
E = 2, μ = 0.6


Amniotic CNEs on hg17: chr4

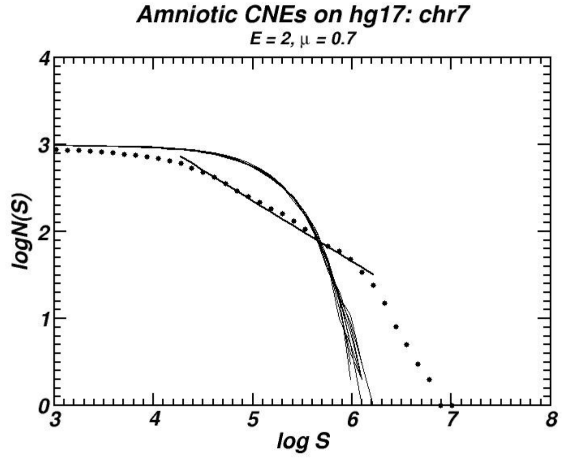
E = 2.5, μ = 1.15

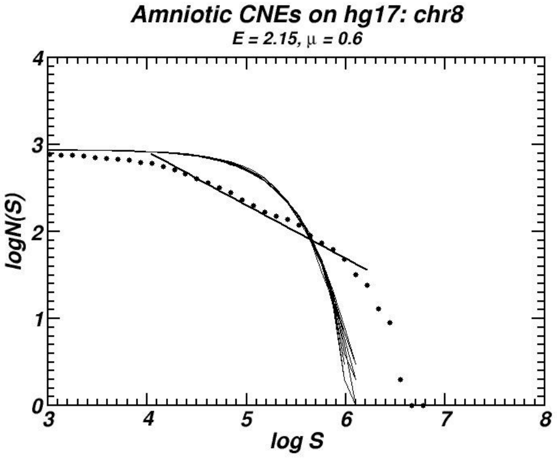

Amniotic CNEs on hg17: chr5

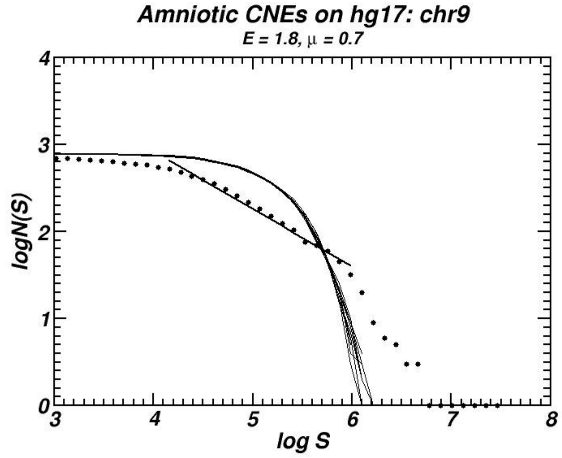
E = 2.05, μ = 0.7

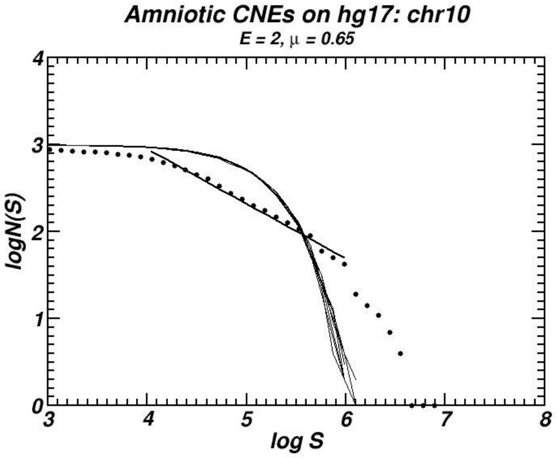

Amniotic CNEs on hg17: chr6

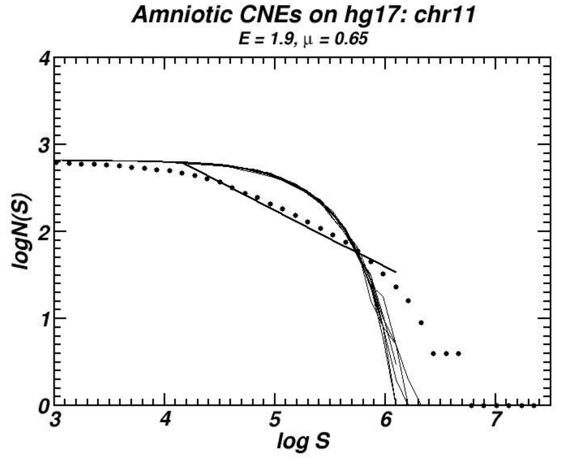
E = 2, μ = 0.78

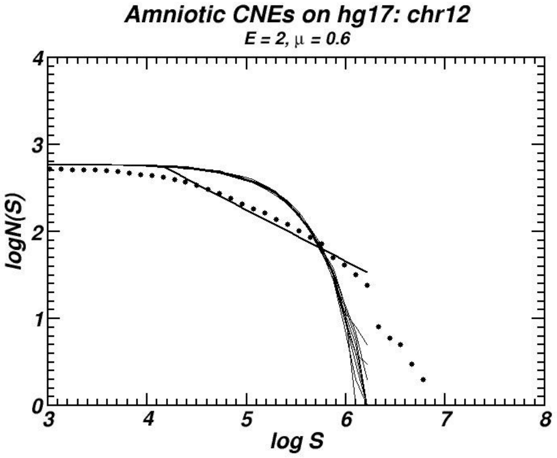

Amniotic CNEs on hg17: chr7
E = 2, μ = 0.7
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

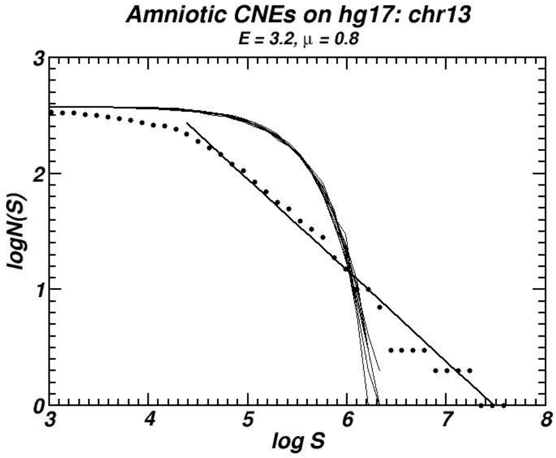

Amniotic CNEs on hg17: chr8
E = 2.15, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

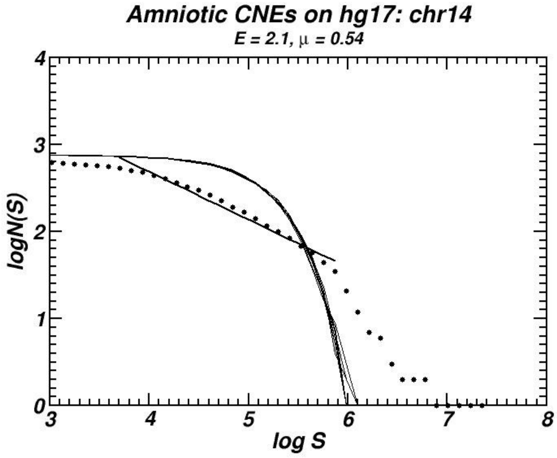

Amniotic CNEs on hg17: chr9
E = 1.8, μ = 0.7
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

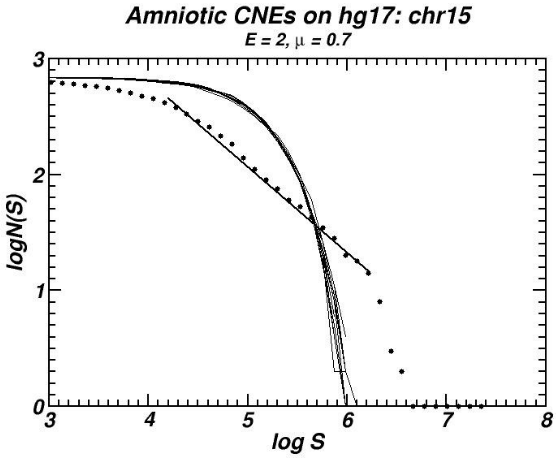

Amniotic CNEs on hg17: chr10
E = 2, μ = 0.65
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

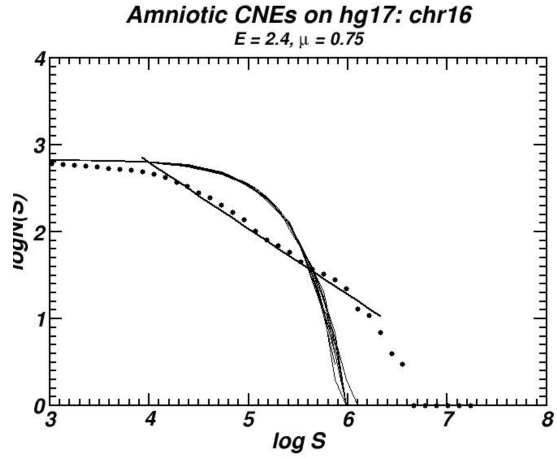

Amniotic CNEs on hg17: chr11
E = 1.9, μ = 0.65
logN(S)
log S
0
1
2
3
4
3
4
5
6
7


Amniotic CNEs on hg17: chr12
E = 2, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


Amniotic CNEs on hg17: chr13
E = 3.2, μ = 0.8
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Amniotic CNEs on hg17: chr14
E = 2.1, μ = 0.54
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


Amniotic CNEs on hg17: chr15
E = 2, μ = 0.7
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Amniotic CNEs on hg17: chr16
E = 2.4, μ = 0.75
logN(S)
log S
0
1
2
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4
3
4
5
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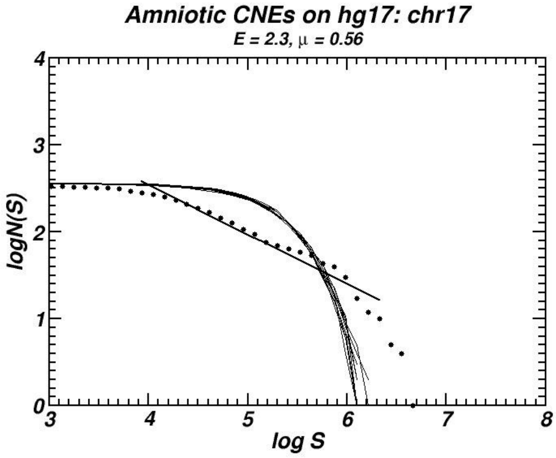
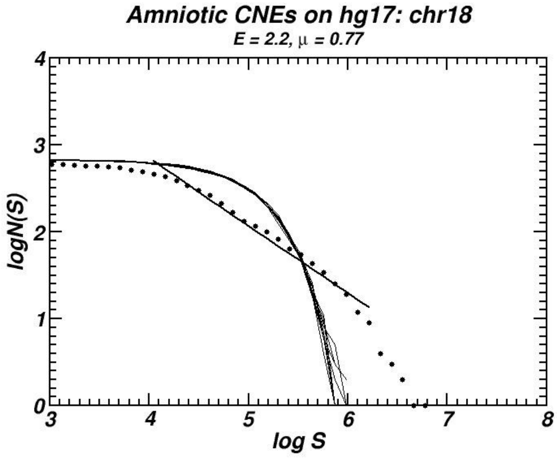
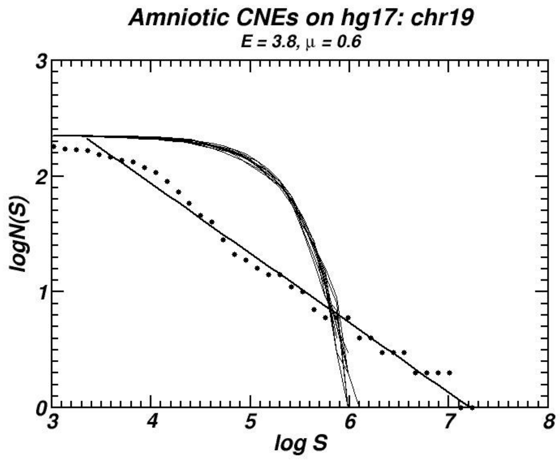
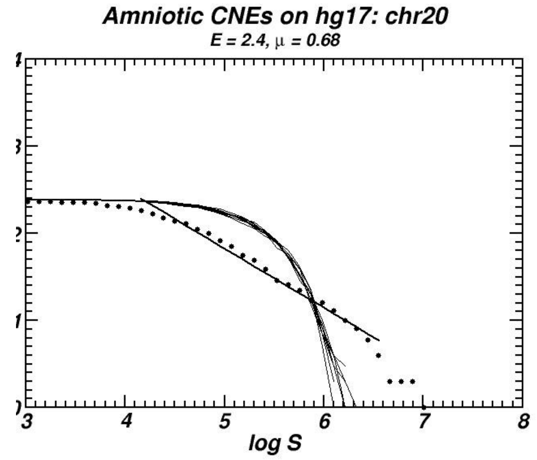
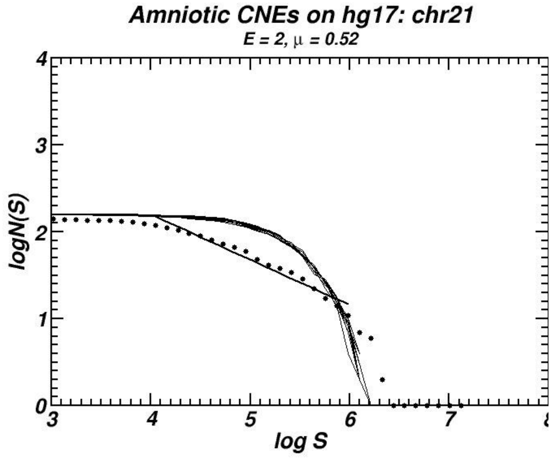
7
8

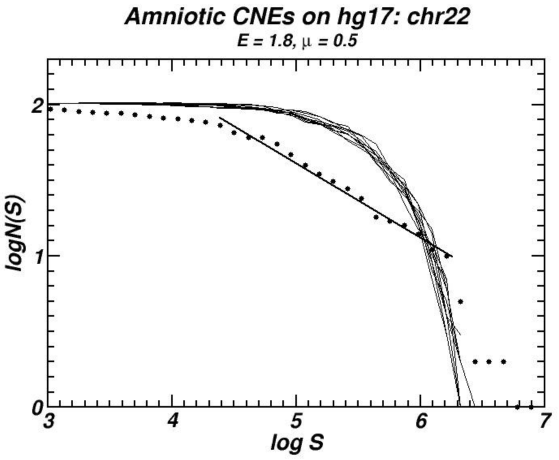

Amniotic CNEs on hg17: chr17
E = 2.3, μ = 0.56
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


Amniotic CNEs on hg17: chr18
E = 2.2, μ = 0.77
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

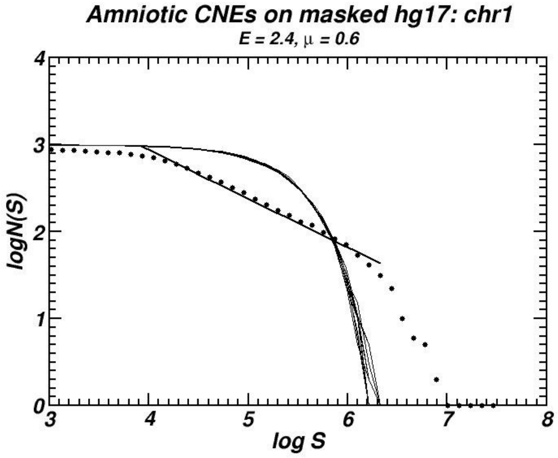

Amniotic CNEs on hg17: chr19
E = 3.8, μ = 0.6
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Amniotic CNEs on hg17: chr20
E = 2.4, μ = 0.68
3
4
5
6
7
8

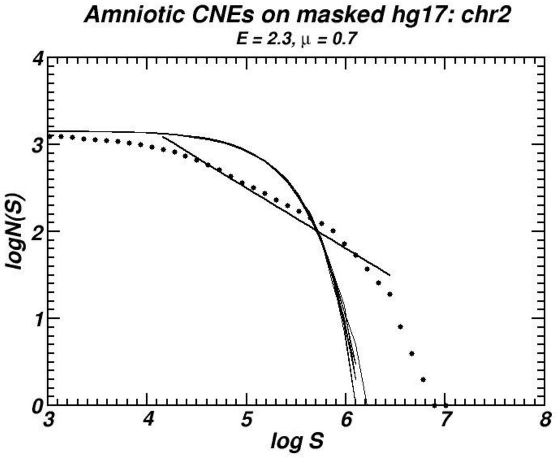

Amniotic CNEs on hg17: chr21
E = 2, μ = 0.52
logN(S)
log S
0
1
2
3
4
3
4
5
6
7


Amniotic CNEs on hg17: chr22
E = 1.8, μ = 0.5
logN(S)
log S
0
1
2
3
4
5
6
7

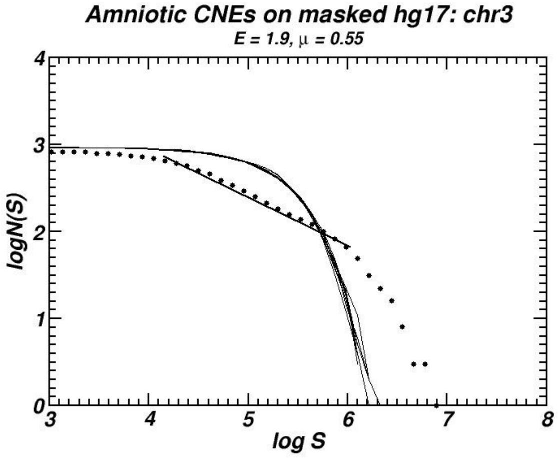
Amniotic CNEs on gene-masked genome


Amniotic CNEs on masked hg17: chr1

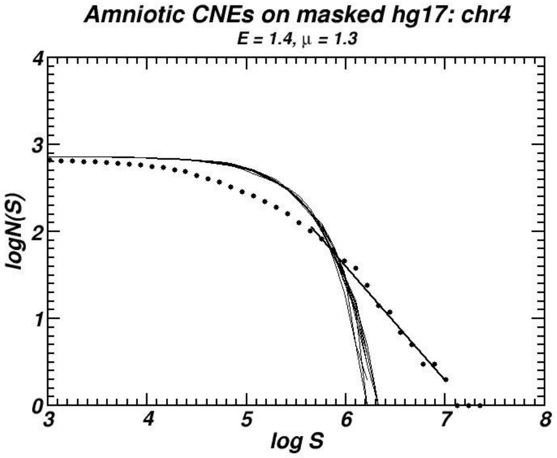
E = 2.4, μ = 0.6


Amniotic CNEs on masked hg17: chr2

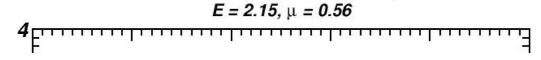
E = 2.3, μ = 0.7


Amniotic CNEs on masked hg17: chr3

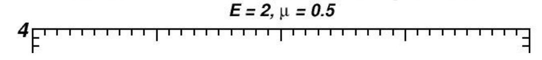
E = 1.9, μ = 0.55


Amniotic CNEs on masked hg17: chr4

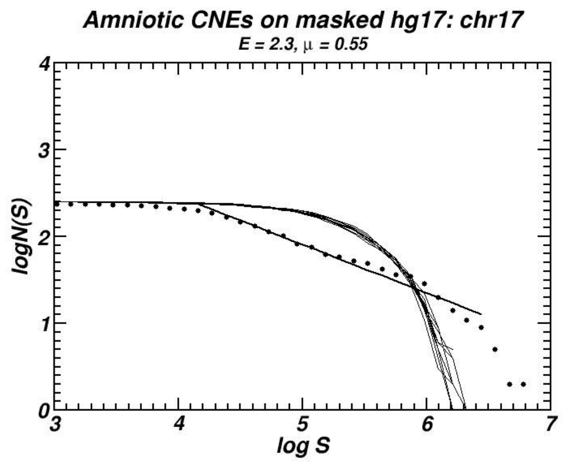
E = 1.4, μ = 1.3


Amniotic CNEs on masked hg17: chr7

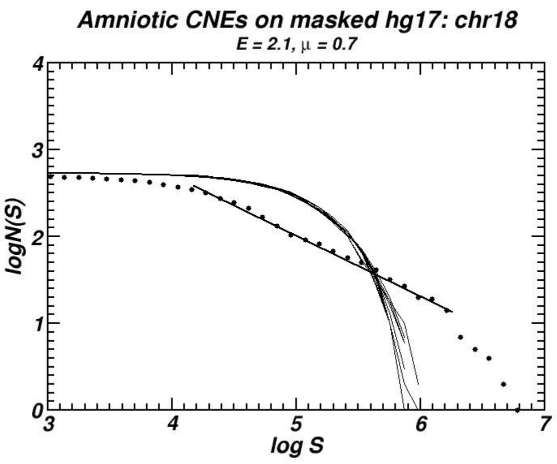
E = 2.15, μ = 0.56


Amniotic CNEs on masked hg17: chr8

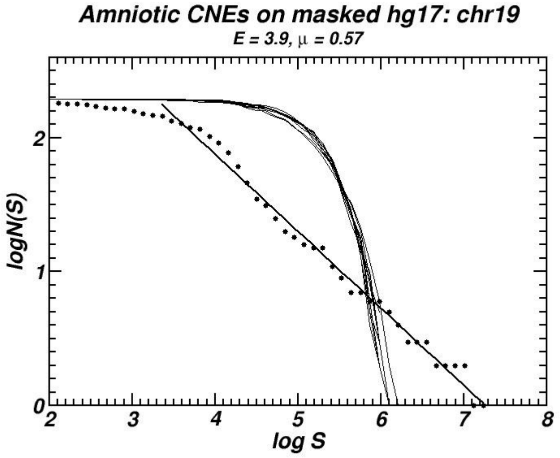
E = 2, μ = 0.5


Amniotic CNEs on masked hg17: chr17

E = 2.3, μ = 0.55

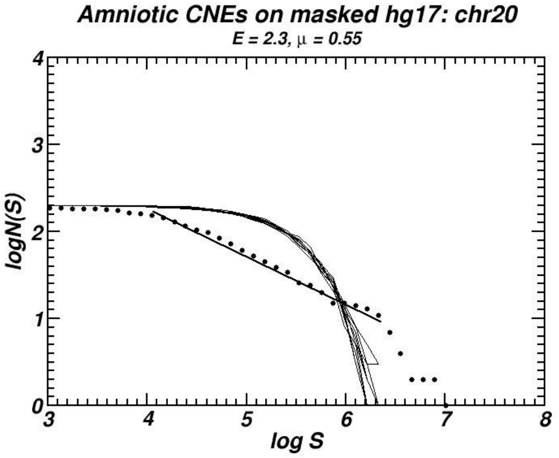

Amniotic CNEs on masked hg17: chr18

E = 2.1, μ = 0.7



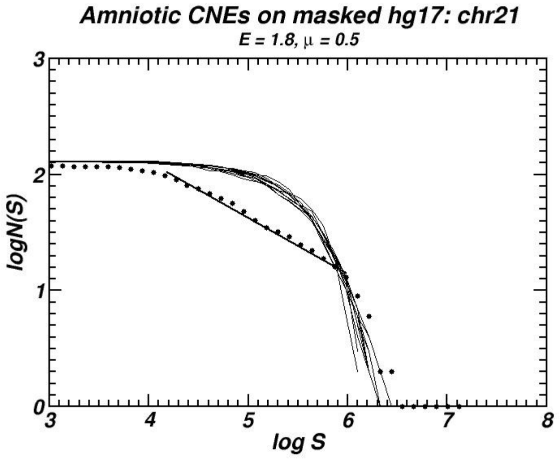
Amniotic CNEs on masked hg17: chr19

$E = 3.9$, $\mu = 0.57$



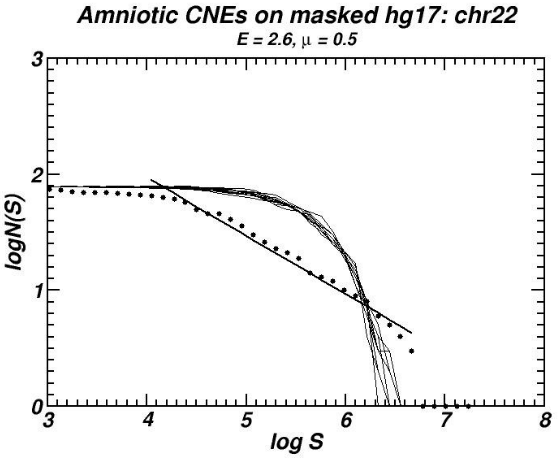
Amniotic CNEs on masked hg17: chr20

$E = 2.3$, $\mu = 0.55$



Amniotic CNEs on masked hg17: chr21

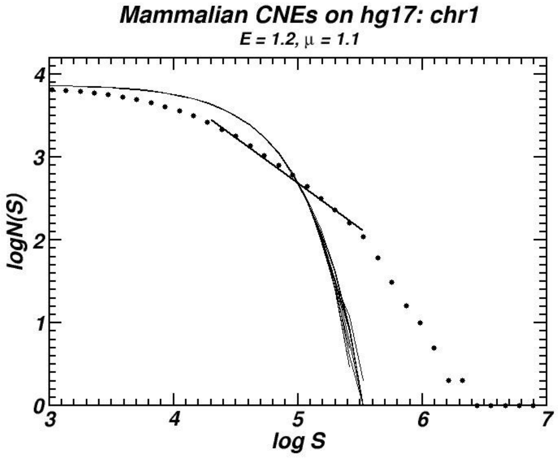
$E = 1.8$, $\mu = 0.5$

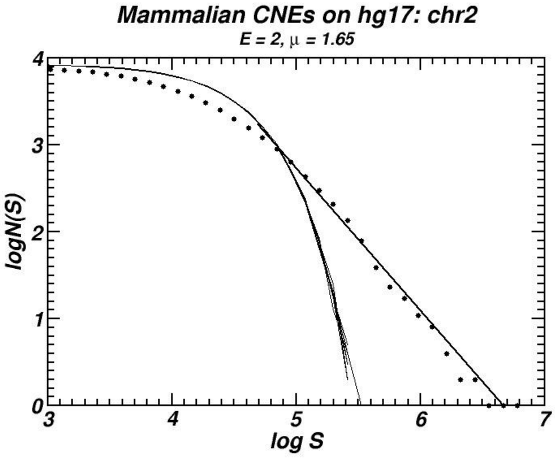


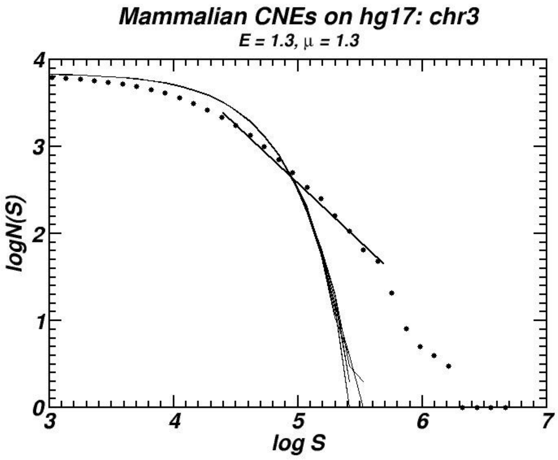
Amniotic CNEs on masked hg17: chr22

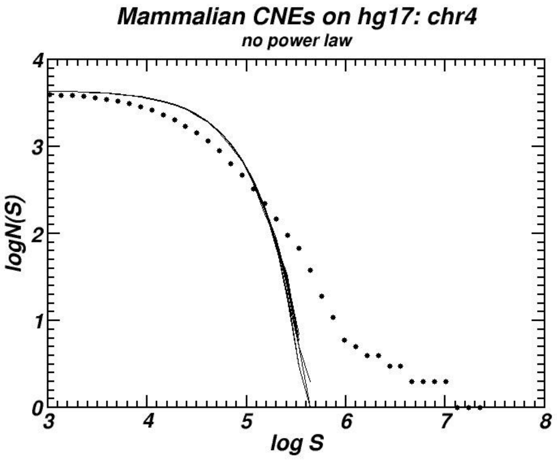
$E = 2.6$, $\mu = 0.5$

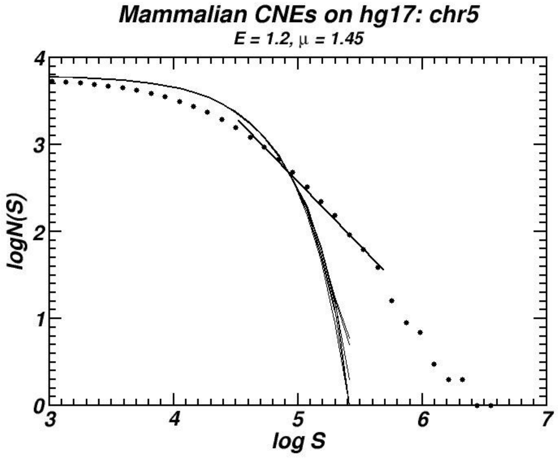
Mammalian CNEs (Dataset iia)

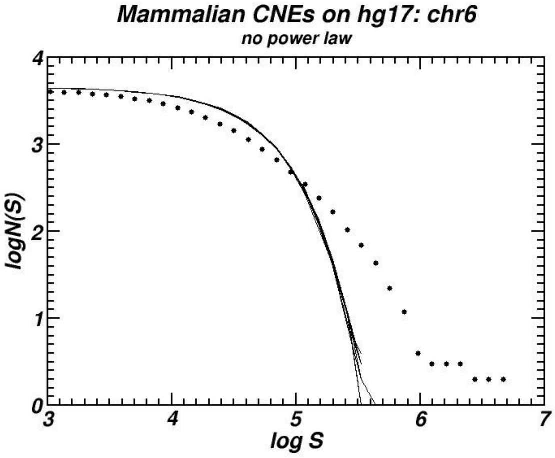


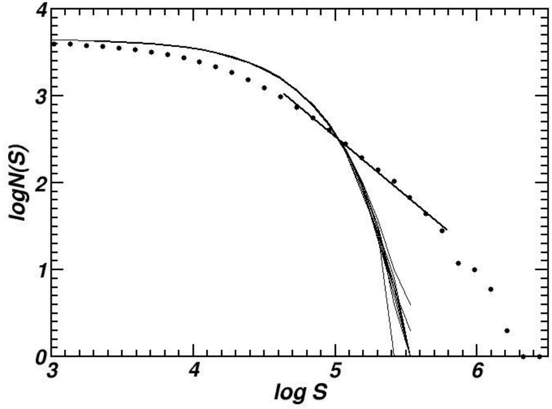






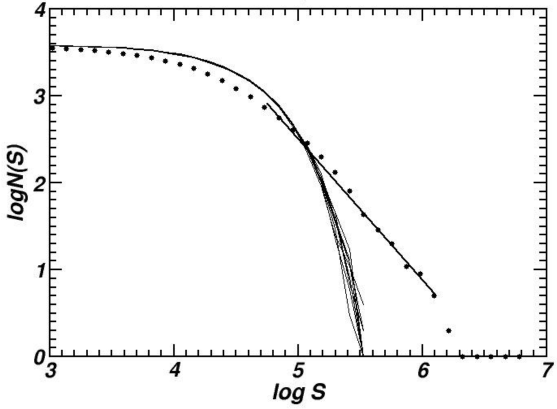






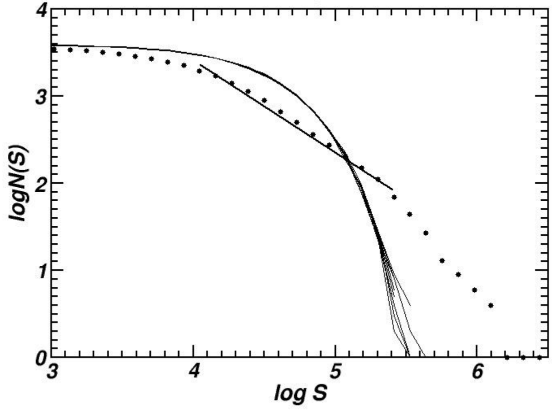
Mammalian CNEs on hg17: chr7

E = 1.2, μ = 1.35



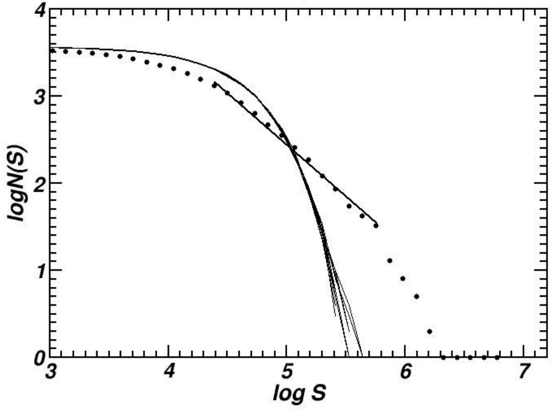
Mammalian CNEs on hg17: chr8

E = 1.4, μ = 1.6



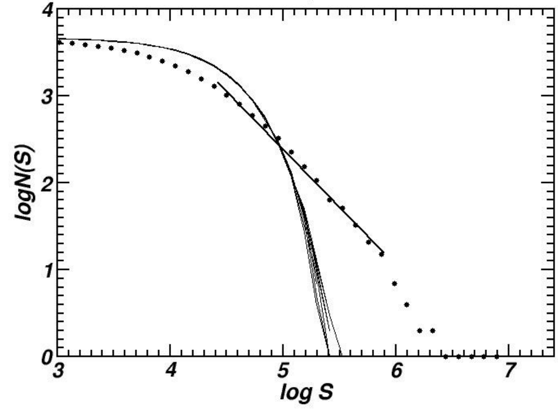
Mammalian CNEs on hg17: chr9

E = 1.4, μ = 1



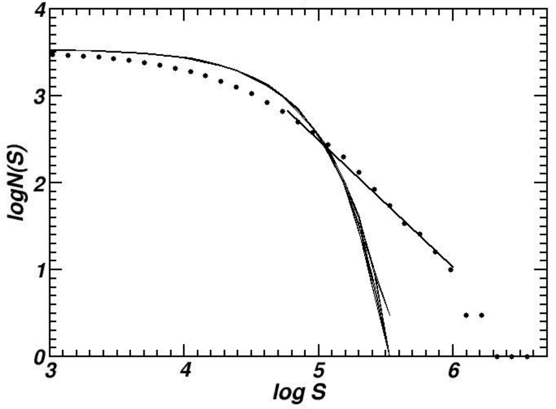
Mammalian CNEs on hg17: chr10

E = 1.4, μ = 1.2



Mammalian CNEs on hg17: chr11

E = 1.5, μ = 1.3

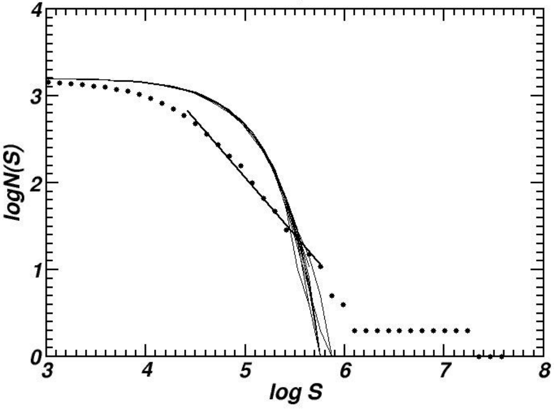


Mammalian CNEs on hg17: chr12

E = 1.25, μ = 1.45

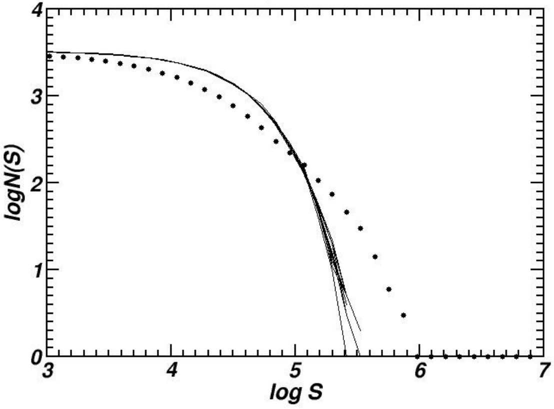
Mammalian CNEs on hg17: chr13

$E = 1.4$, $\mu = 1.3$



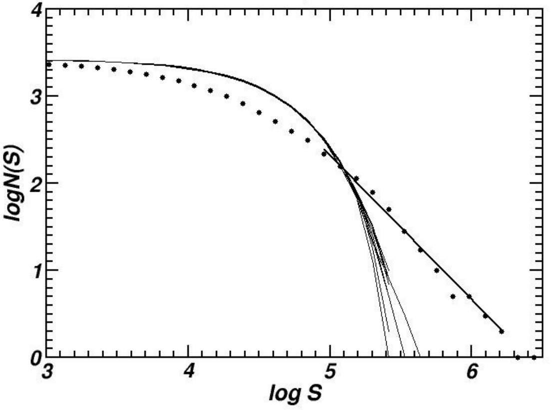
Mammalian CNEs on hg17: chr14

no power law



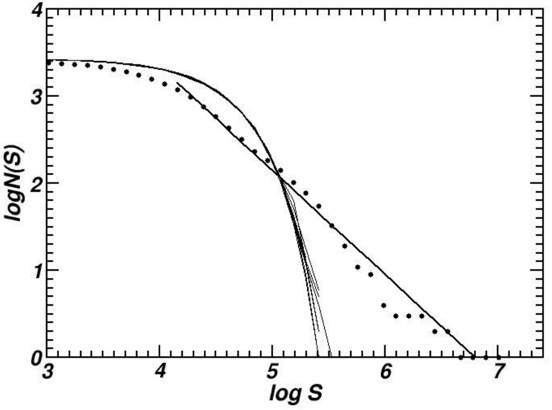
Mammalian CNEs on hg17: chr15

$E = 1.25$, $\mu = 1.7$



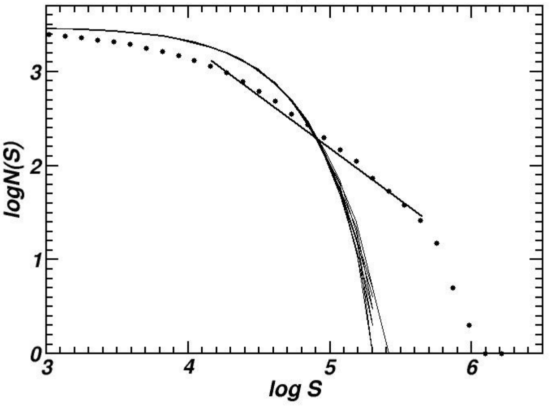
Mammalian CNEs on hg17: chr16

$E = 2.7$, $\mu = 1.2$



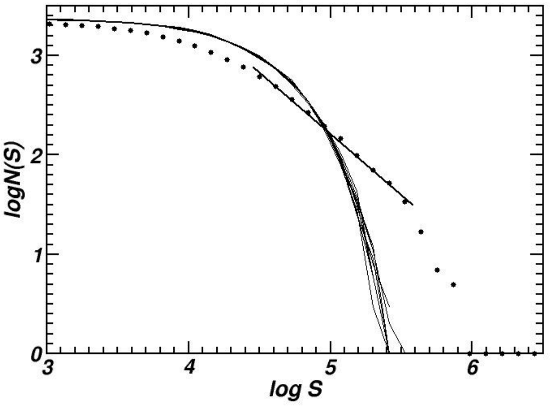
Mammalian CNEs on hg17: chr17

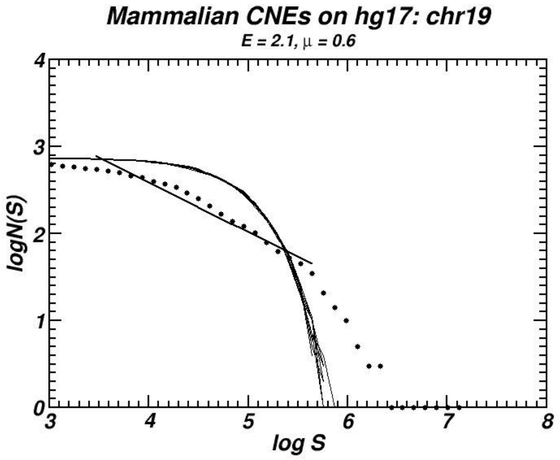
$E = 1.5$, $\mu = 1.1$



Mammalian CNEs on hg17: chr18

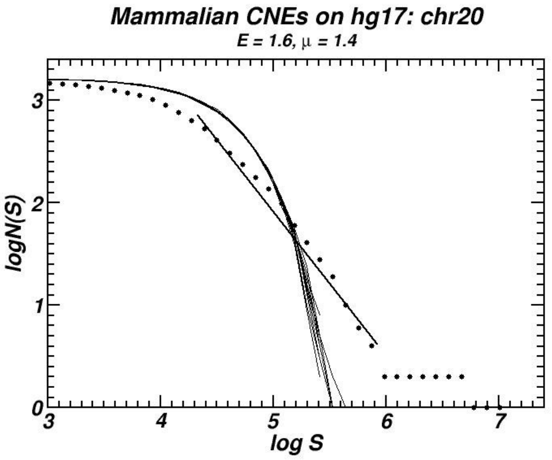
$E = 1.1$, $\mu = 1.2$





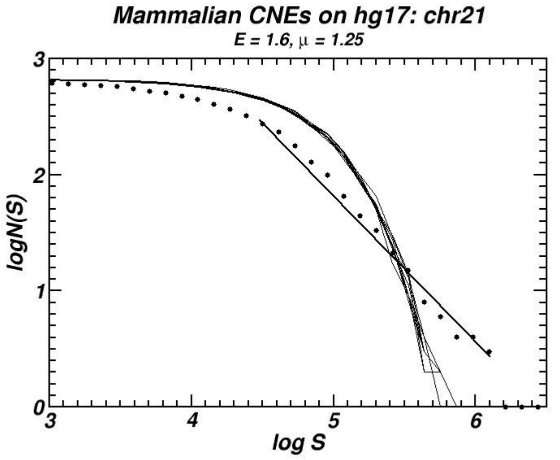
Mammalian CNEs on hg17: chr19

$E = 2.1$, $\mu = 0.6$



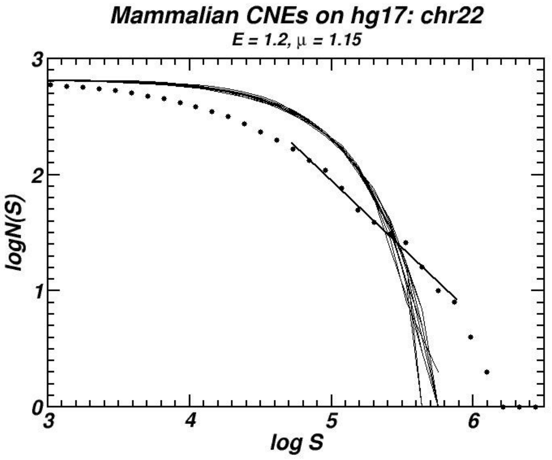
Mammalian CNEs on hg17: chr20

$E = 1.6$, $\mu = 1.4$



Mammalian CNEs on hg17: chr21

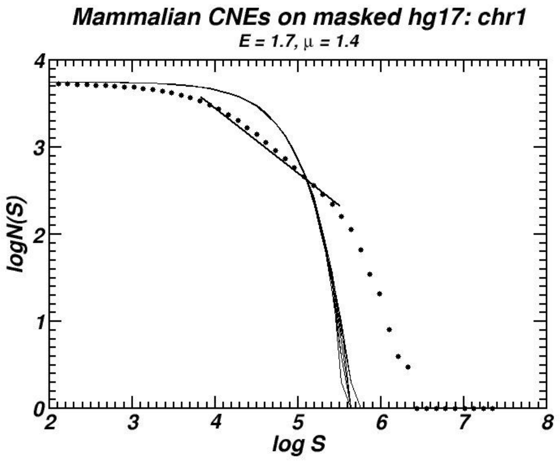
$E = 1.6$, $\mu = 1.25$

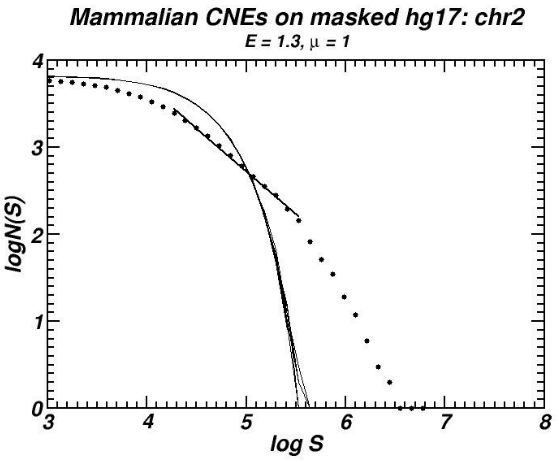


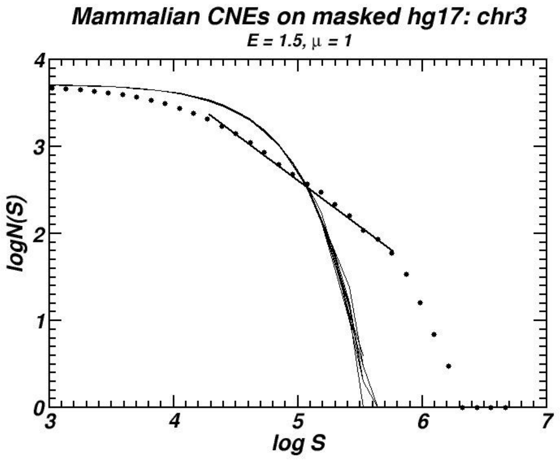
Mammalian CNEs on hg17: chr22

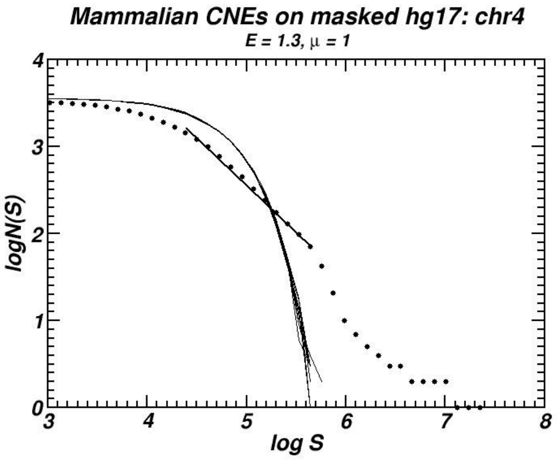
$E = 1.2$, $\mu = 1.15$

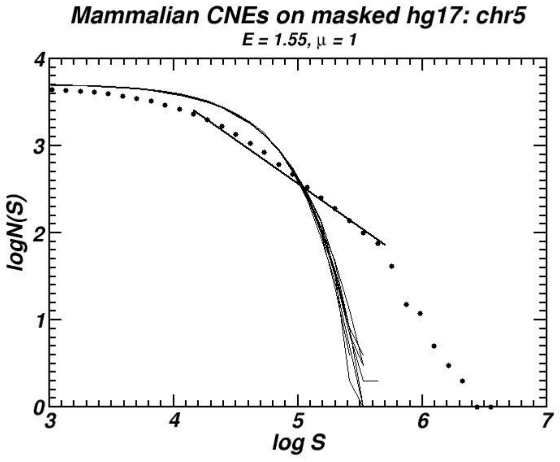
Mammalian CNEs on gene-masked genome

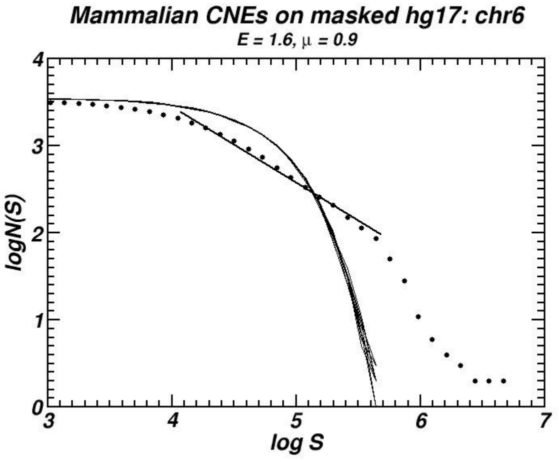


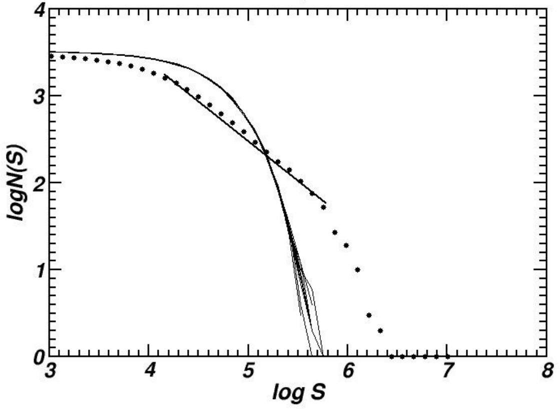






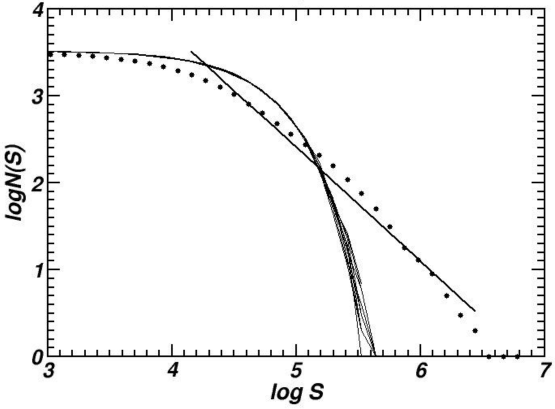






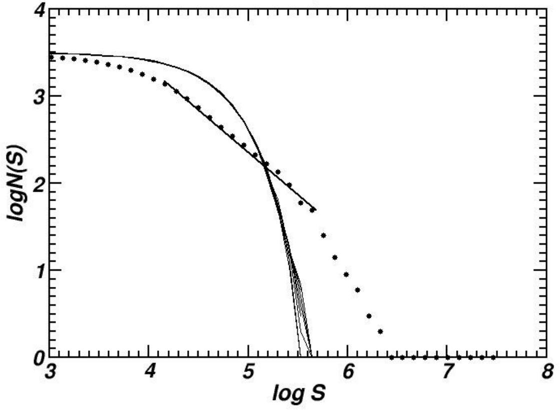
Mammalian CNEs on masked hg17: chr7

E = 1.6, $\mu = 0.9$



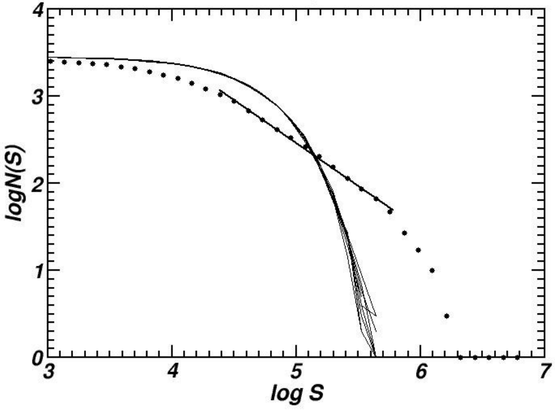
Mammalian CNEs on masked hg17: chr8

E = 2.3, $\mu = 1.3$



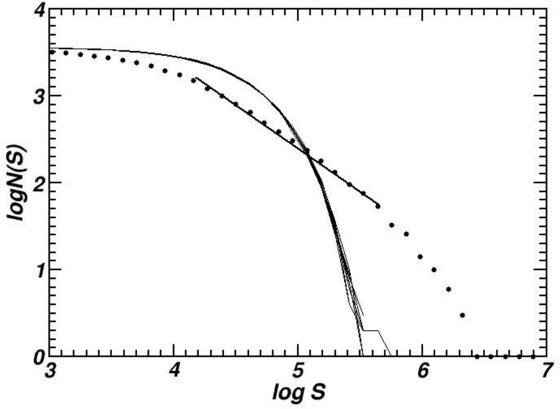
Mammalian CNEs on masked hg17: chr9

E = 1.5, $\mu = 1$



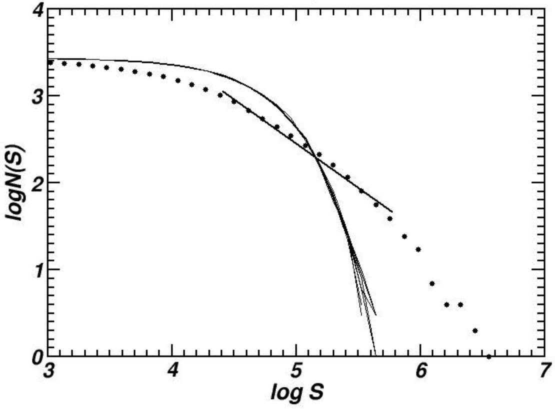
Mammalian CNES on masked hg17: chr10

E = 1.4, $\mu = 1$



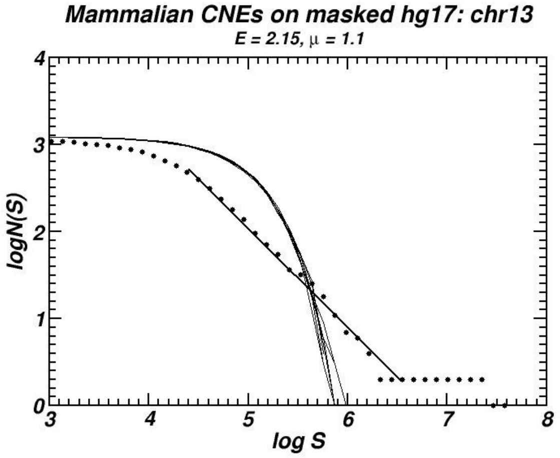
Mammalian CNEs on hg17: chr11

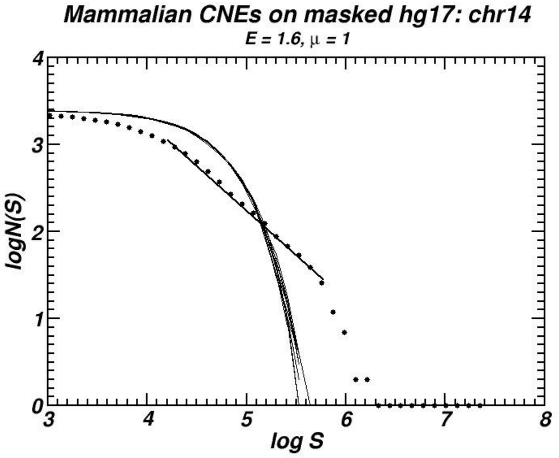
E = 1.5, $\mu = 1$

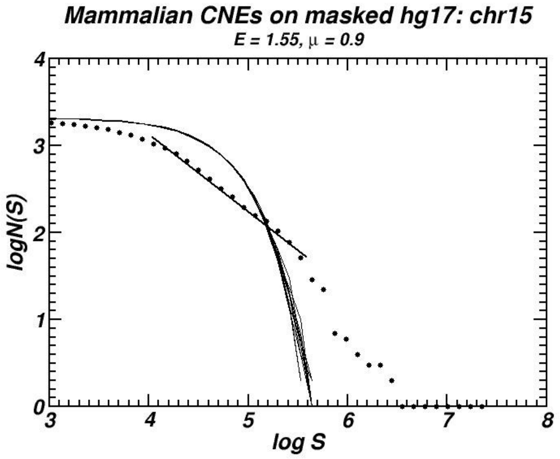


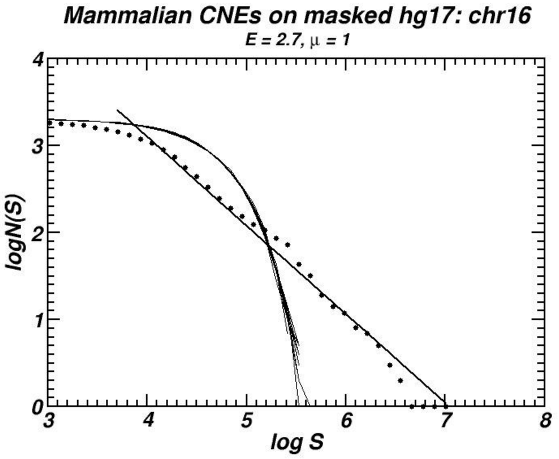
Mammalian CNEs on masked hg17: chr12

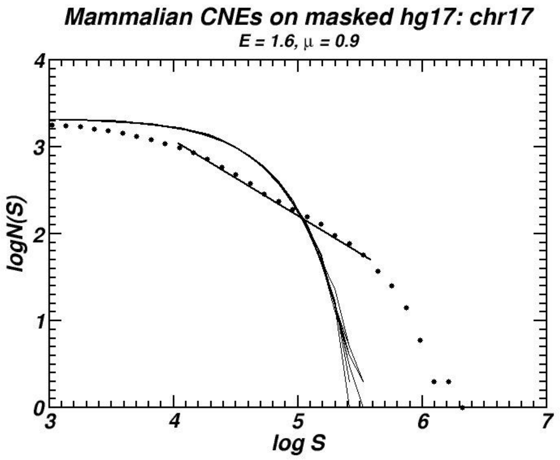
E = 1.4, $\mu = 1$

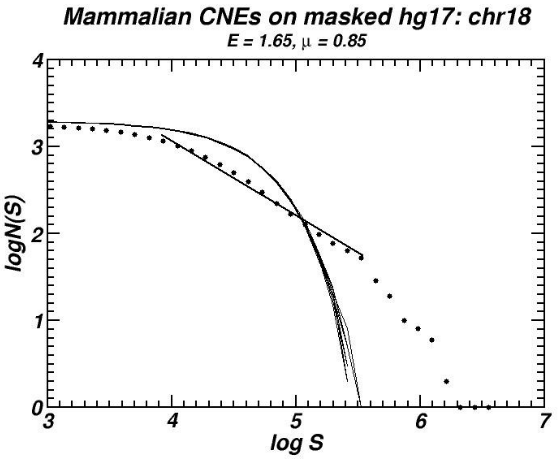

Mammalian CNEs on masked hg17: chr13
E = 2.15, μ = 1.1
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

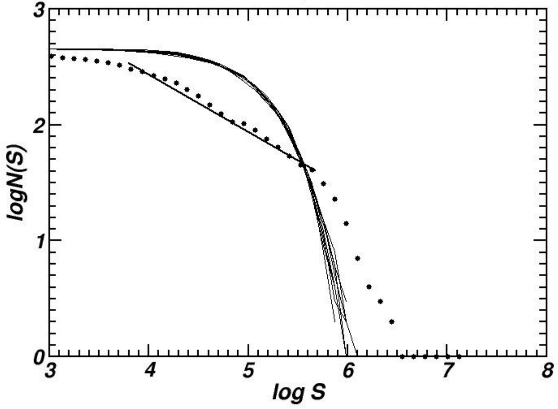

Mammalian CNEs on masked hg17: chr14
E = 1.6, μ = 1
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


Mammalian CNEs on masked hg17: chr15
E = 1.55, μ = 0.9
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


Mammalian CNEs on masked hg17: chr16
E = 2.7, μ = 1
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

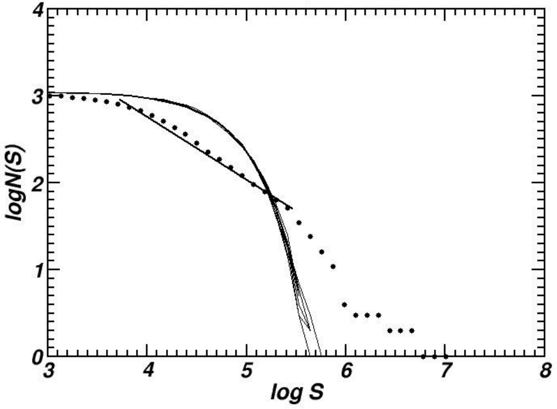

Mammalian CNEs on masked hg17: chr17
E = 1.6, μ = 0.9
logN(S)
log S
0
1
2
3
4
3
4
5
6
7


Mammalian CNEs on masked hg17: chr18
E = 1.65, μ = 0.85
logN(S)
log S
0
1
2
3
4
3
4
5
6
7



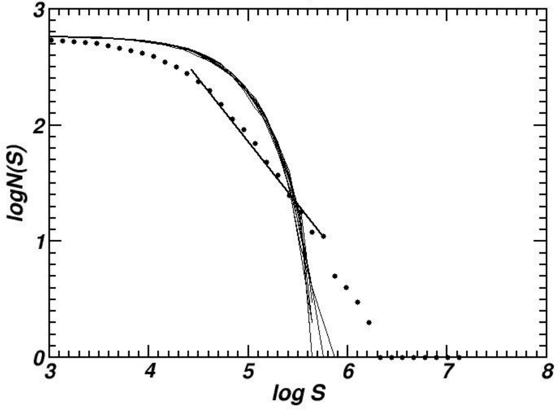
Mammalian CNEs on masked hg17: chr19

E = 1.9, $\mu = 0.5$



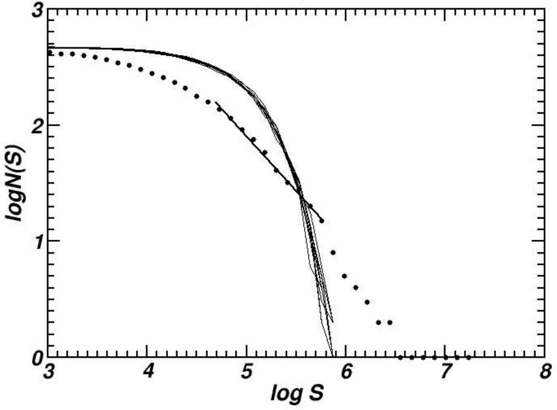
Mammalian CNEs on masked hg17: chr20

E = 1.75, $\mu = 0.7$



Mammalian CNEs on masked hg17: chr21

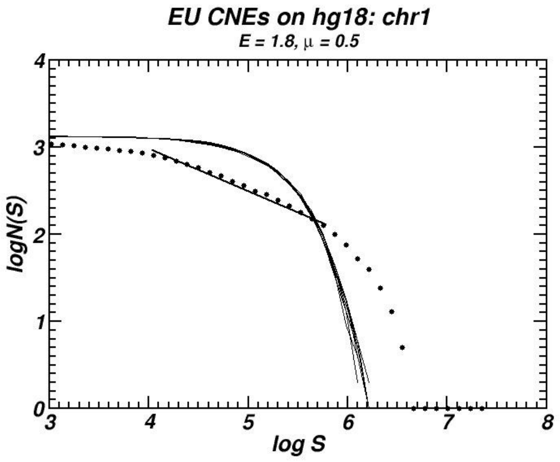
E = 1.35, $\mu = 1.1$

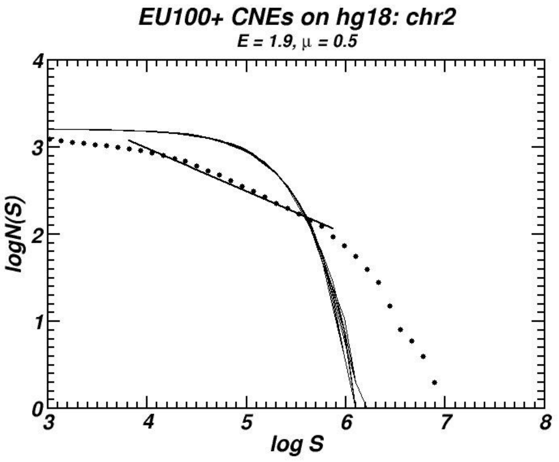


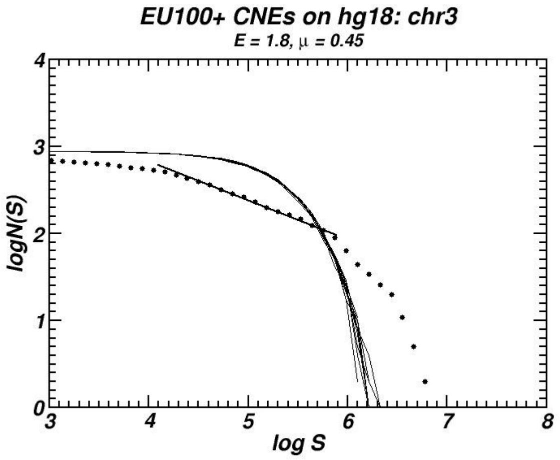
Mammalian CNEs on masked hg17: chr22

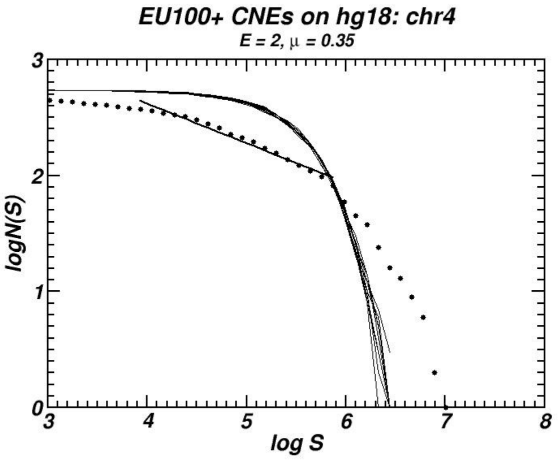
E = 1.1, $\mu = 0.9$

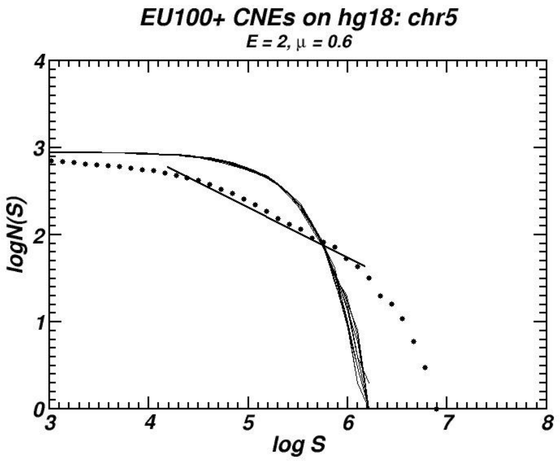
EU100+ CNEs (Dataset i)

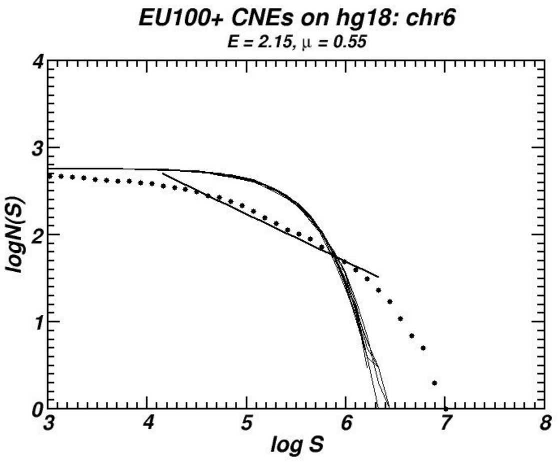


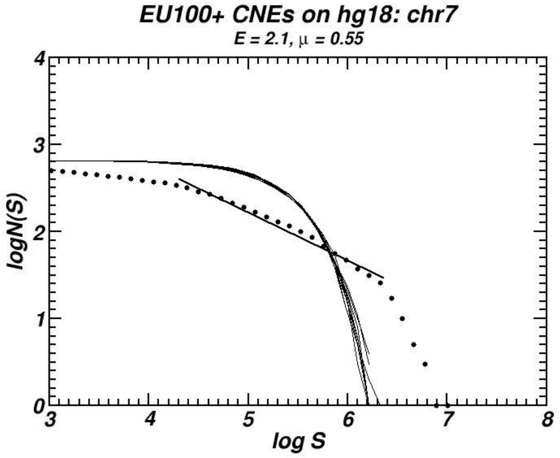


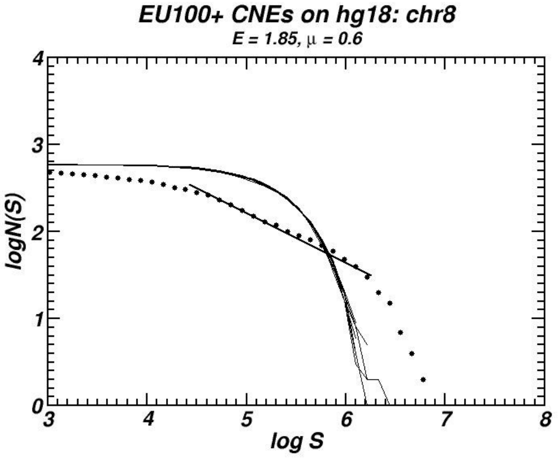









EU100+ CNEs on hg18: chr7
E = 2.1, μ = 0.55
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr8
E = 1.85, μ = 0.6
logN(S)
log S
0
1
2
3
4
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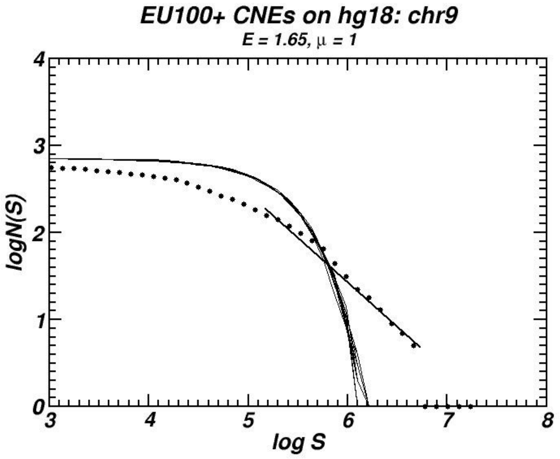
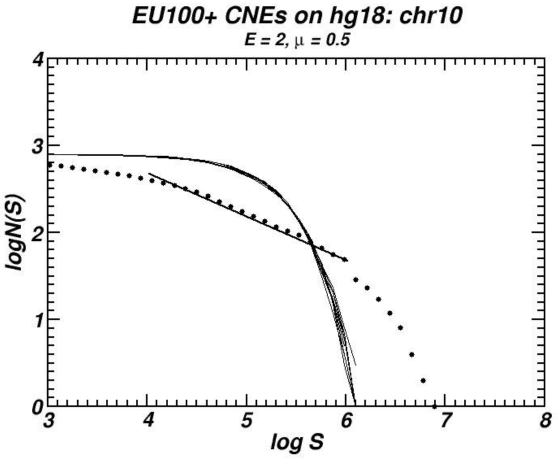
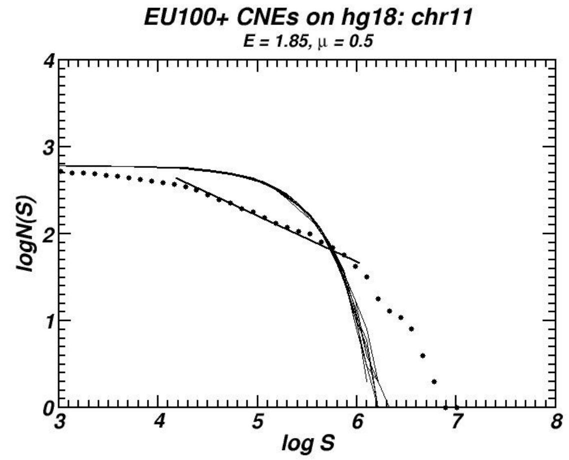
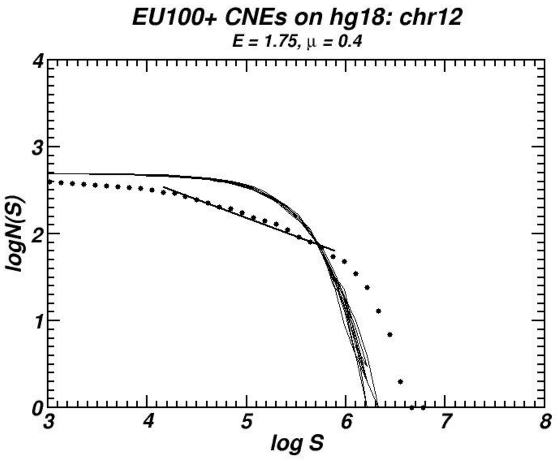
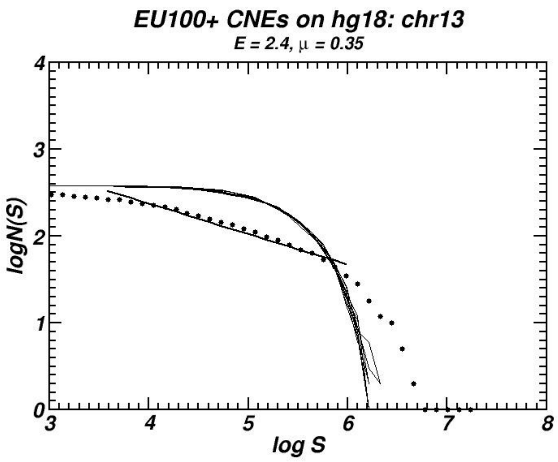
8

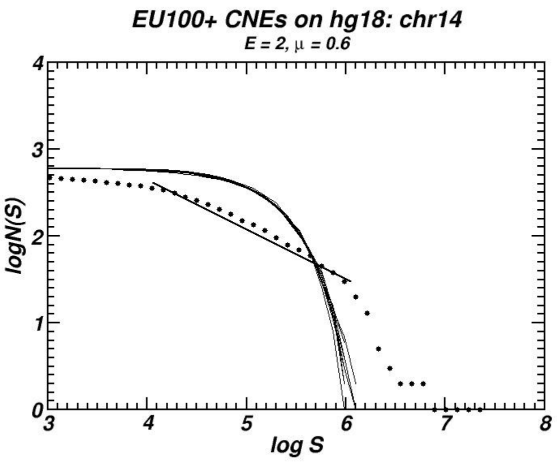

EU100+ CNEs on hg18: chr9
E = 1.65, μ = 1
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr10
E = 2, μ = 0.5
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr11
E = 1.85, μ = 0.5
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr12
E = 1.75, μ = 0.4
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr13
E = 2.4, μ = 0.35
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr14
E = 2, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
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5
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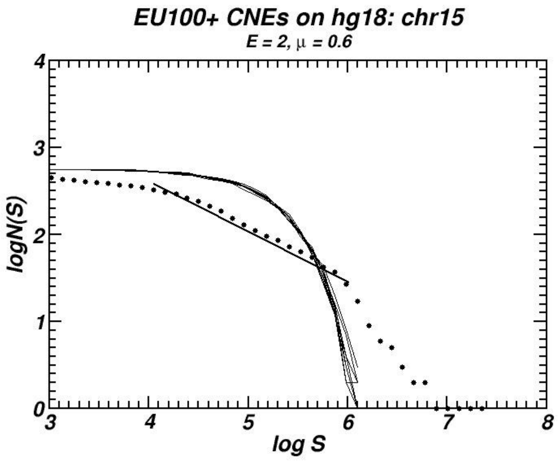
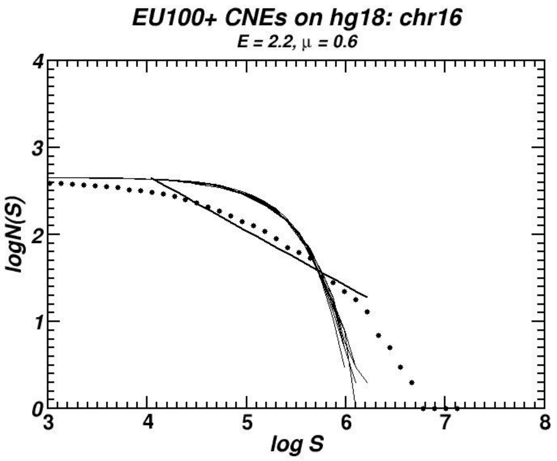
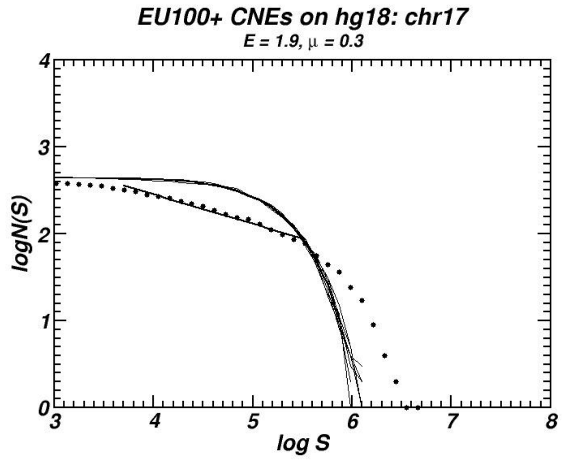
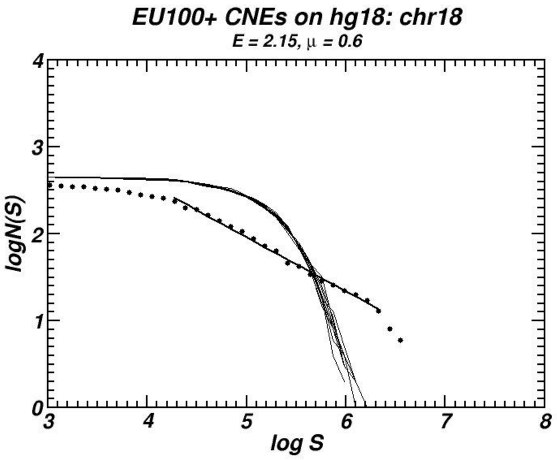
7
8


EU100+ CNEs on hg18: chr15
E = 2, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

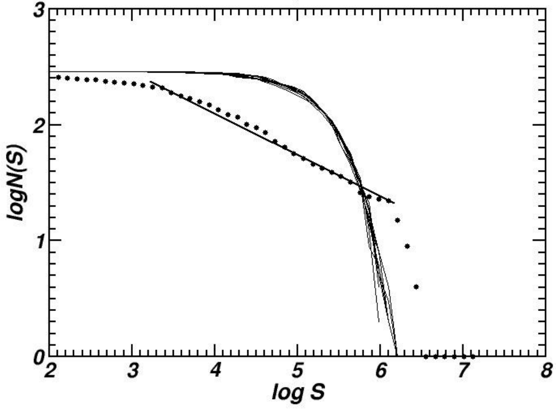

EU100+ CNEs on hg18: chr16
E = 2.2, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr17
E = 1.9, μ = 0.3
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8


EU100+ CNEs on hg18: chr18
E = 2.15, μ = 0.6
logN(S)
log S
0
1
2
3
4
3
4
5
6
7
8

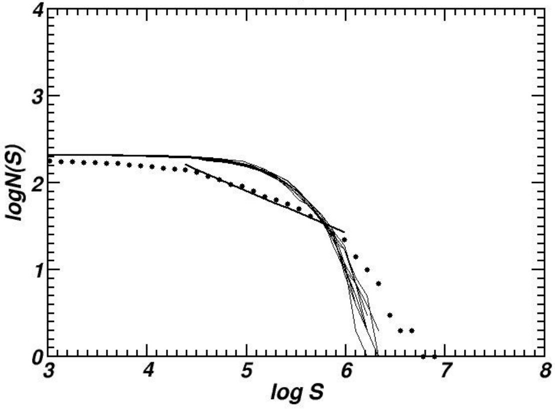
EU100+ CNEs on hg18: chr19

E = 3, μ = 0.4



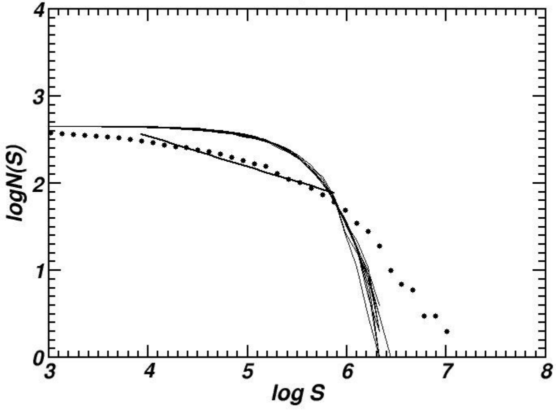
EU100+ CNEs on hg18: chr20

E = 1.6, μ = 0.5

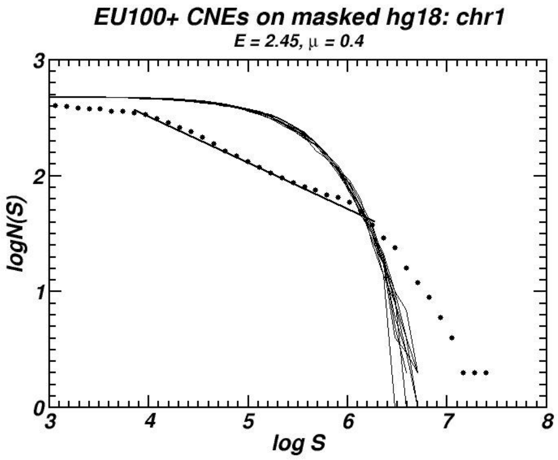


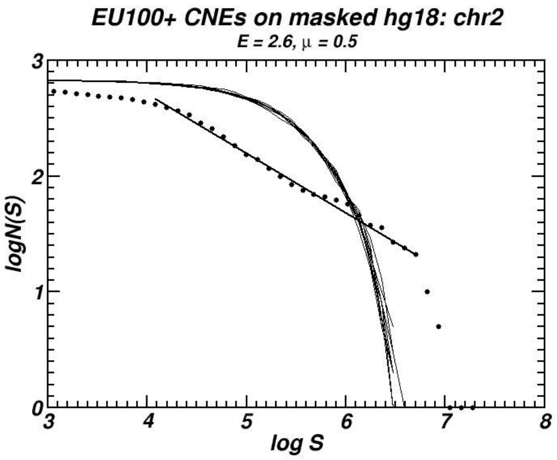
EU100+ CNEs on hg18: chrX

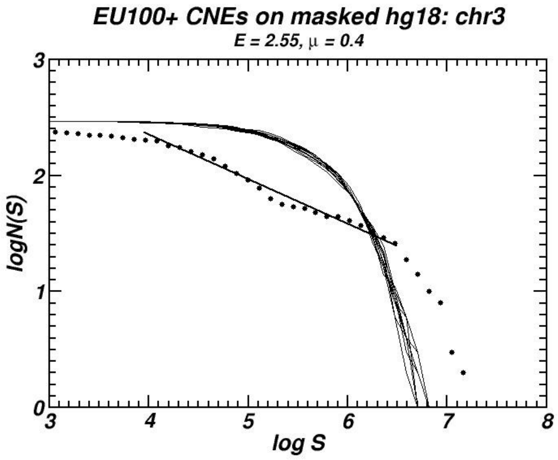
E = 1.9, μ = 0.35

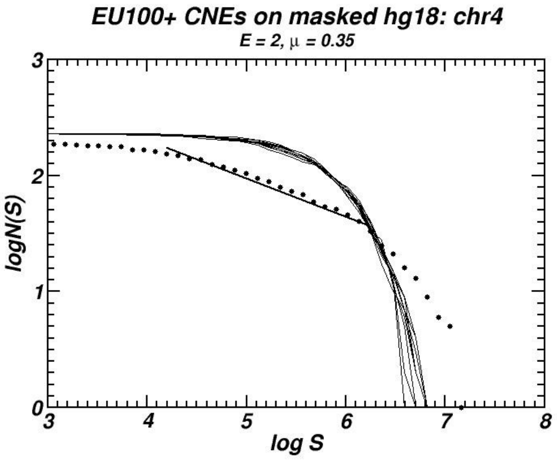


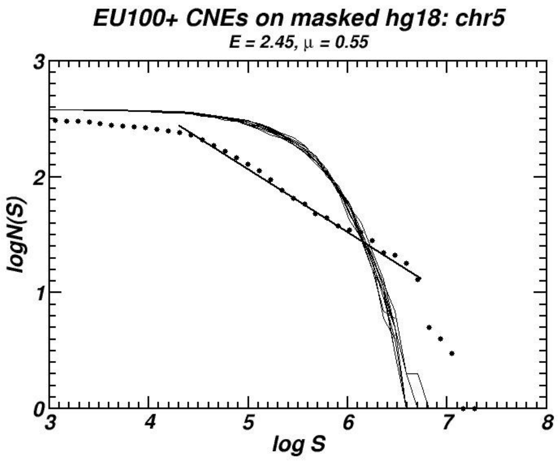
EU100+ CNEs on gene-masked genome

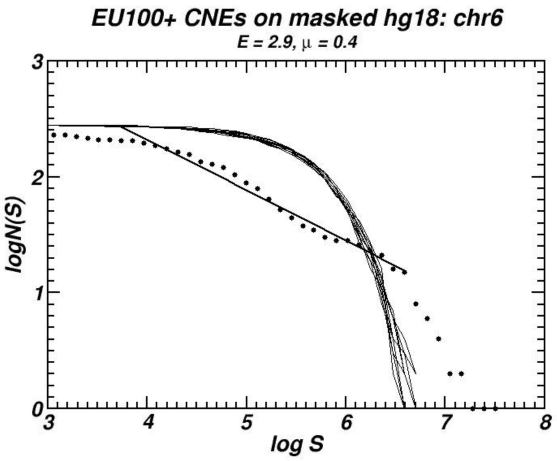


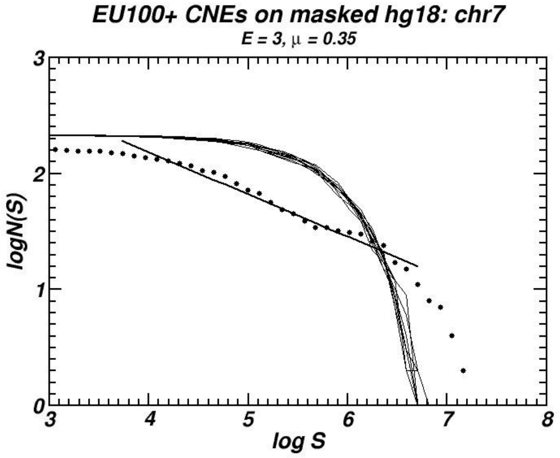




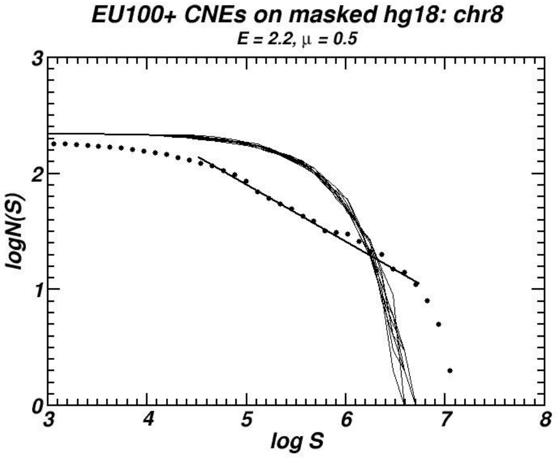




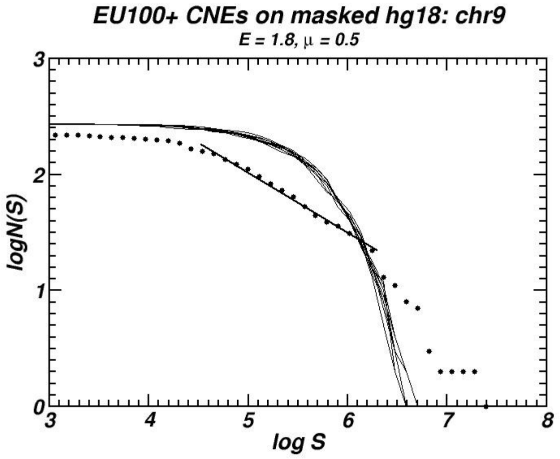



EU100+ CNEs on masked hg18: chr7

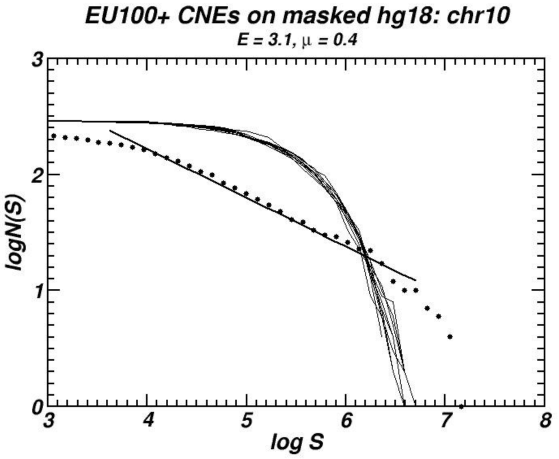
E = 3, μ = 0.35


EU100+ CNEs on masked hg18: chr8

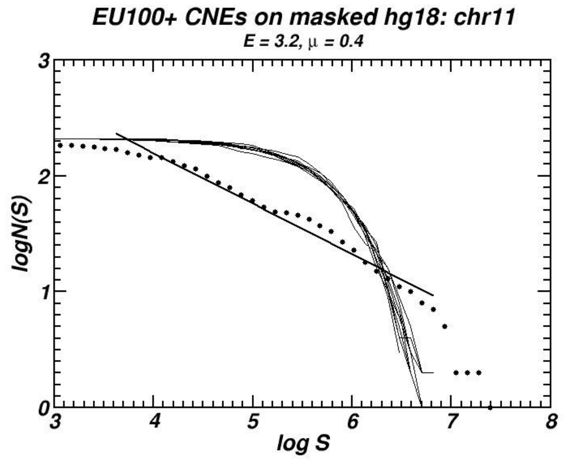
E = 2.2, μ = 0.5


EU100+ CNEs on masked hg18: chr9

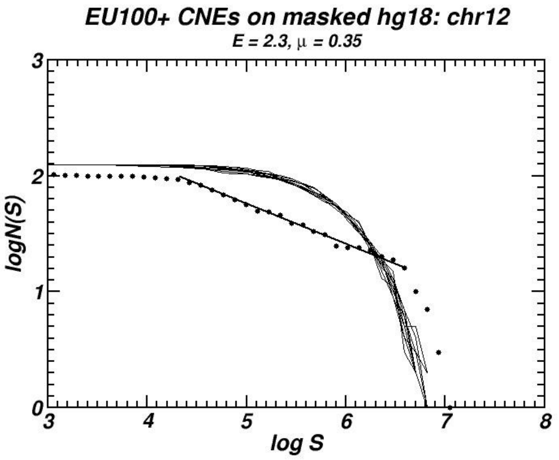
E = 1.8, μ = 0.5


EU100+ CNEs on masked hg18: chr10

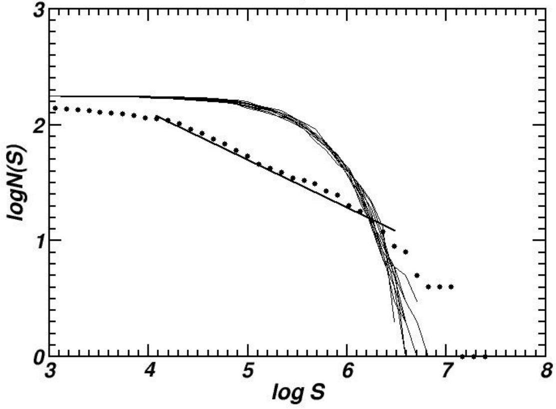
E = 3.1, μ = 0.4


EU100+ CNEs on masked hg18: chr11

E = 3.2, μ = 0.4

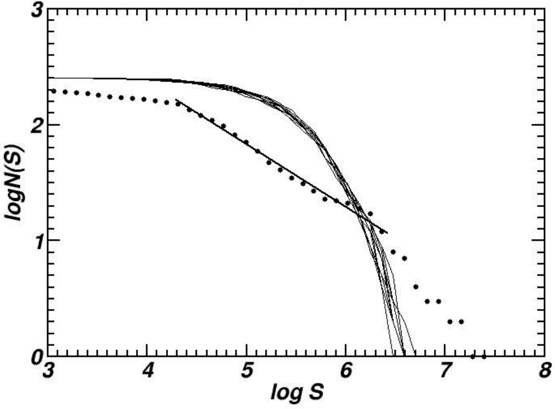

EU100+ CNEs on masked hg18: chr12

E = 2.3, μ = 0.35



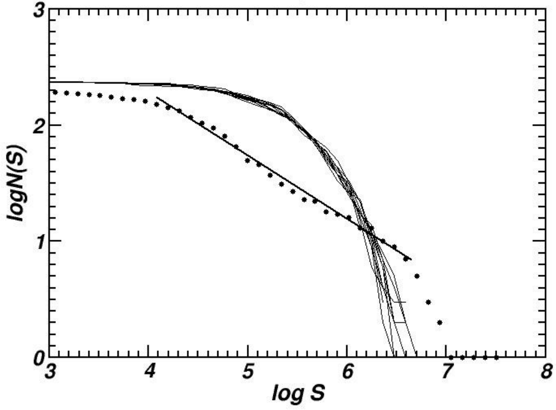
EU100+ CNEs on masked hg18: chr13

E = 2.4, μ = 0.4



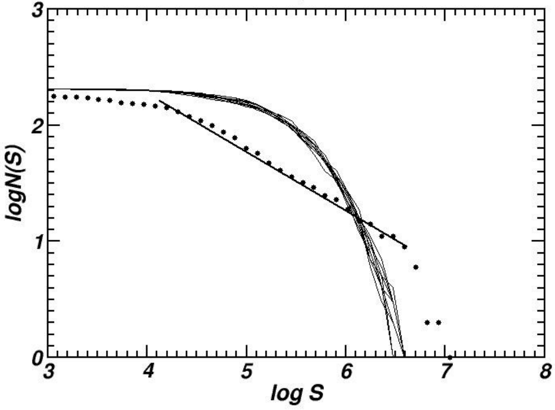
EU100+ CNEs on masked hg18: chr14

E = 2.15, μ = 0.55



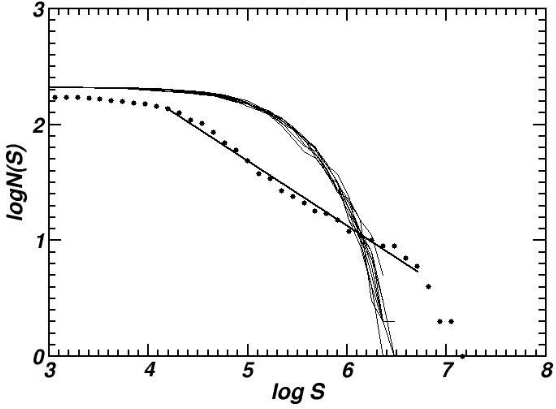
EU100+ CNEs on masked hg18: chr15

E = 2.6, μ = 0.55



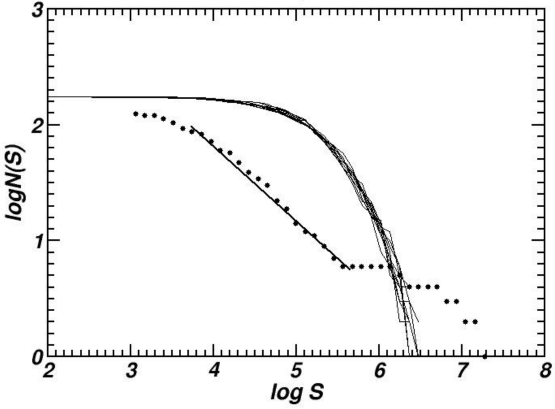
EU100+ CNEs on masked hg18: chr16

E = 2.5, μ = 0.5



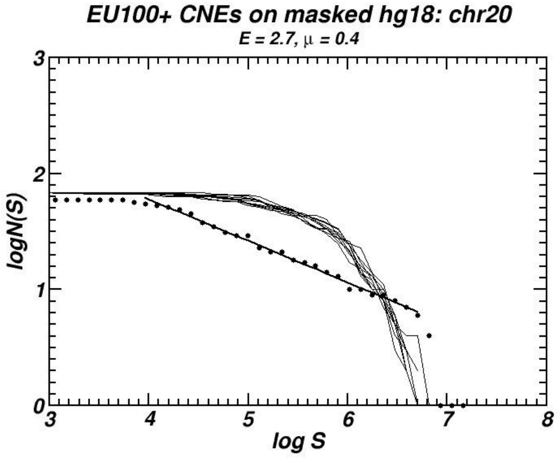
EU100+ CNEs on masked hg18: chr18

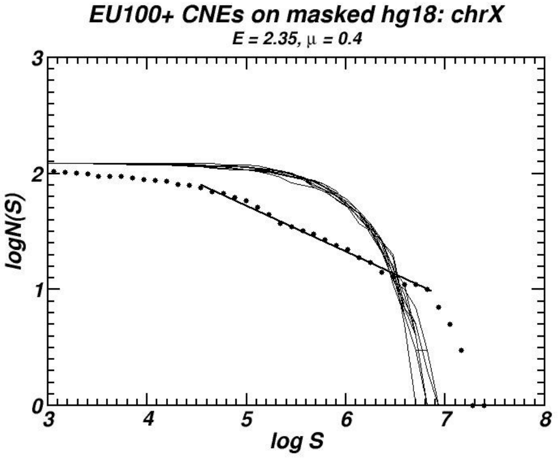
E = 2.55, μ = 0.55



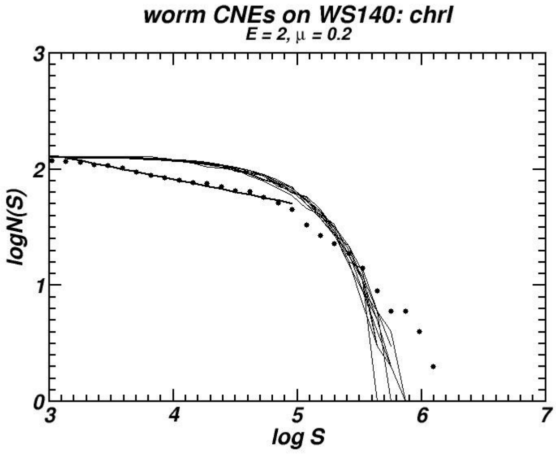
EU100+ CNEs on masked hg18: chr19

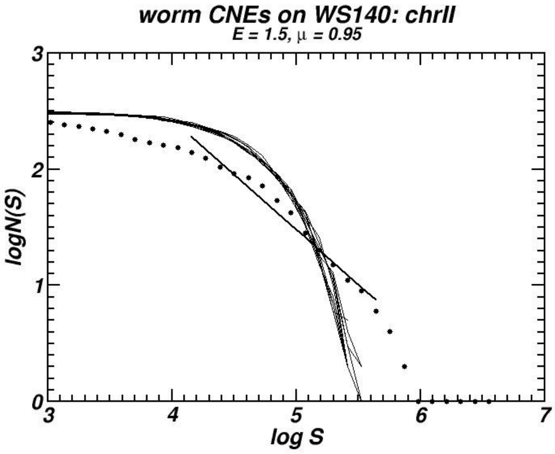
E = 1.9, μ = 0.6

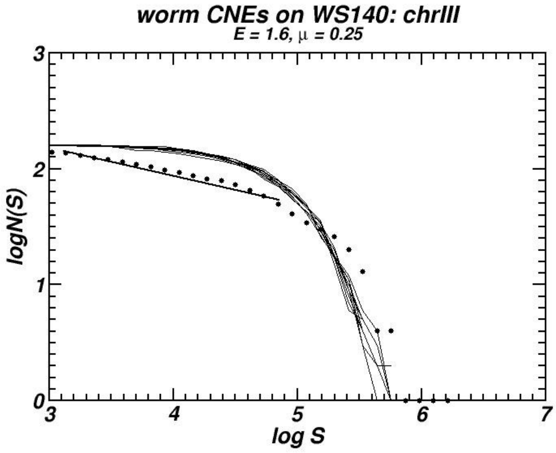

EU100+ CNEs on masked hg18: chr20
E = 2.7, μ = 0.4
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

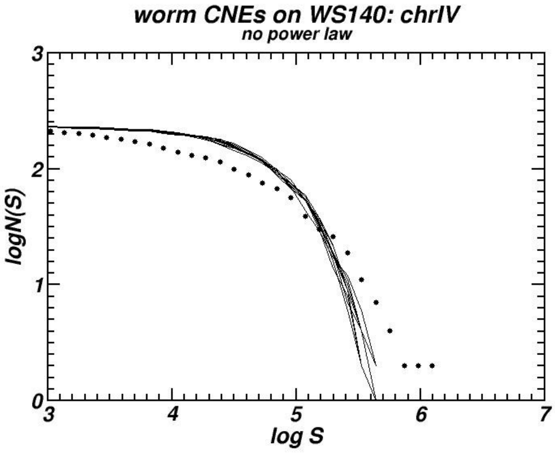

EU100+ CNEs on masked hg18: chrX
E = 2.35, μ = 0.4
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

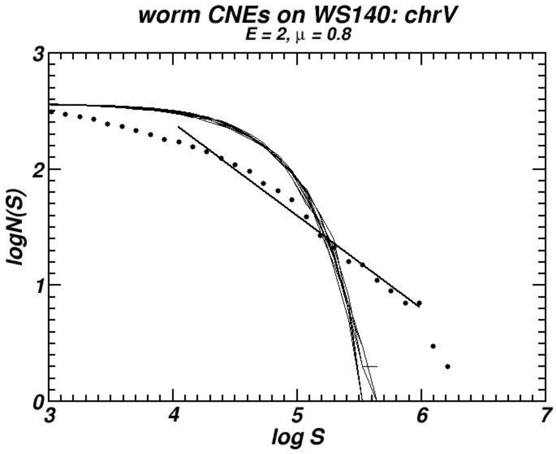
Worm CNEs (Dataset ix)


worm CNEs on WS140: chrI
E = 2, μ = 0.2

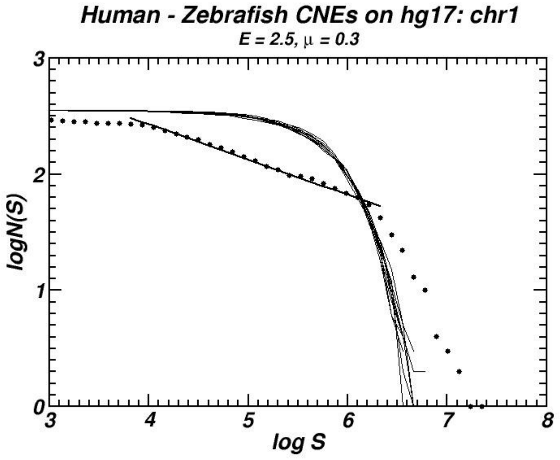

worm CNEs on WS140: chrII
E = 1.5, μ = 0.95

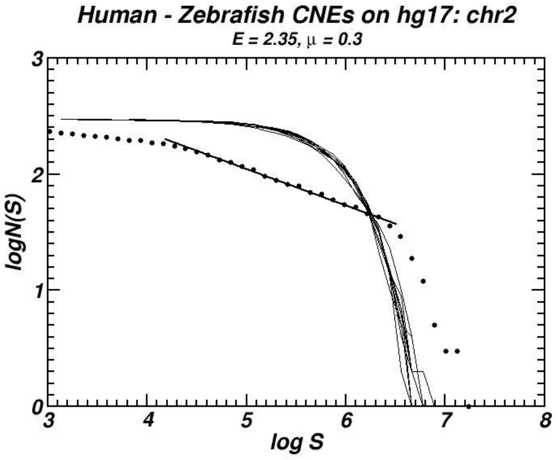

worm CNEs on WS140: chrIII
E = 1.6, μ = 0.25

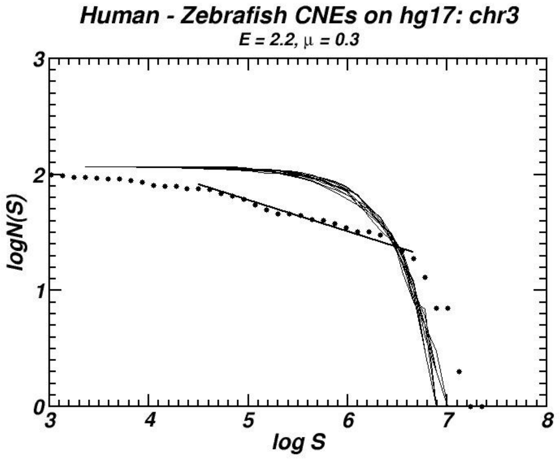

worm CNEs on WS140: chrIV
no power law

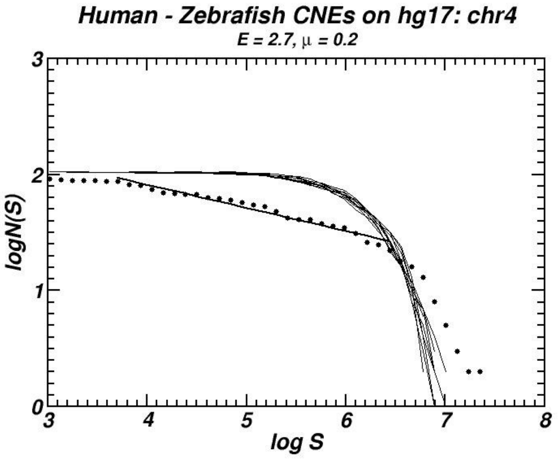

worm CNEs on WS140: chrV
E = 2, μ = 0.8

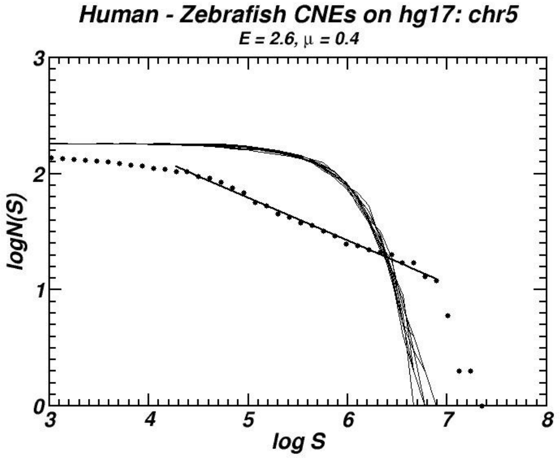
Human-Zebrafish CNEs (Dataset v)

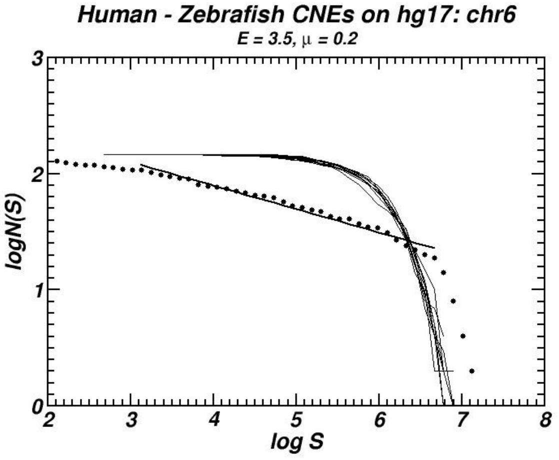


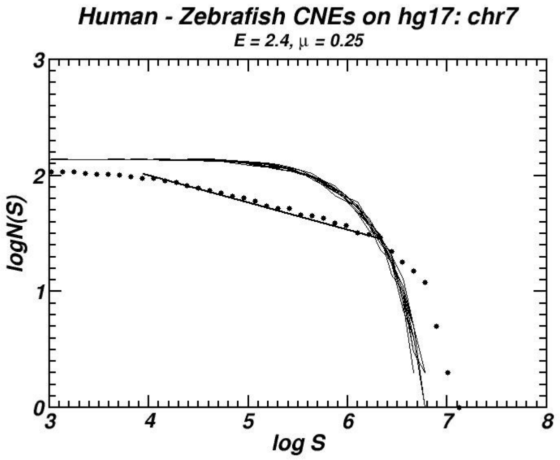


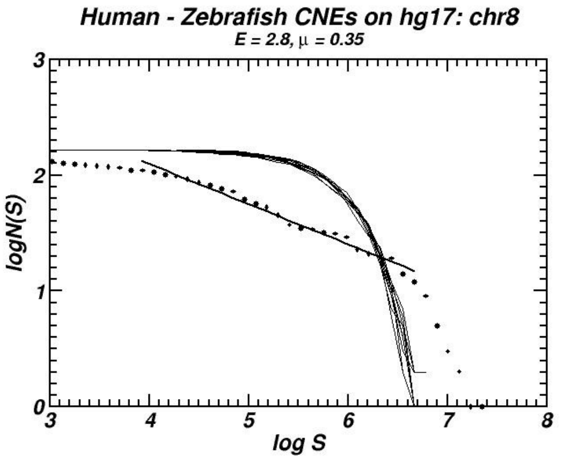


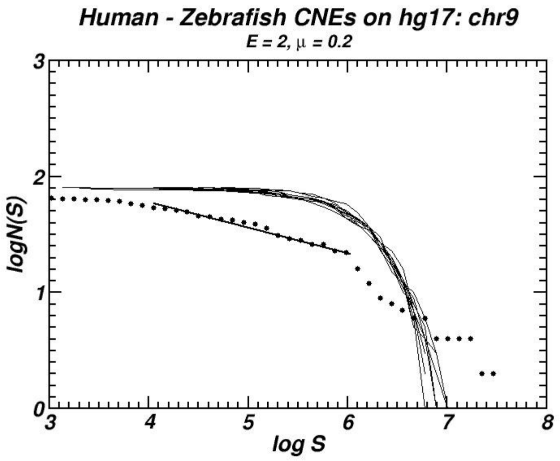


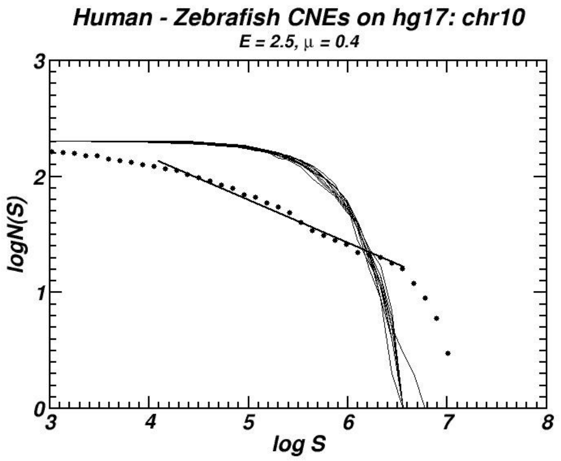


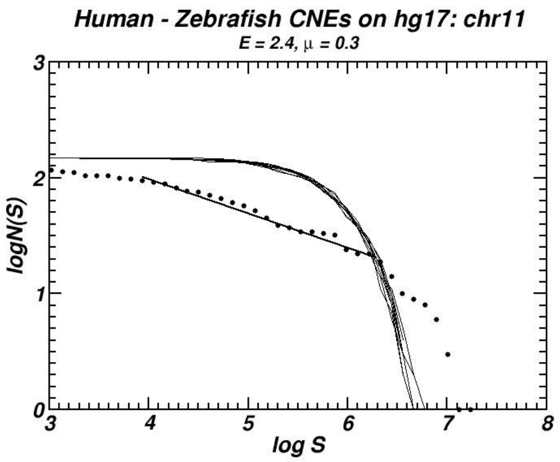


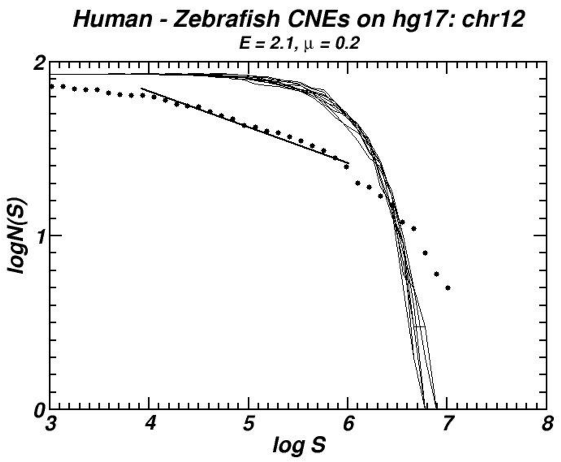

Human - Zebrafish CNEs on hg17: chr7
E = 2.4, μ = 0.25
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

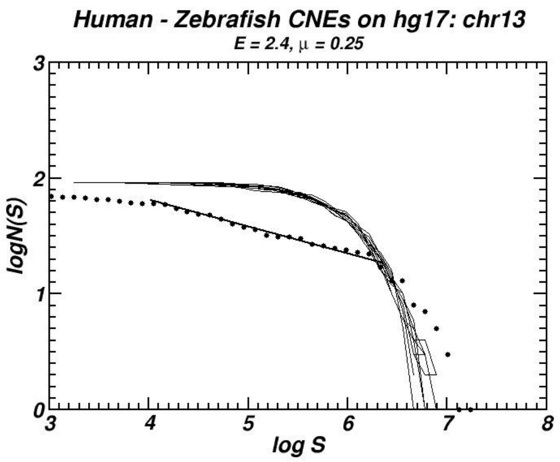

Human - Zebrafish CNEs on hg17: chr8
E = 2.8, μ = 0.35
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

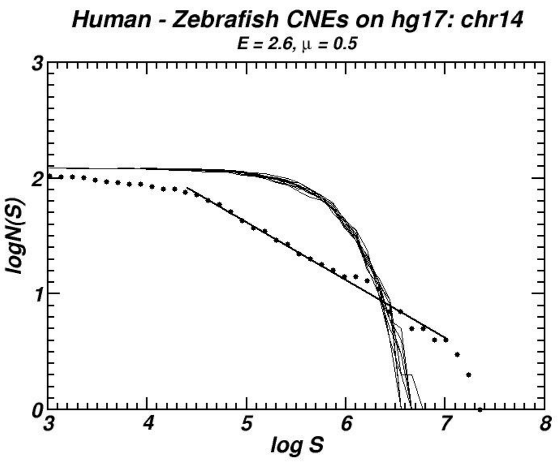

Human - Zebrafish CNEs on hg17: chr9
E = 2, μ = 0.2
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

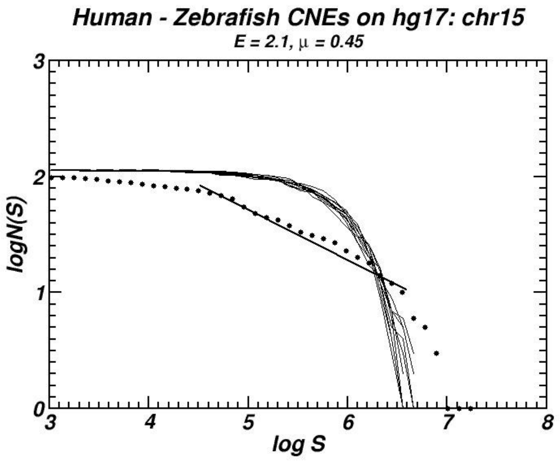

Human - Zebrafish CNEs on hg17: chr10
E = 2.5, μ = 0.4
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

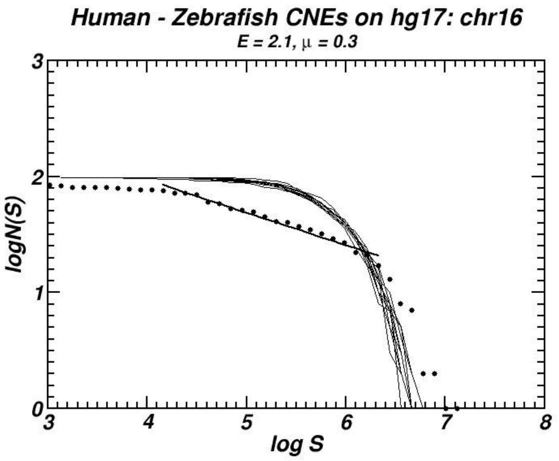

Human - Zebrafish CNEs on hg17: chr11
E = 2.4, μ = 0.3
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

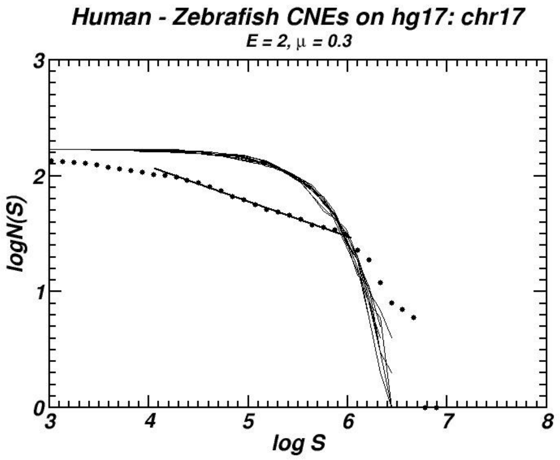

Human - Zebrafish CNEs on hg17: chr12
E = 2.1, μ = 0.2
logN(S)
log S
0
1
2
3
4
5
6
7
8

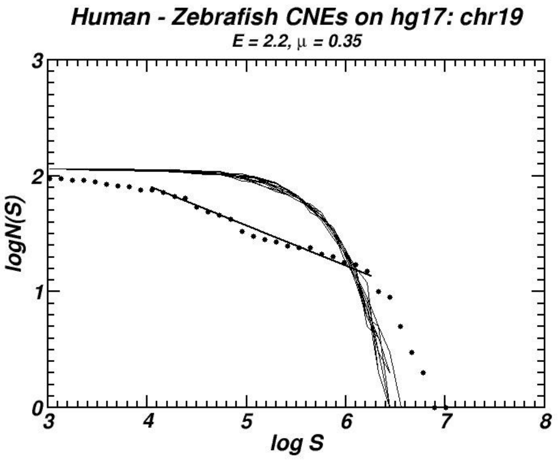

Human - Zebrafish CNEs on hg17: chr13
E = 2.4, μ = 0.25
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

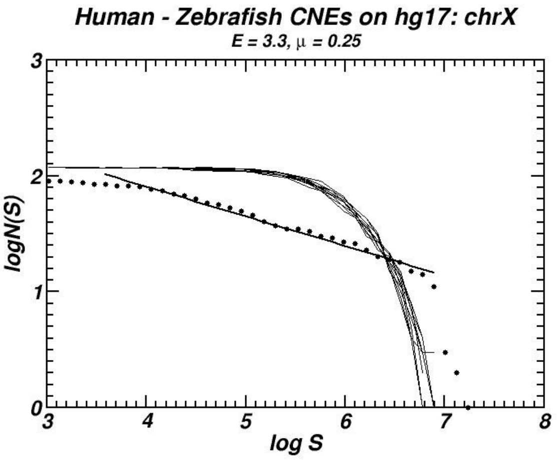

Human - Zebrafish CNEs on hg17: chr14
E = 2.6, μ = 0.5
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Human - Zebrafish CNEs on hg17: chr15
E = 2.1, μ = 0.45
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

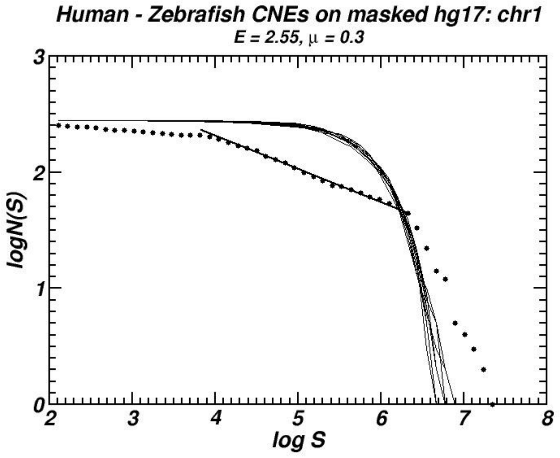

Human - Zebrafish CNEs on hg17: chr16
E = 2.1, μ = 0.3
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

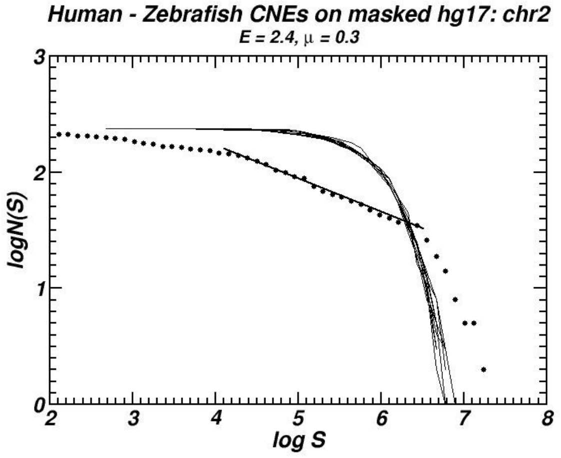

Human - Zebrafish CNEs on hg17: chr17
E = 2, μ = 0.3
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

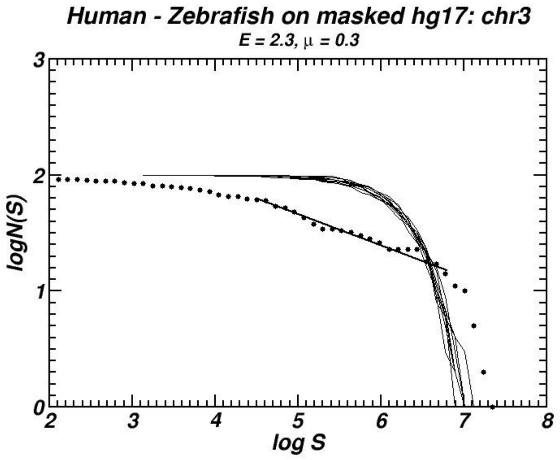

Human - Zebrafish CNEs on hg17: chr19
E = 2.2, μ = 0.35
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

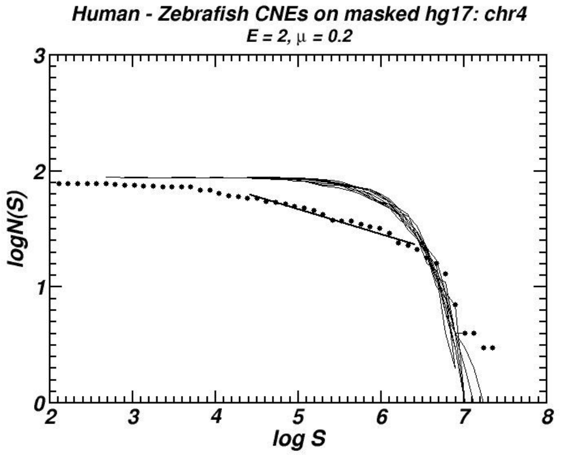

Human - Zebrafish CNEs on hg17: chrX
E = 3.3, μ = 0.25
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

Human-Zebrafish CNEs on gene-masked genome

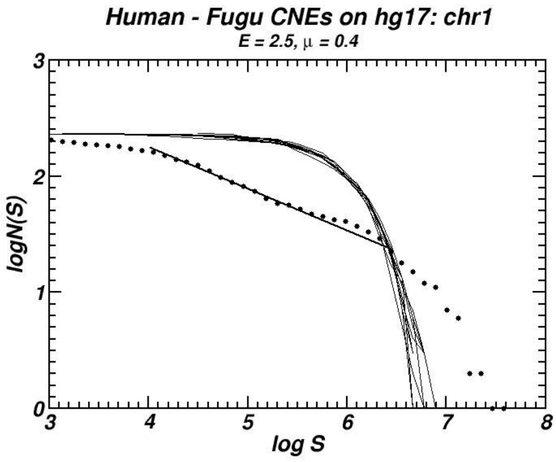


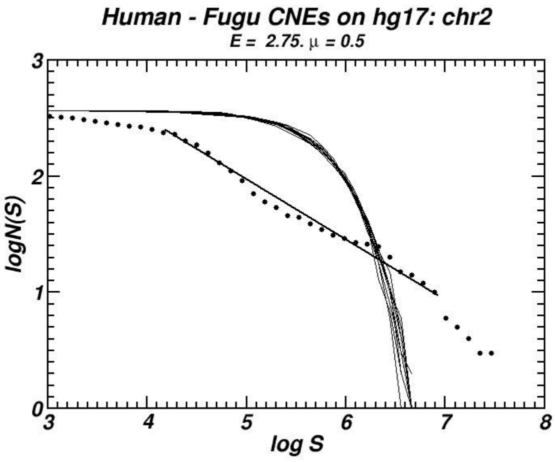


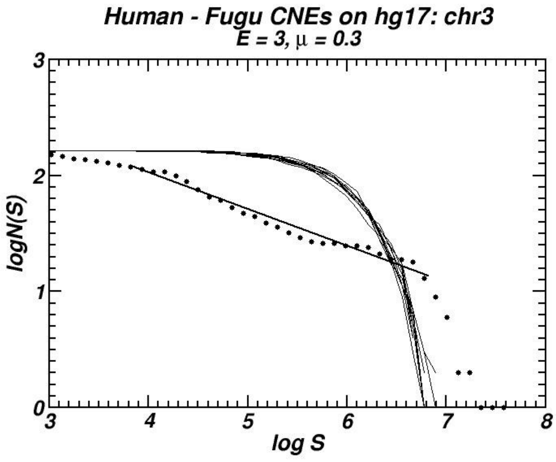


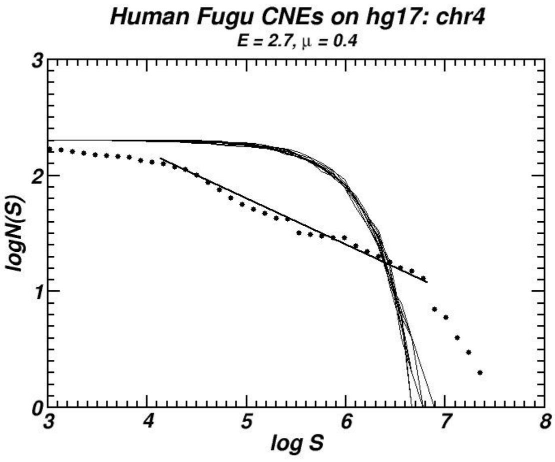


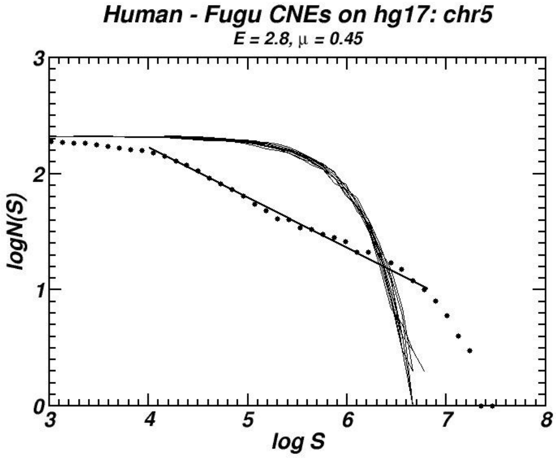
Human-Fugu CNEs (Dataset iv)

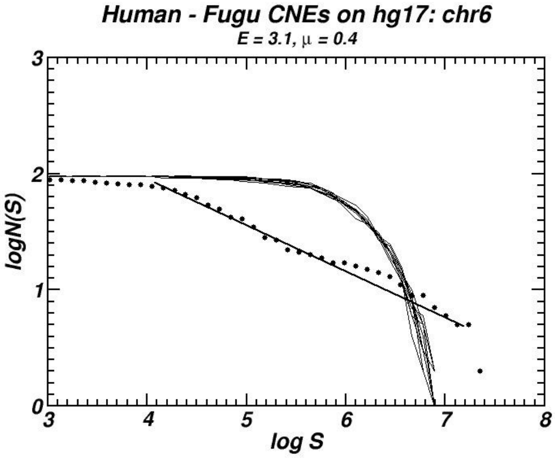


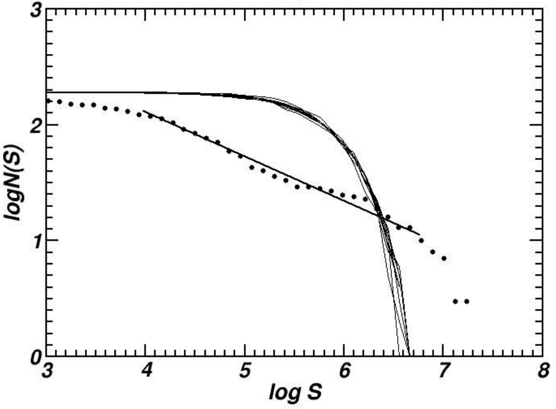




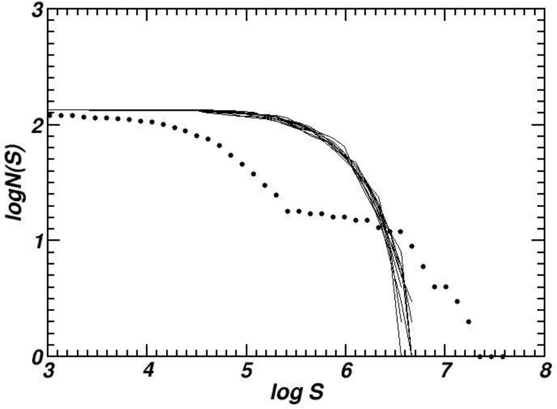




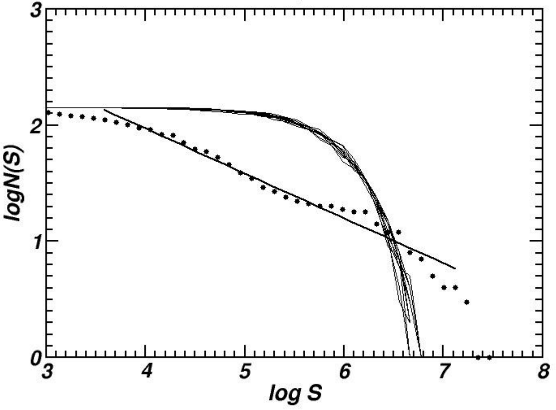



Human - Fugu CNEs on hg17: chr7

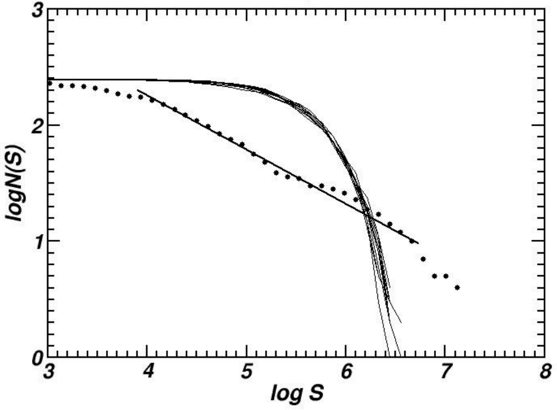
$E = 2.8$, $\mu = 0.4$


Human - Fugu CNEs on hg17: chr8

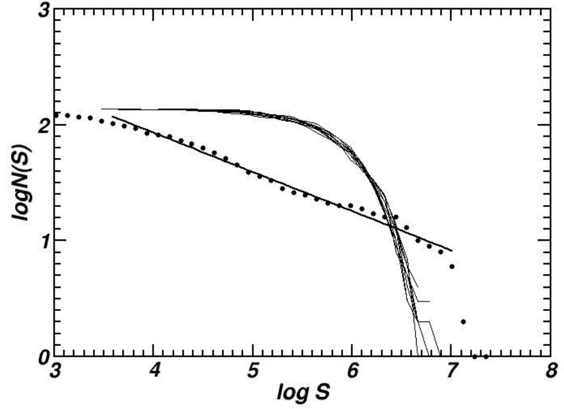
no power law


Human - Fugu CNEs on hg17: chr9

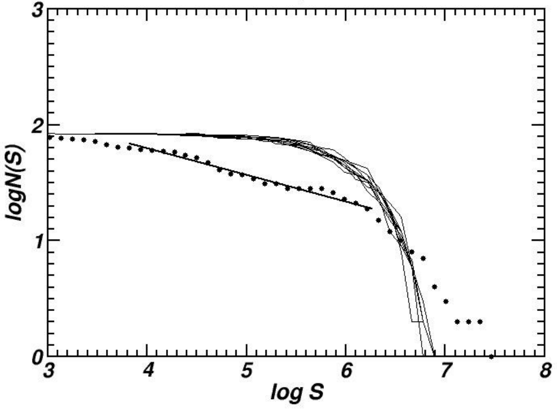
$E = 3.5$, $\mu = 0.4$


Human - Fugu CNEs on hg17: chr10

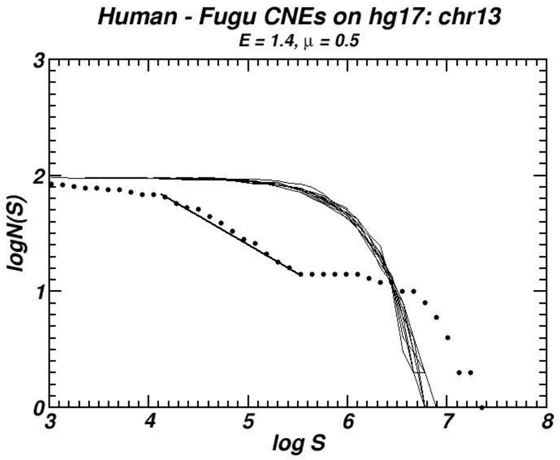
$E = 2.85$, $\mu = 0.5$


Human - Fugu CNEs on hg17: chr11

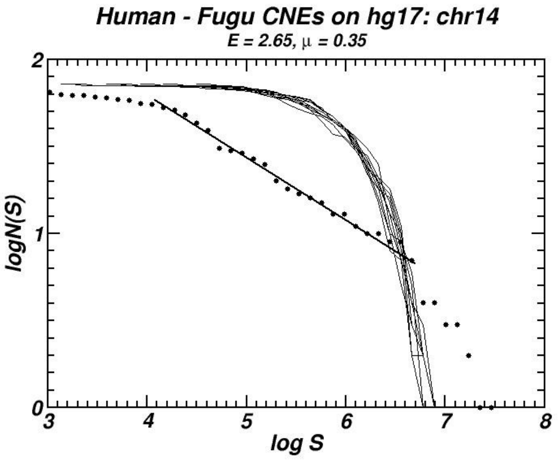
$E = 3.4$, $\mu = 0.34$


Human - Fugu CNEs on hg17: chr12

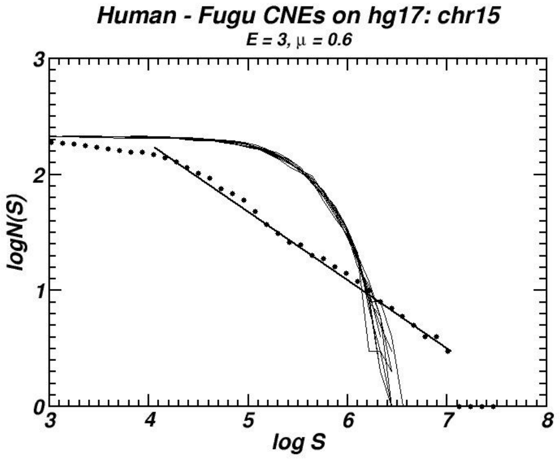
$E = 2.45$, $\mu = 0.25$


Human - Fugu CNEs on hg17: chr13

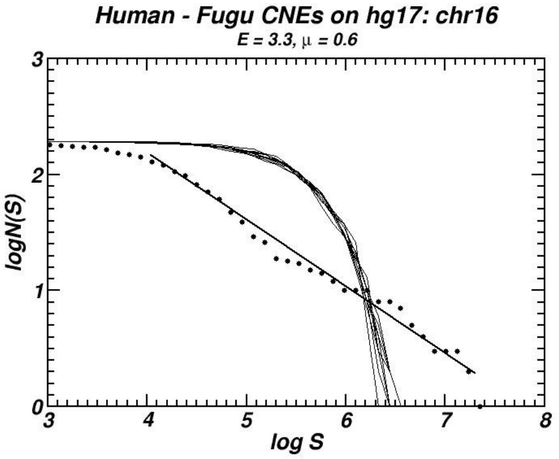
$E = 1.4, \mu = 0.5$


Human - Fugu CNEs on hg17: chr14

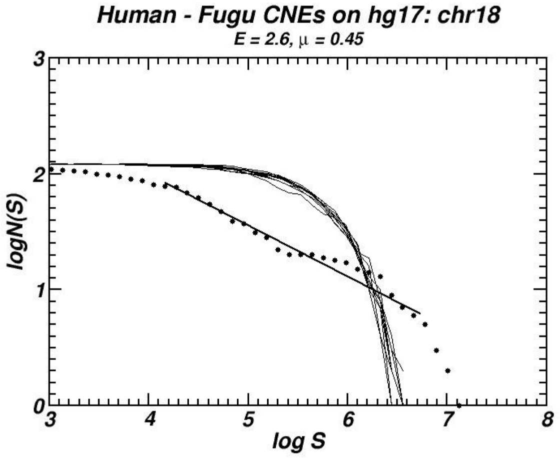
$E = 2.65, \mu = 0.35$


Human - Fugu CNEs on hg17: chr15

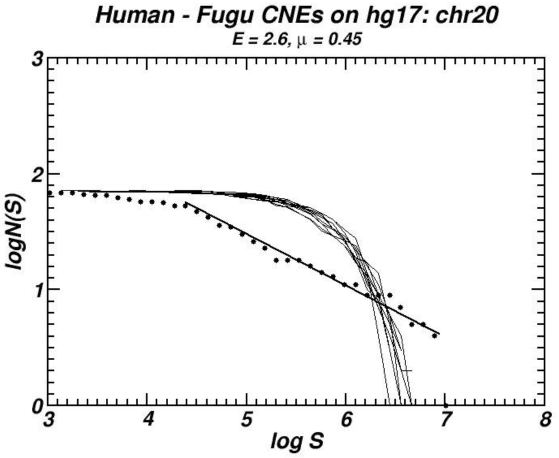
$E = 3, \mu = 0.6$


Human - Fugu CNEs on hg17: chr16

$E = 3.3, \mu = 0.6$

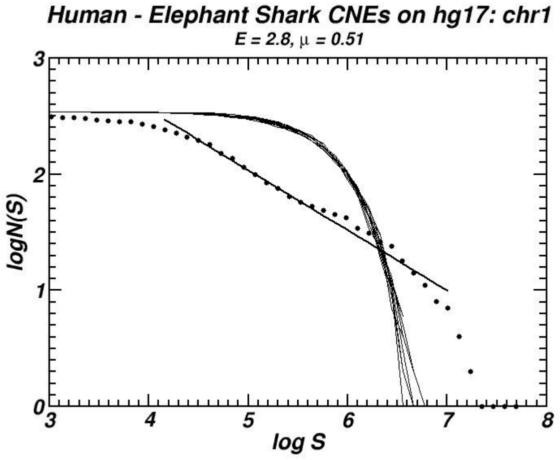

Human - Fugu CNEs on hg17: chr18

$E = 2.6, \mu = 0.45$

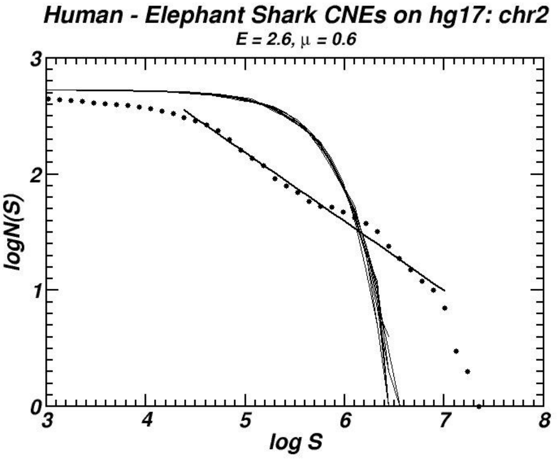

Human - Fugu CNEs on hg17: chr20

$E = 2.6, \mu = 0.45$

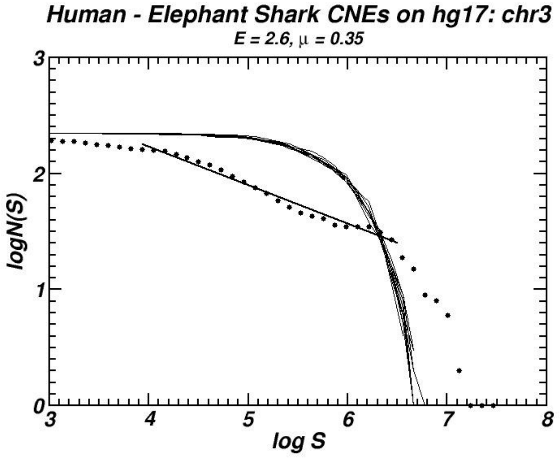
Human-Elephant Shark CNEs (Dataset vi)


Human - Elephant Shark CNEs on hg17: chr1

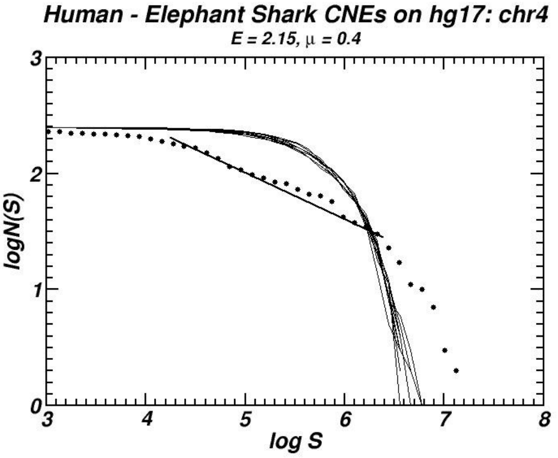
E = 2.8, μ = 0.51


Human - Elephant Shark CNEs on hg17: chr2

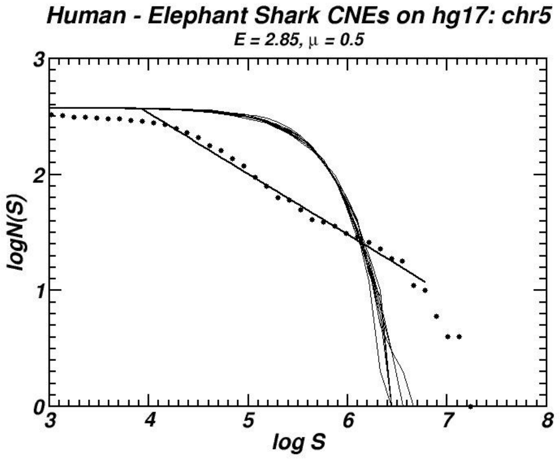
E = 2.6, μ = 0.6


Human - Elephant Shark CNEs on hg17: chr3

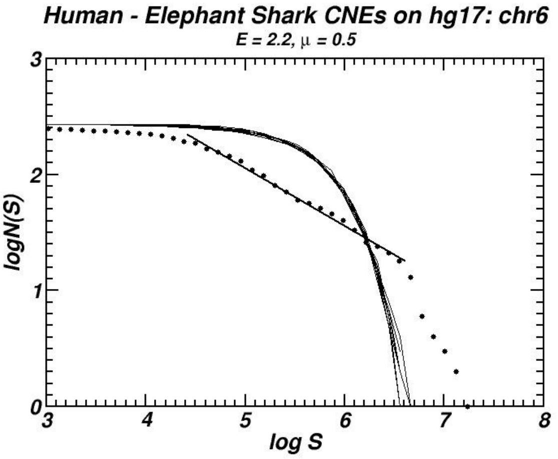
E = 2.6, μ = 0.35


Human - Elephant Shark CNEs on hg17: chr4

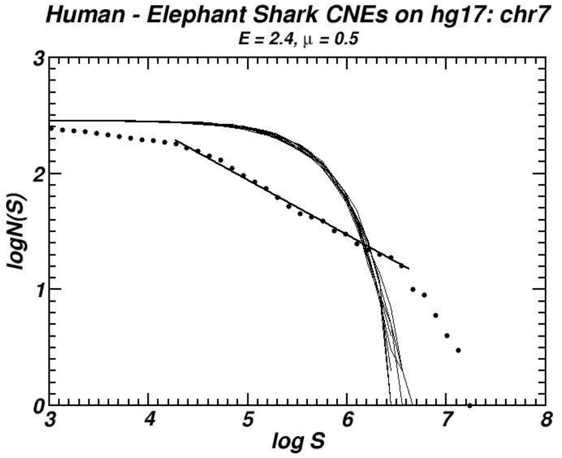
E = 2.15, μ = 0.4

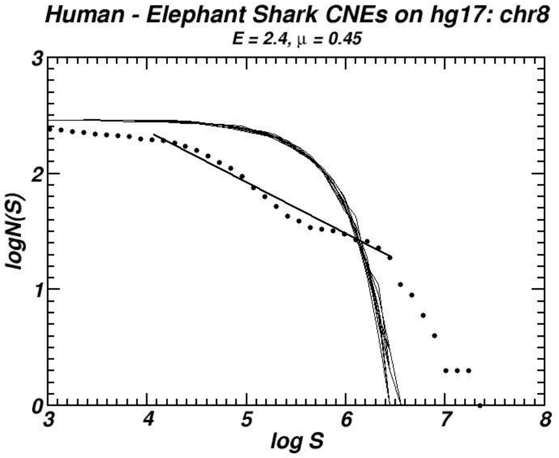

Human - Elephant Shark CNEs on hg17: chr5

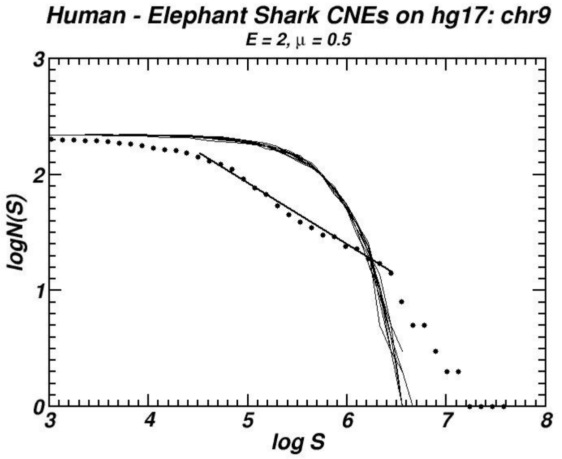
E = 2.85, μ = 0.5

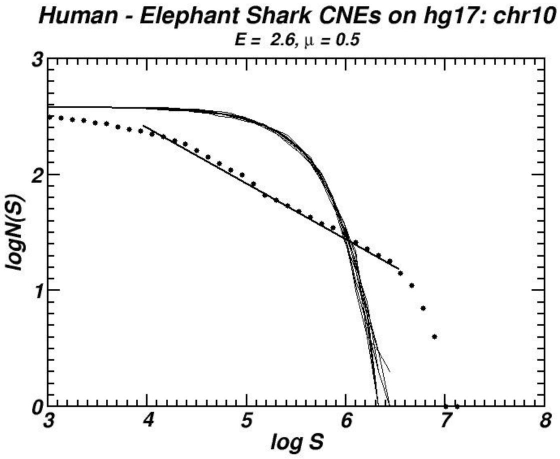

Human - Elephant Shark CNEs on hg17: chr6

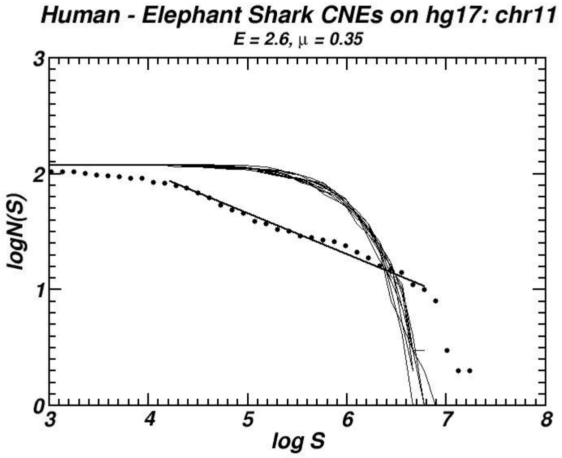
E = 2.2, μ = 0.5

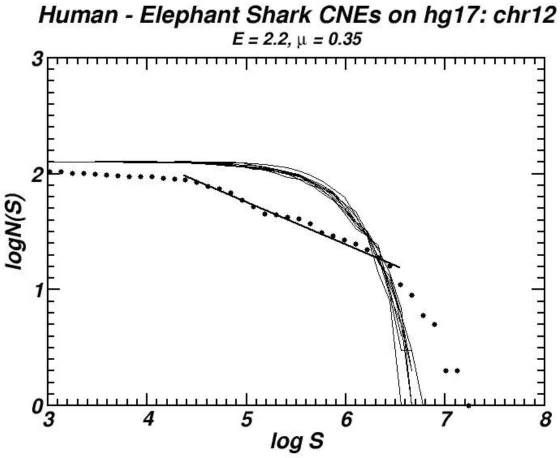

Human - Elephant Shark CNEs on hg17: chr7

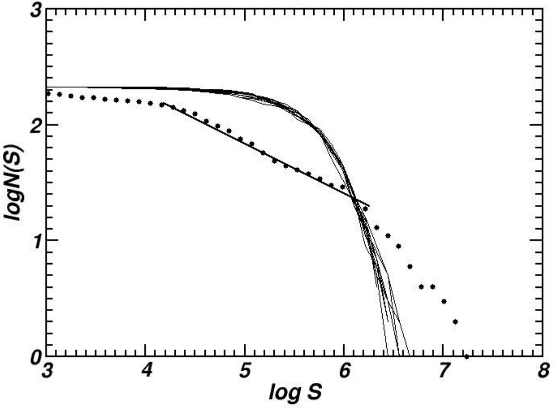

Human - Elephant Shark CNEs on hg17: chr8


Human - Elephant Shark CNEs on hg17: chr9

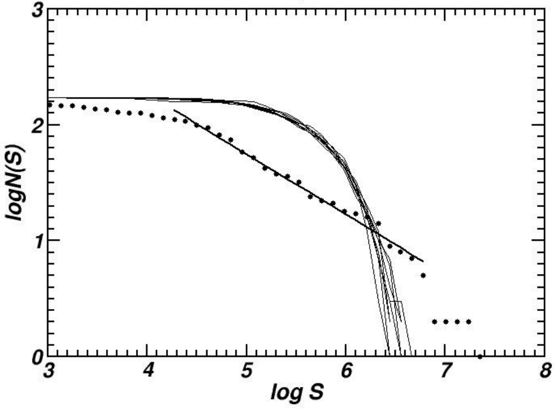

Human - Elephant Shark CNEs on hg17: chr10


Human - Elephant Shark CNEs on hg17: chr11

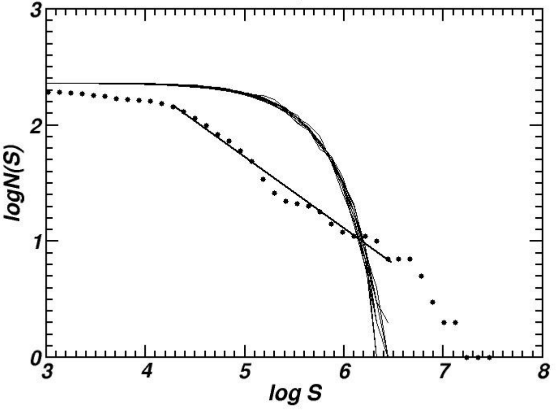

Human - Elephant Shark CNEs on hg17: chr12


Human - Elephant Shark CNEs on hg17: chr13

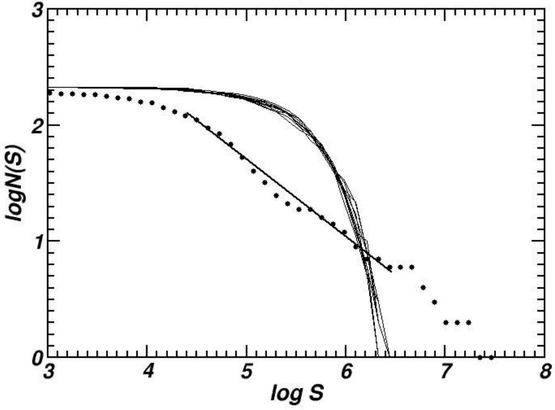
$E = 2.1$, $\mu = 0.45$


Human - Elephant Shark CNEs on hg17: chr14

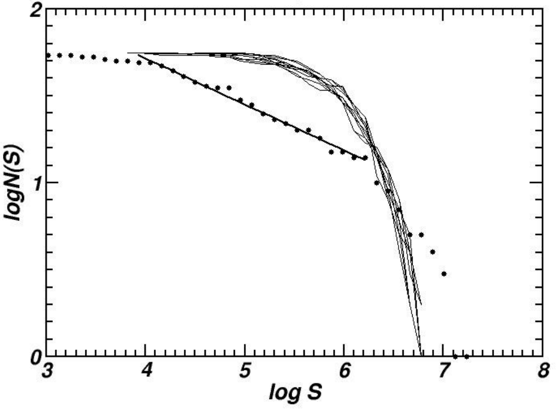
$E = 2.5$, $\mu = 0.5$


Human - Elephant Shark CNEs on hg17: chr15

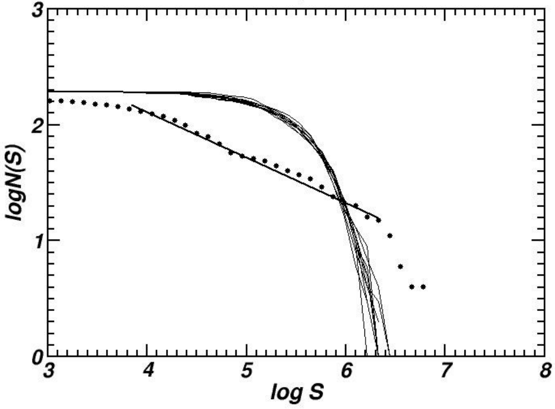
$E = 2.2$, $\mu = 0.6$


Human - Elephant Shark CNEs on hg17: chr16

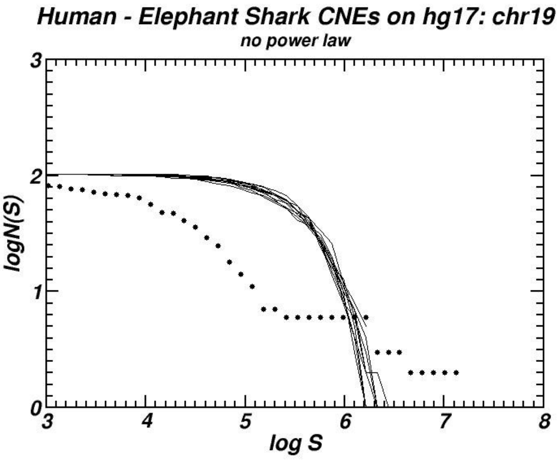
$E = 2.1$, $\mu = 0.7$

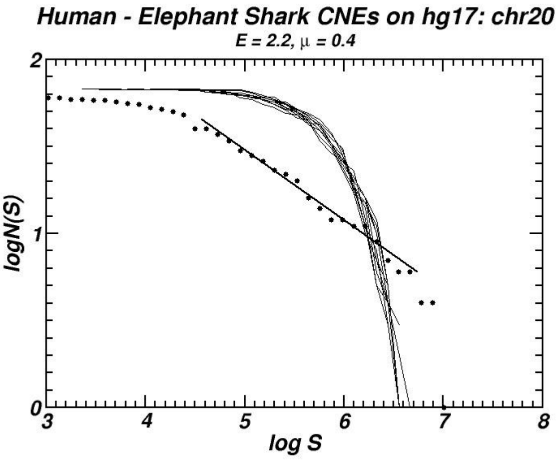

Human - Elephant Shark CNEs on hg17: chr17

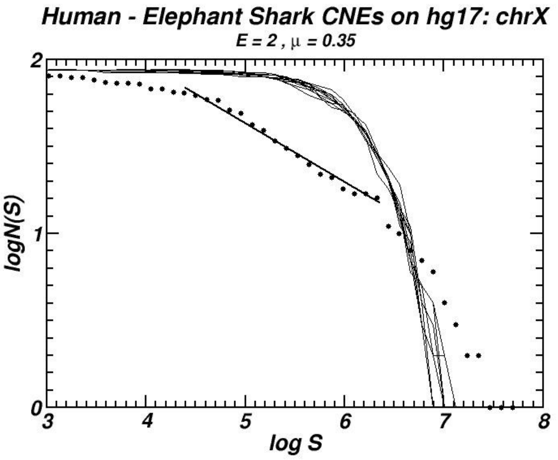
$E = 2.3$, $\mu = 0.25$


Human - Elephant Shark CNEs on hg17: chr18

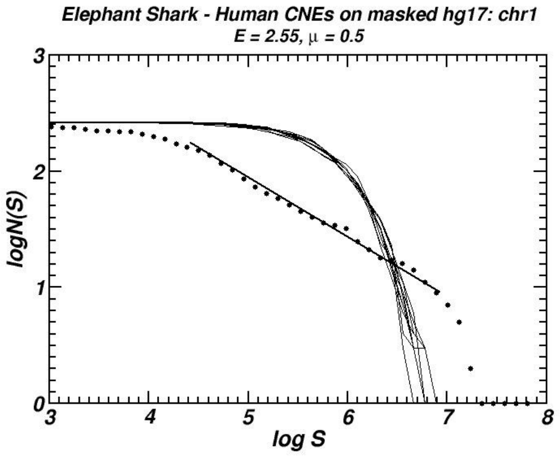
$E = 2.5$, $\mu = 0.4$

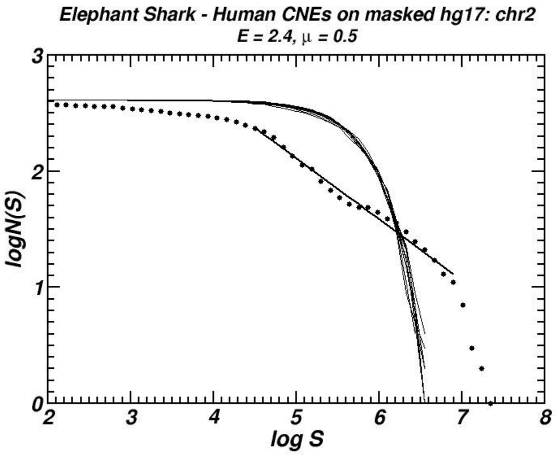

Human - Elephant Shark CNEs on hg17: chr19
no power law
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

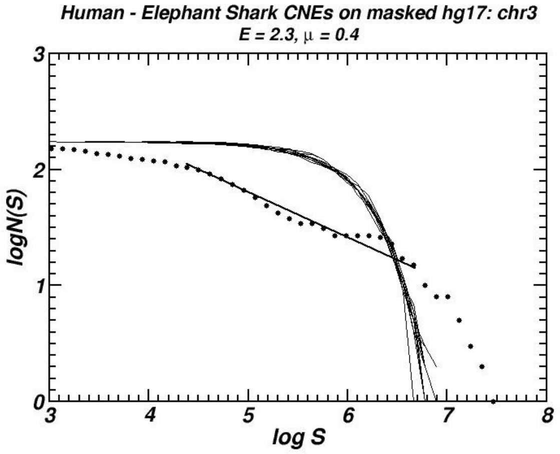

Human - Elephant Shark CNEs on hg17: chr20
E = 2.2, μ = 0.4
logN(S)
log S
0
1
2
3
4
5
6
7
8

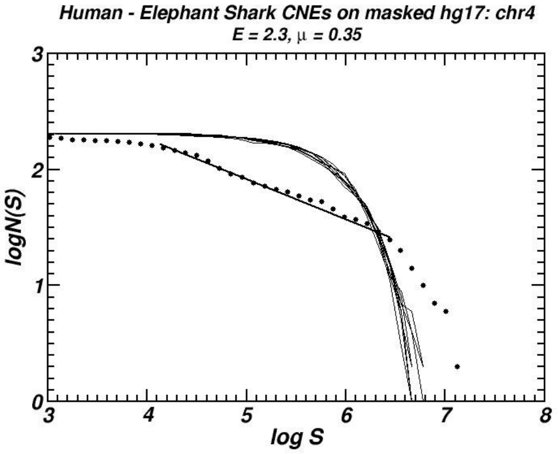

Human - Elephant Shark CNEs on hg17: chrX
E = 2 , μ = 0.35
logN(S)
log S
0
1
2
3
4
5
6
7
8

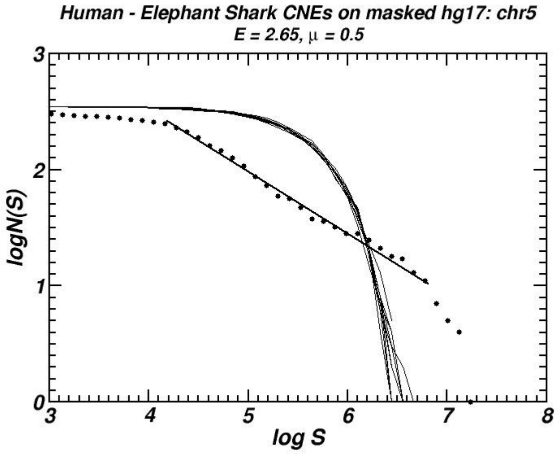
Human-Elephant Shark CNEs on gene-masked genome

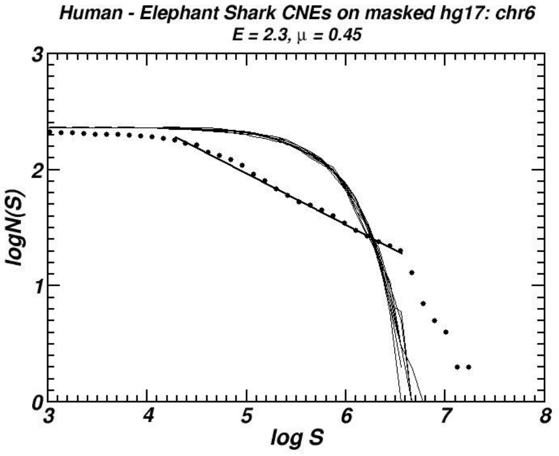


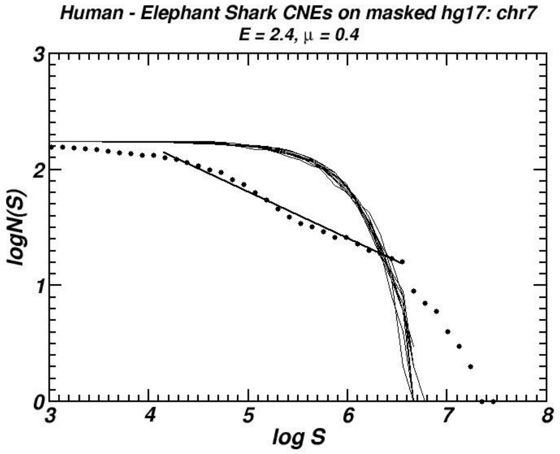


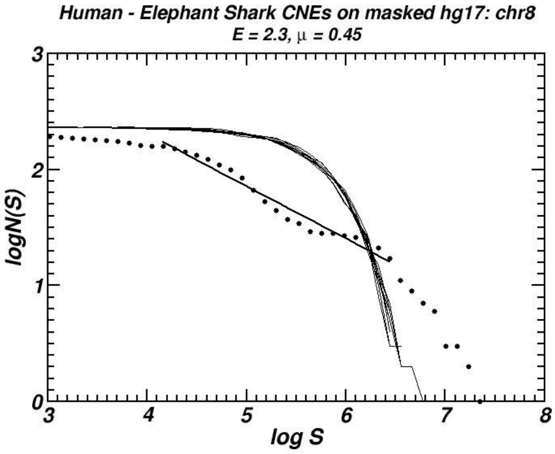


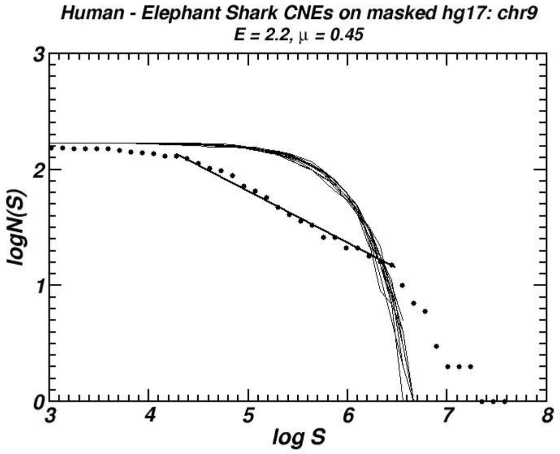


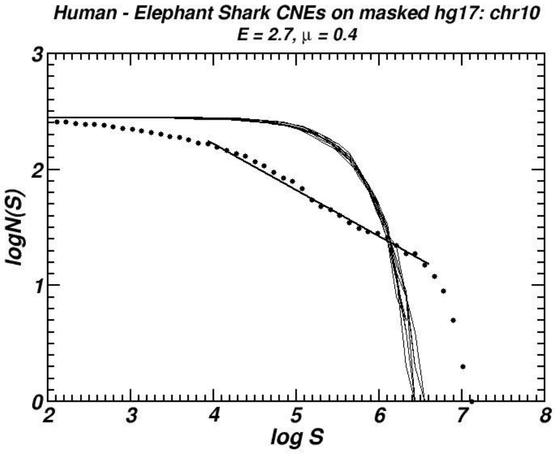


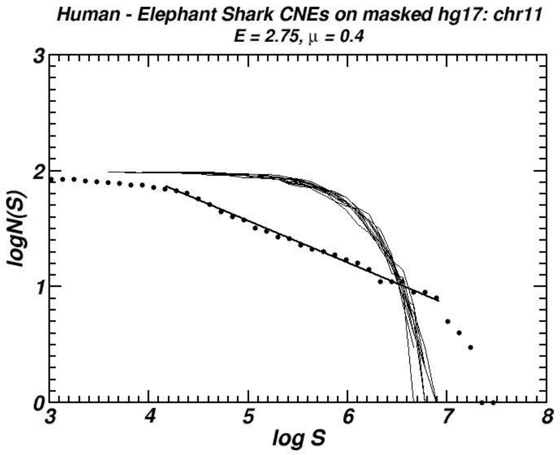


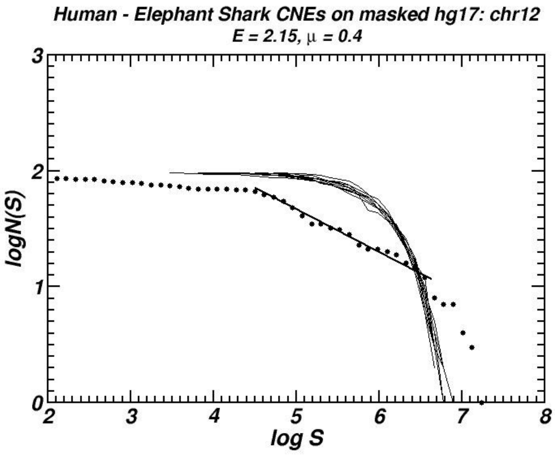

Human - Elephant Shark CNEs on masked hg17: chr7
E = 2.4, μ = 0.4

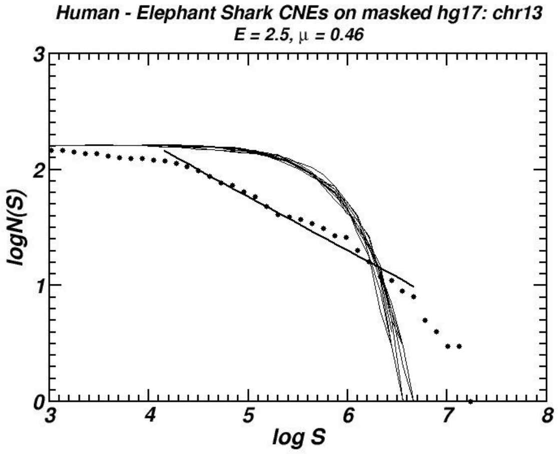

Human - Elephant Shark CNEs on masked hg17: chr8
E = 2.3, μ = 0.45


Human - Elephant Shark CNEs on masked hg17: chr9
E = 2.2, μ = 0.45

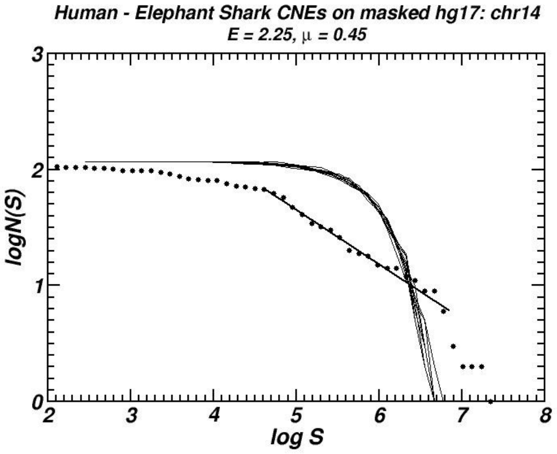

Human - Elephant Shark CNEs on masked hg17: chr10
E = 2.7, μ = 0.4


Human - Elephant Shark CNEs on masked hg17: chr11
E = 2.75, μ = 0.4

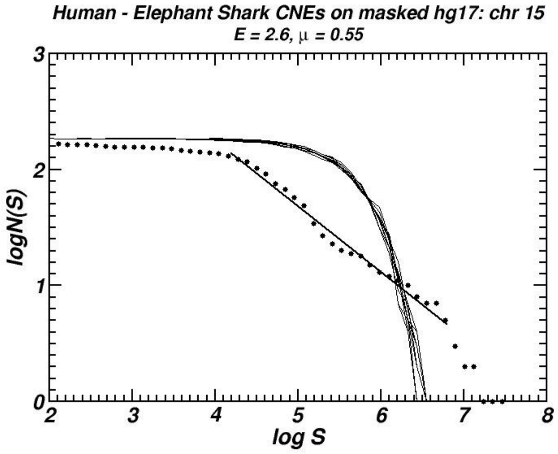

Human - Elephant Shark CNEs on masked hg17: chr12
E = 2.15, μ = 0.4


Human - Elephant Shark CNEs on masked hg17: chr13

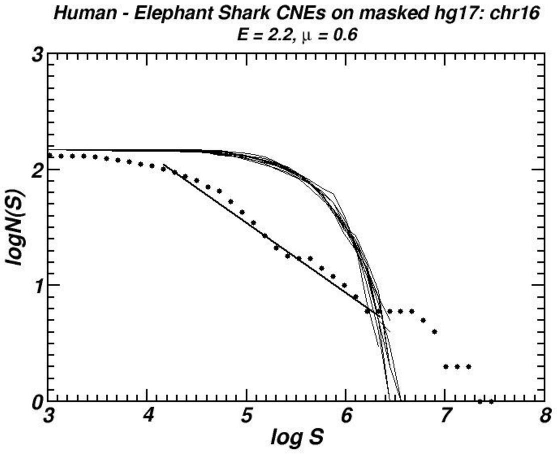
$E = 2.5$, $\mu = 0.46$


Human - Elephant Shark CNEs on masked hg17: chr14

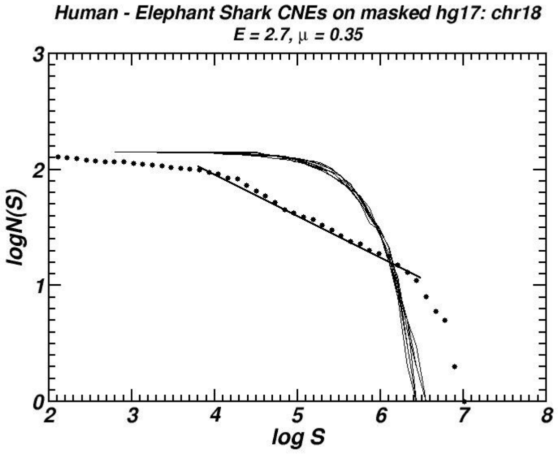
$E = 2.25$, $\mu = 0.45$


Human - Elephant Shark CNEs on masked hg17: chr 15

$E = 2.6$, $\mu = 0.55$

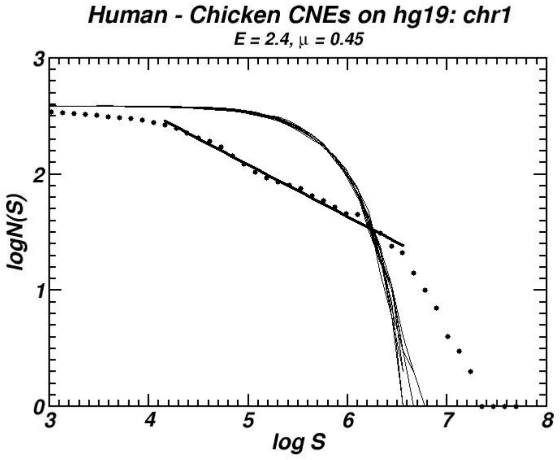

Human - Elephant Shark CNEs on masked hg17: chr16

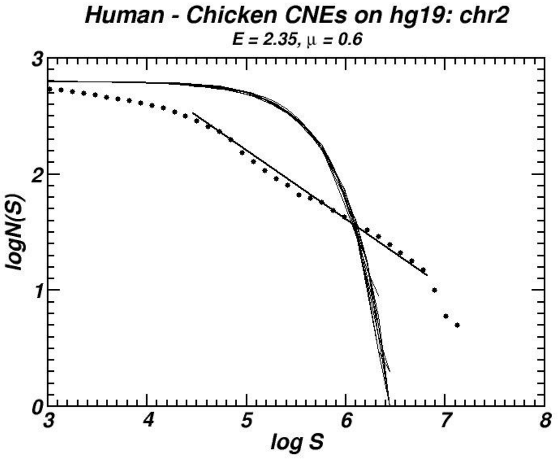
$E = 2.2$, $\mu = 0.6$

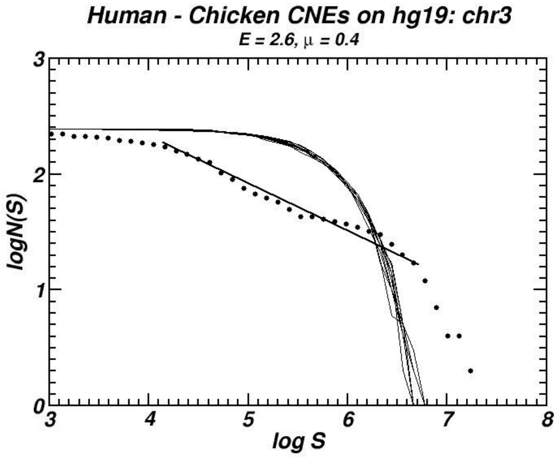

Human - Elephant Shark CNEs on masked hg17: chr18

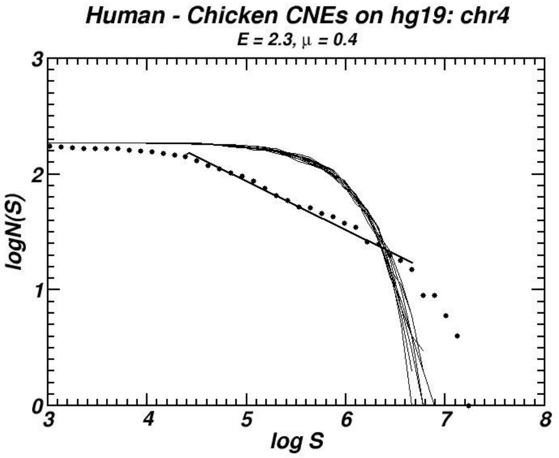
$E = 2.7$, $\mu = 0.35$

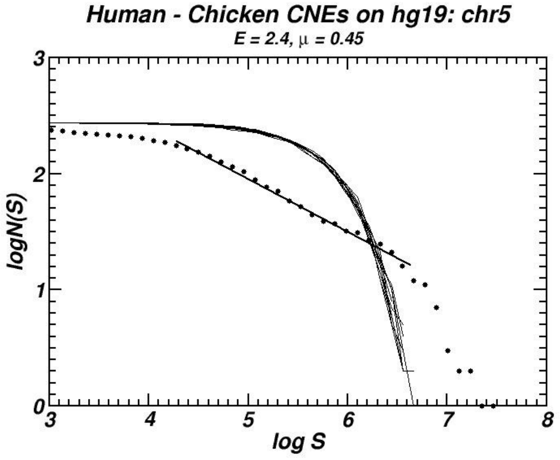
Human-Chicken UCNEs (Dataset iii)

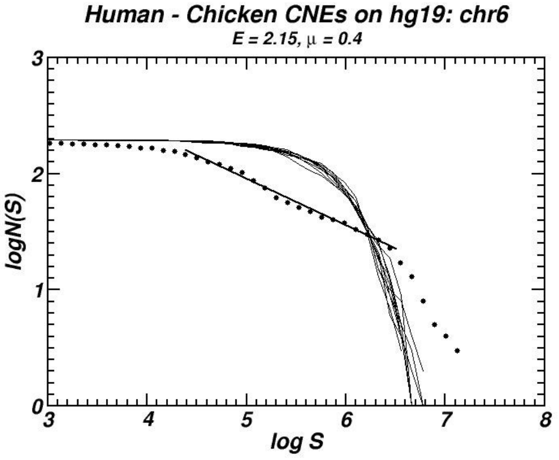


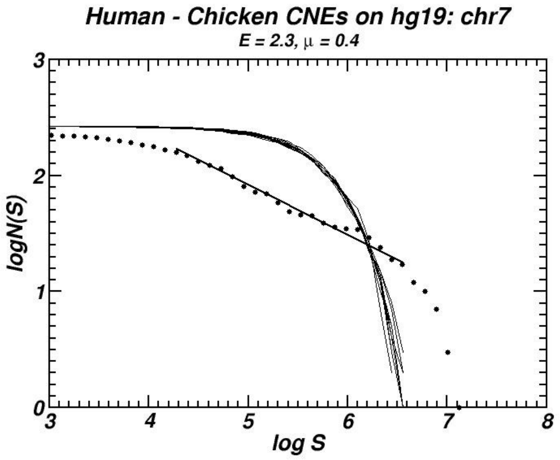




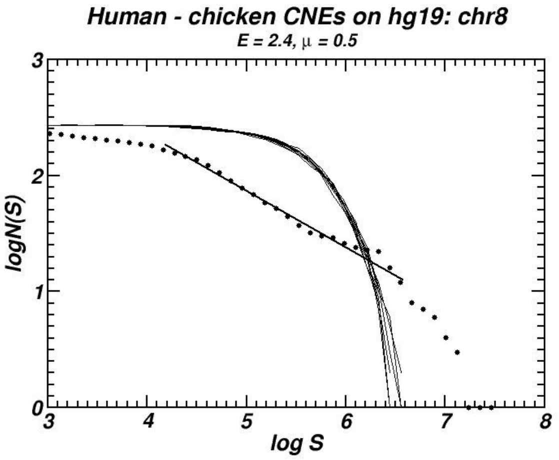




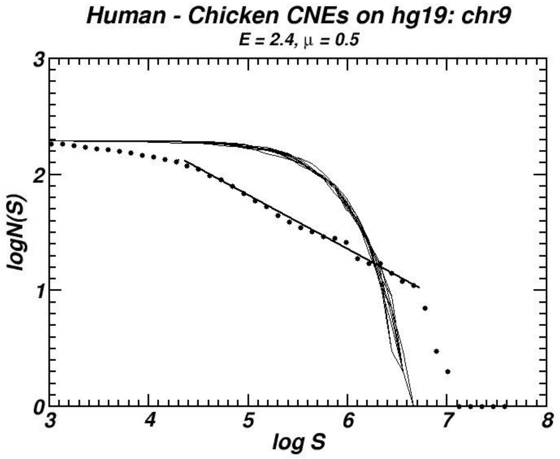



Human - Chicken CNEs on hg19: chr7

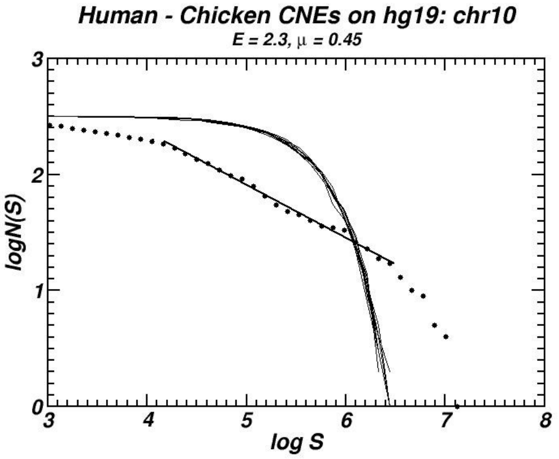
E = 2.3, μ = 0.4


Human - chicken CNEs on hg19: chr8

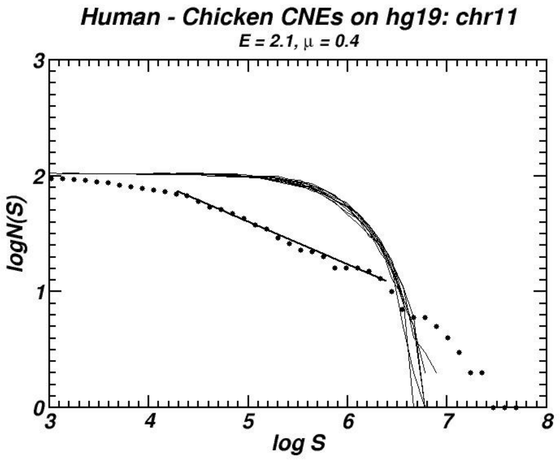
E = 2.4, μ = 0.5


Human - Chicken CNEs on hg19: chr9

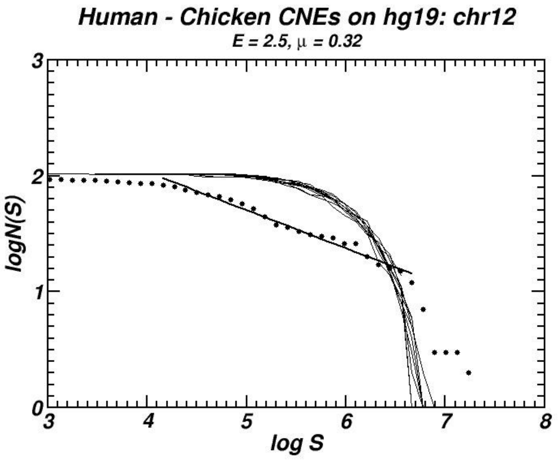
E = 2.4, μ = 0.5


Human - Chicken CNEs on hg19: chr10

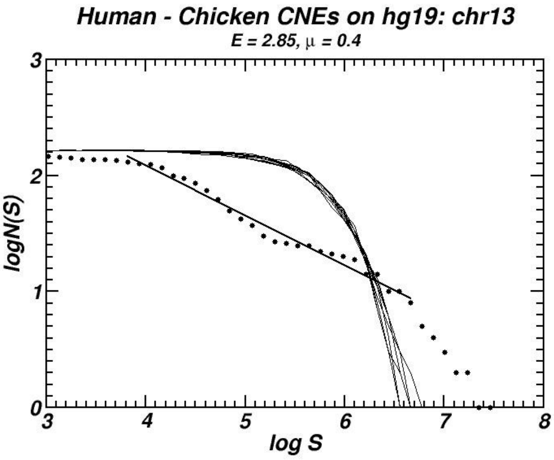
E = 2.3, μ = 0.45

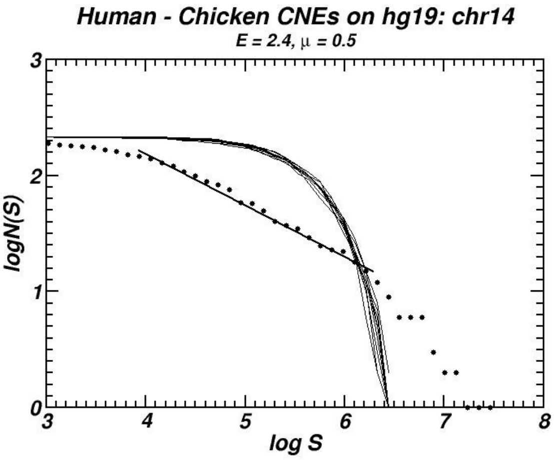

Human - Chicken CNEs on hg19: chr11

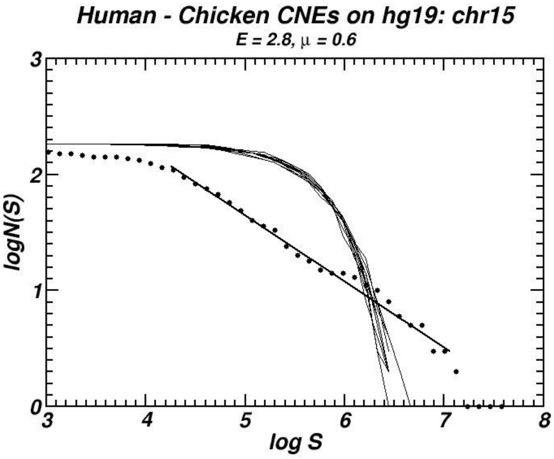
E = 2.1, μ = 0.4

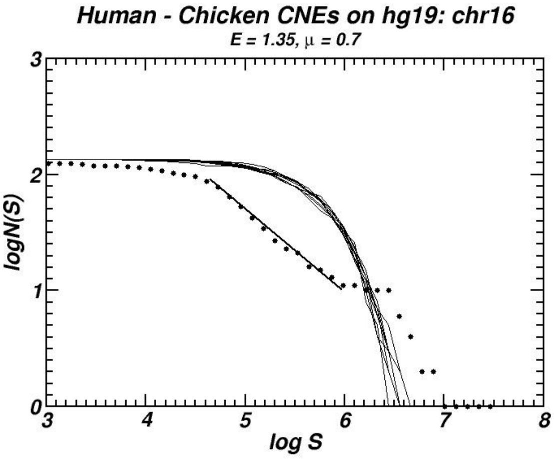

Human - Chicken CNEs on hg19: chr12

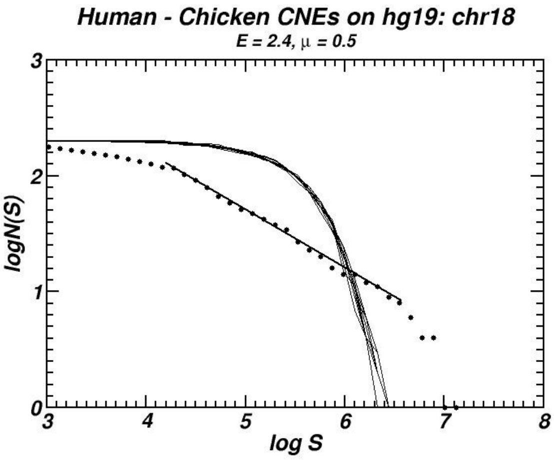
E = 2.5, μ = 0.32


Human - Chicken CNEs on hg19: chr13
E = 2.85, μ = 0.4
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

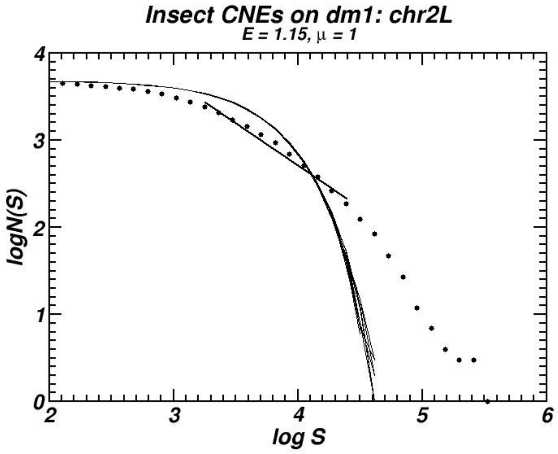

Human - Chicken CNEs on hg19: chr14
E = 2.4, μ = 0.5
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Human - Chicken CNEs on hg19: chr15
E = 2.8, μ = 0.6
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

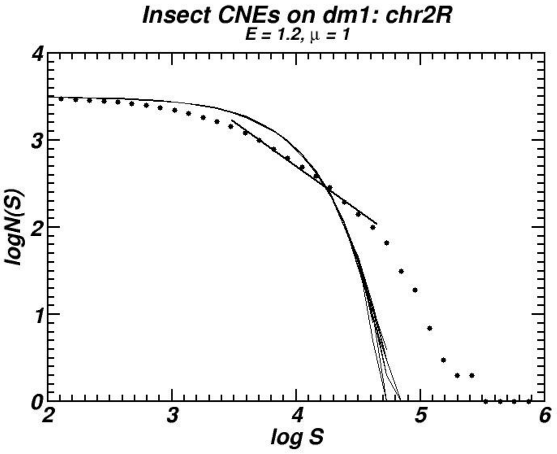

Human - Chicken CNEs on hg19: chr16
E = 1.35, μ = 0.7
logN(S)
log S
0
1
2
3
3
4
5
6
7
8


Human - Chicken CNEs on hg19: chr18
E = 2.4, μ = 0.5
logN(S)
log S
0
1
2
3
3
4
5
6
7
8

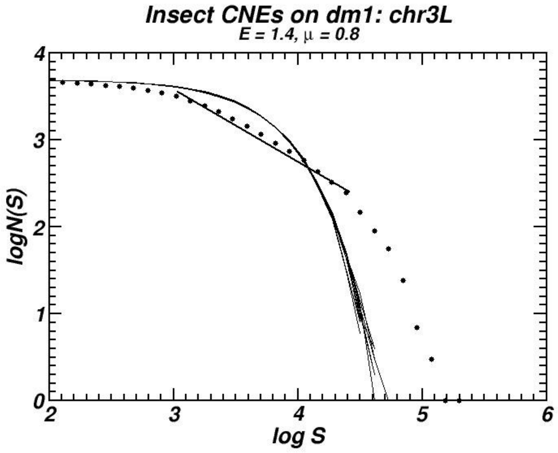
Insect CNEs (Dataset viii)


Insect CNEs on dm1: chr2L

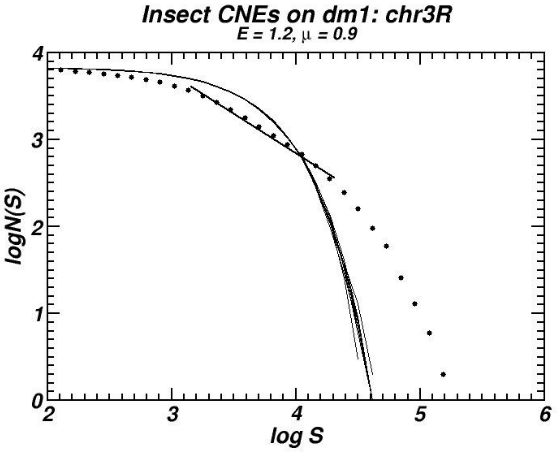
E = 1.15, μ = 1


Insect CNEs on dm1: chr2R

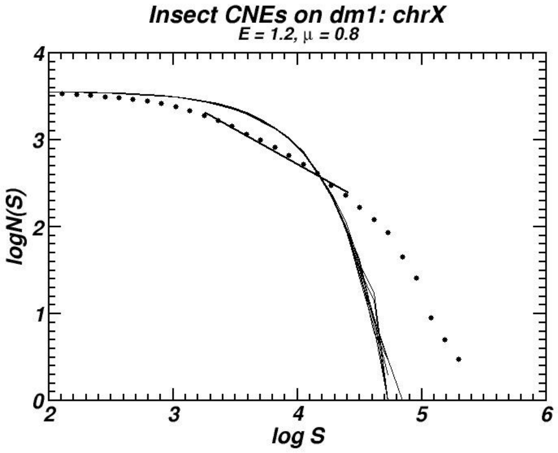
E = 1.2, μ = 1


Insect CNEs on dm1: chr3L

E = 1.4, μ = 0.8

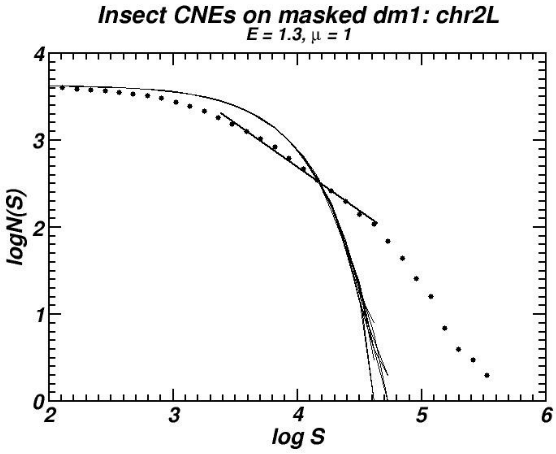

Insect CNEs on dm1: chr3R

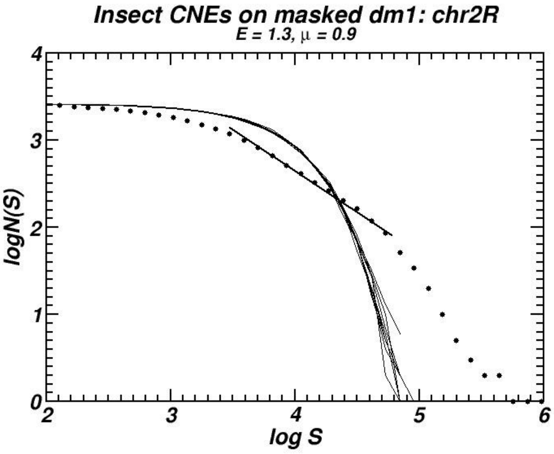
E = 1.2, μ = 0.9

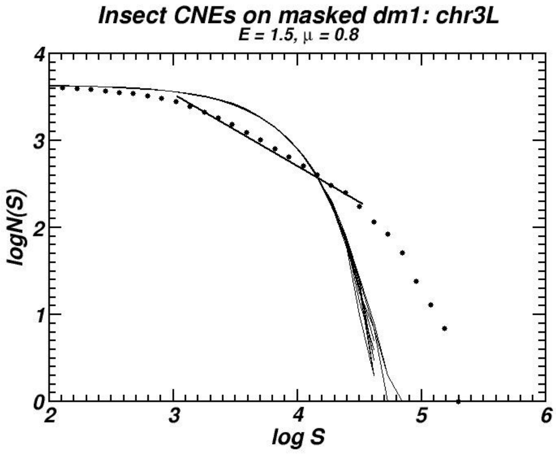

Insect CNEs on dm1: chrX

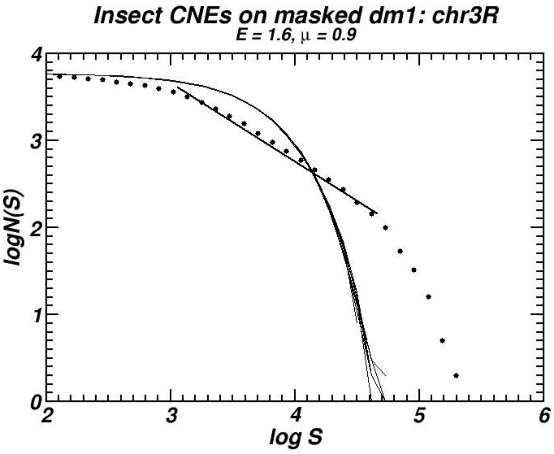
E = 1.2, μ = 0.8

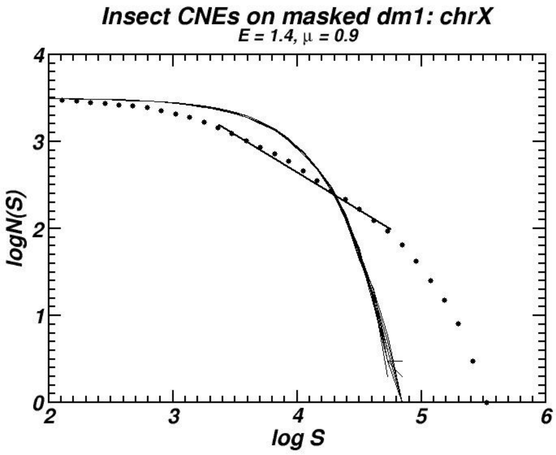
Insect CNEs on gene-masked genome


Insect CNEs on masked dm1: chr2L
E = 1.3, μ = 1

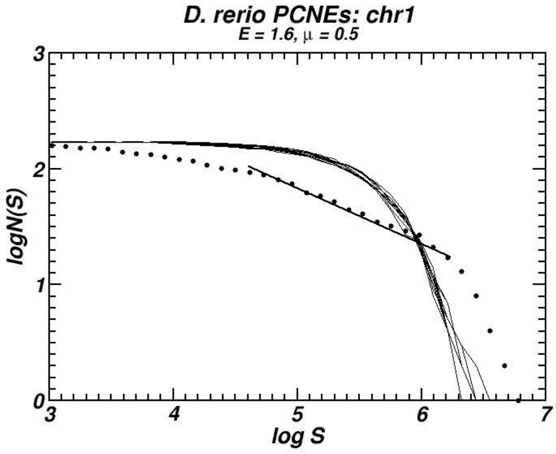

Insect CNEs on masked dm1: chr2R
E = 1.3, μ = 0.9

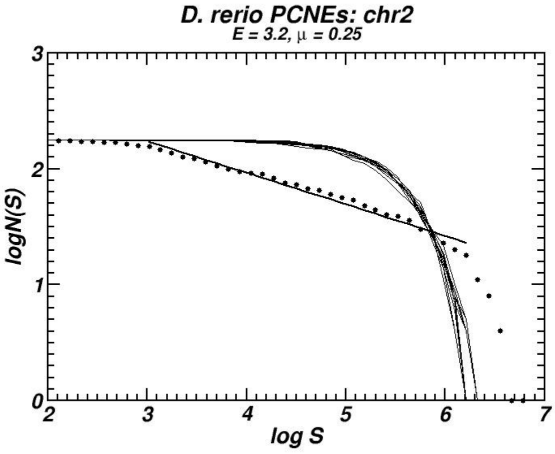

Insect CNEs on masked dm1: chr3L
E = 1.5, μ = 0.8

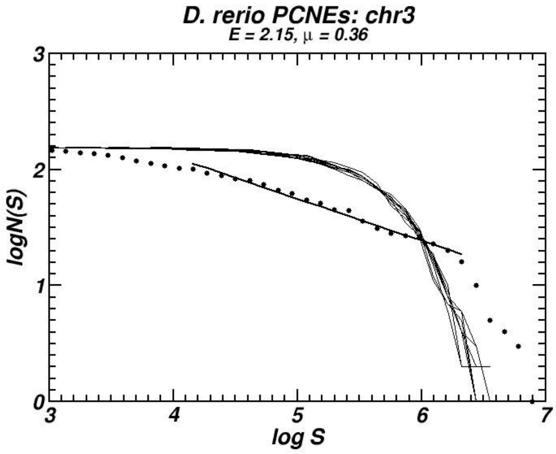

Insect CNEs on masked dm1: chr3R
E = 1.6, μ = 0.9

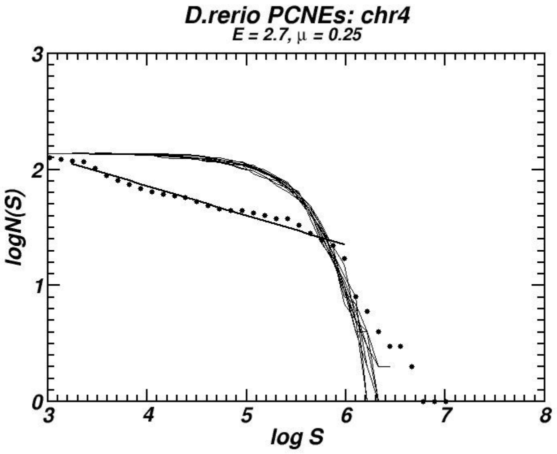

Insect CNEs on masked dm1: chrX
E = 1.4, μ = 0.9

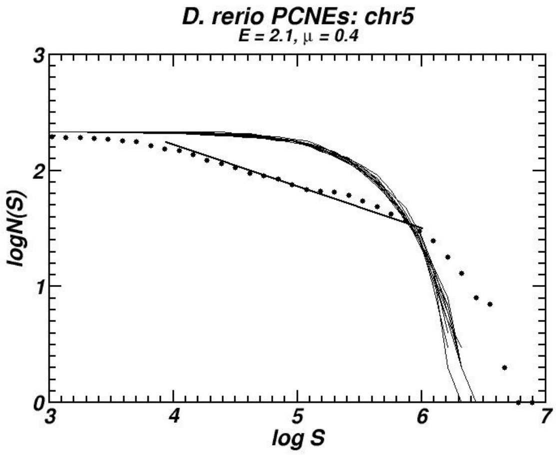
D.rerio PCNEs (Dataset vii)

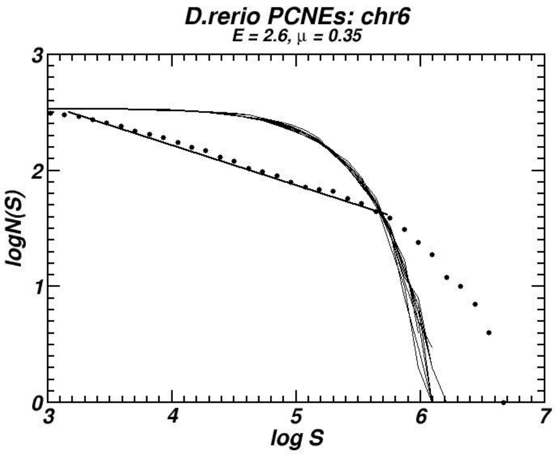


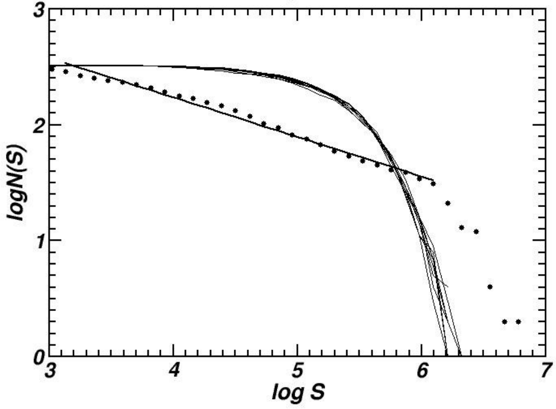






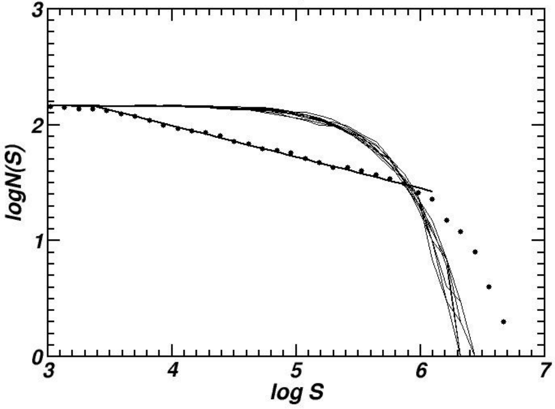






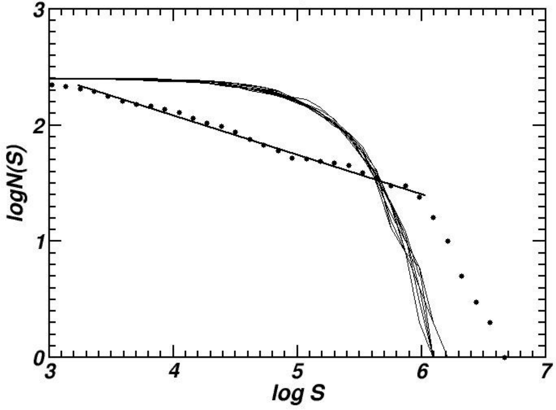
D. rerio PCNEs: chr7

E = 3, μ = 0.35



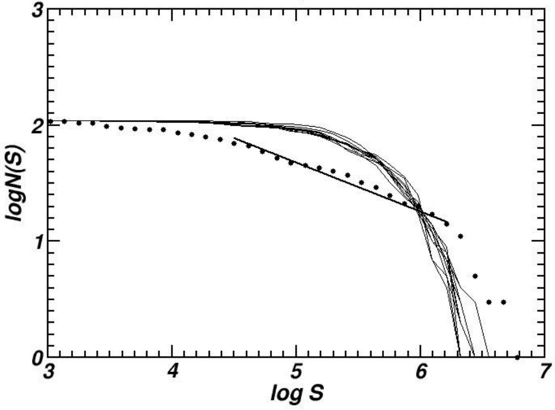
D.rerio PCNEs: chr8

E = 2.7, μ = 0.3



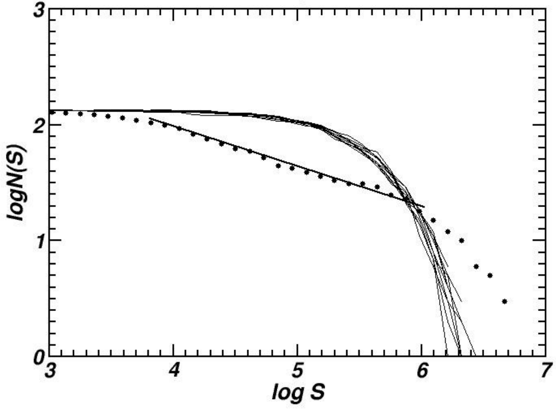
D. rerio PCNEs: chr9

E = 2.8, μ = 0.35



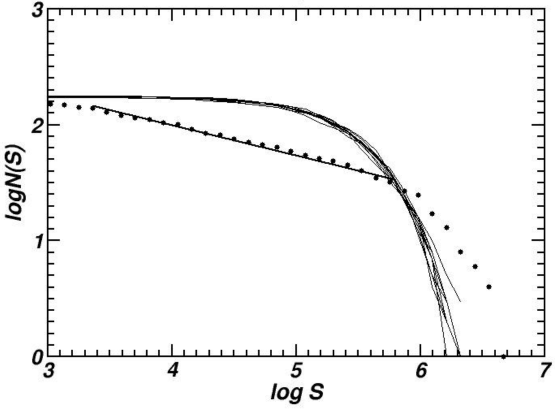
D. rerio PCNEs: chr10

E = 1.7, μ = 0.4



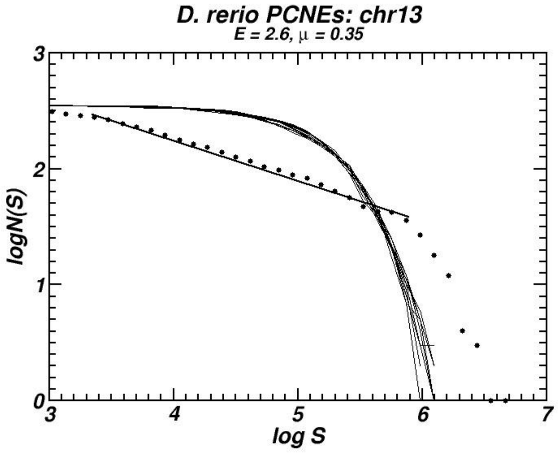
D. rerio PCNEs: chr11

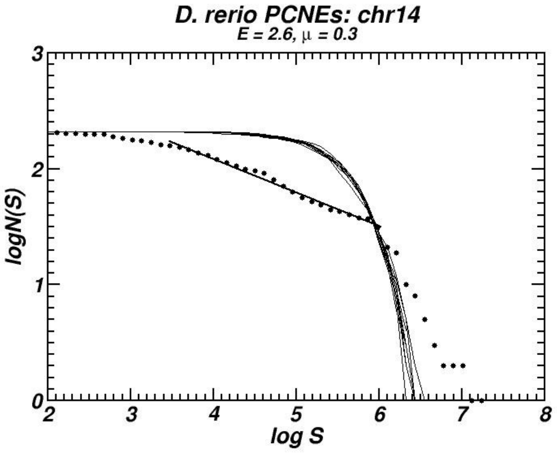
E = 2.2, μ = 0.35

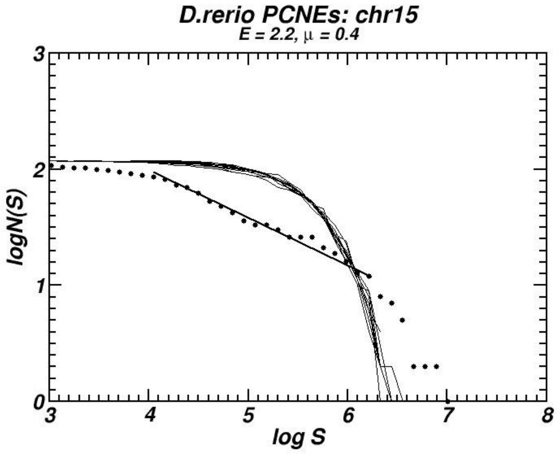


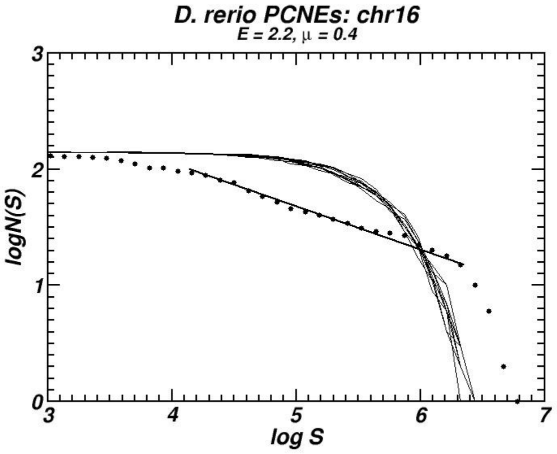
D. rerio PCNEs: chr12

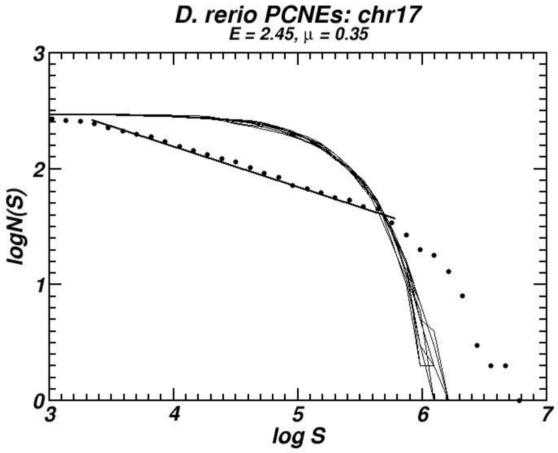
E = 2.4, μ = 0.3

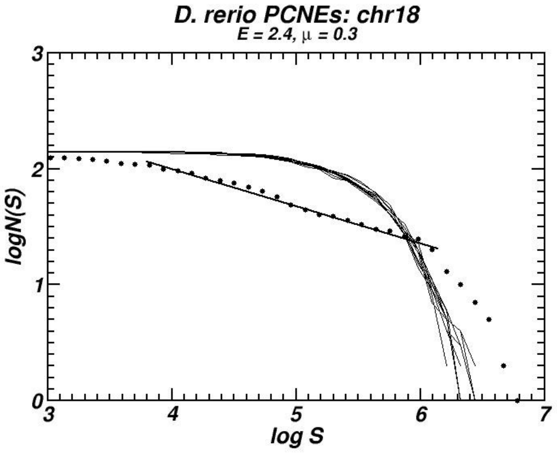

D. rerio PCNEs: chr13
E = 2.6, μ = 0.35

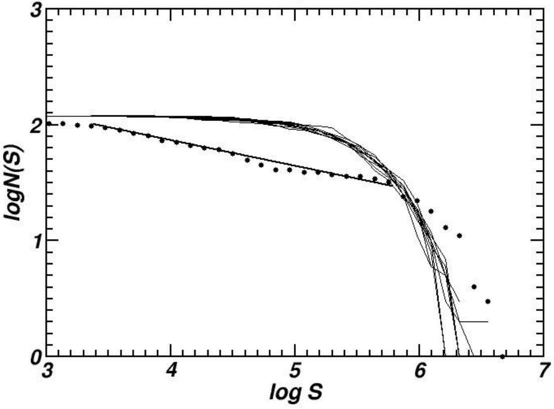

D. rerio PCNEs: chr14
E = 2.6, μ = 0.3


D.rerio PCNEs: chr15
E = 2.2, μ = 0.4


D. rerio PCNEs: chr16
E = 2.2, μ = 0.4

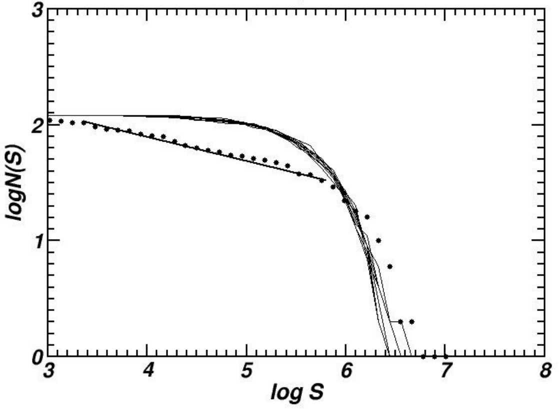

D. rerio PCNEs: chr17
E = 2.45, μ = 0.35


D. rerio PCNEs: chr18
E = 2.4, μ = 0.3



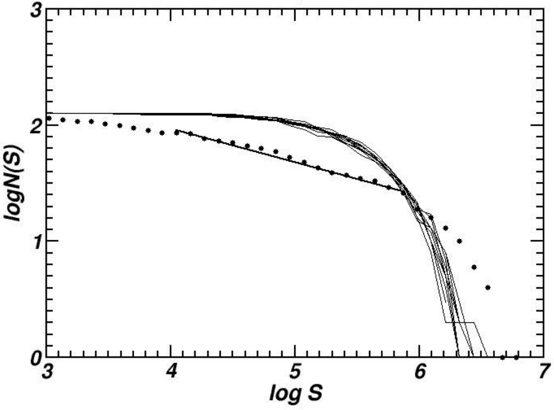
D. rerio PCNEs: chr19

E = 2.4, μ = 0.2



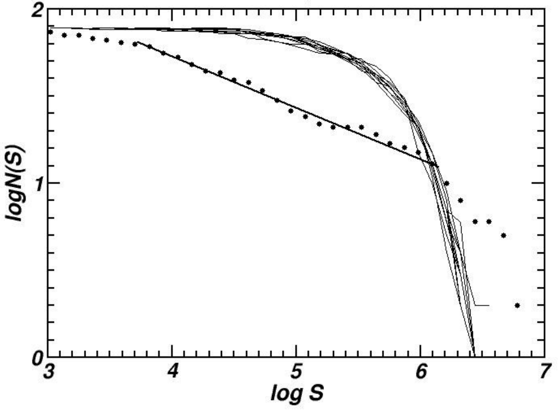
D. rerio PCNEs: chr20

E = 2.5, μ = 0.2



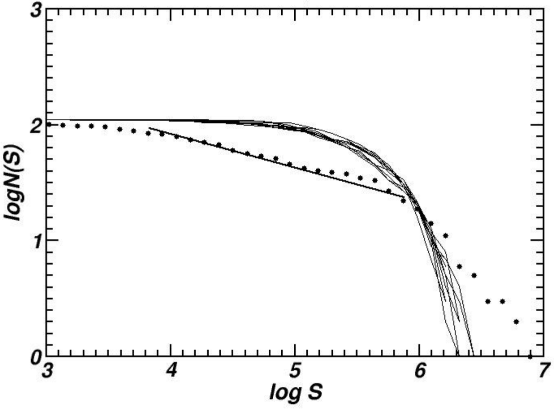
D. rerio PCNEs: chr21

E = 1.8, μ = 0.3



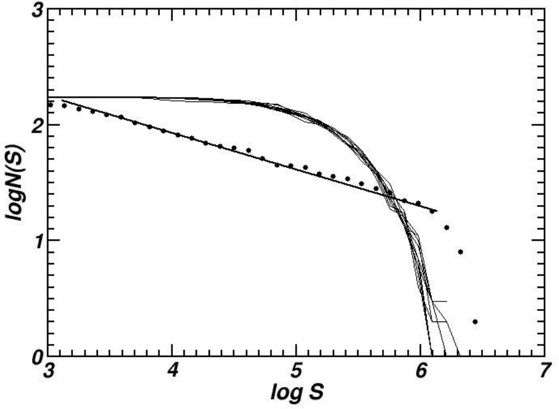
D. rerio PCNEs: chr22

E = 2.45, μ = 0.3



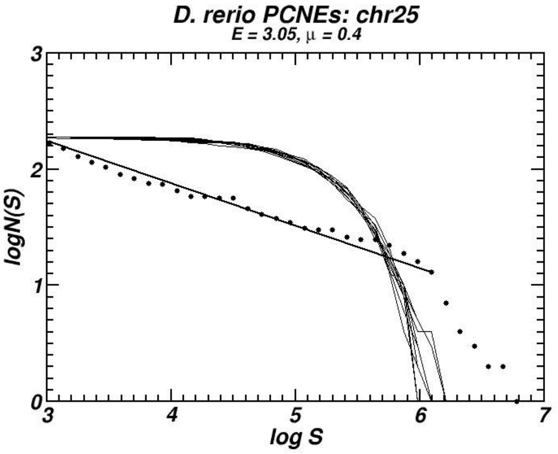
D. rerio PCNEs: chr23

E = 2.05, μ = 0.3

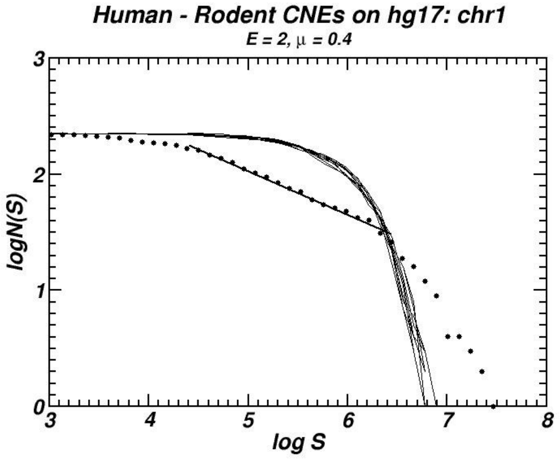


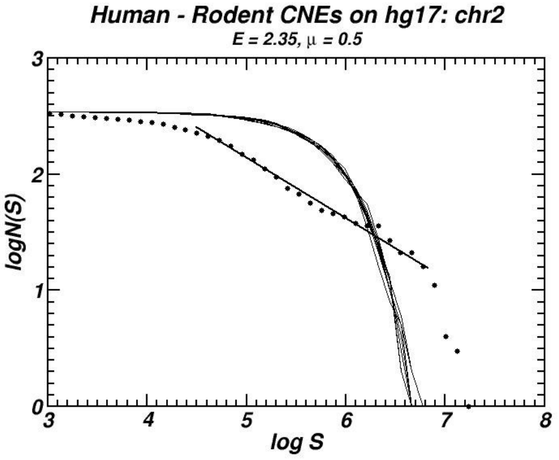
D. rerio PCNEs: chr24

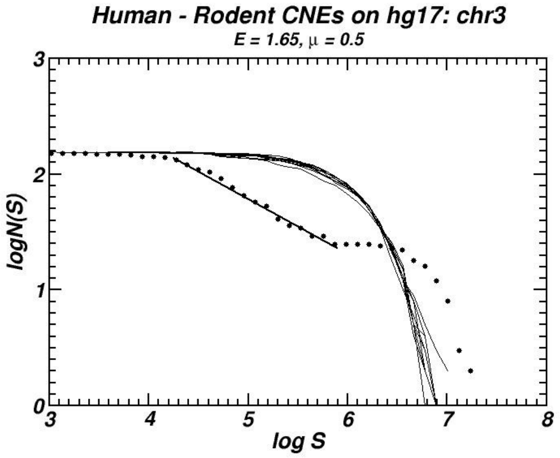
E = 3, μ = 0.3

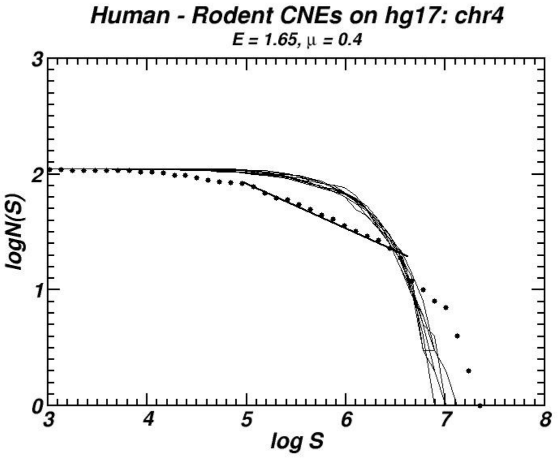

D. rerio PCNEs: chr25
E = 3.05, μ = 0.4
logN(S)
log S
0
1
2
3
3
4
5
6
7

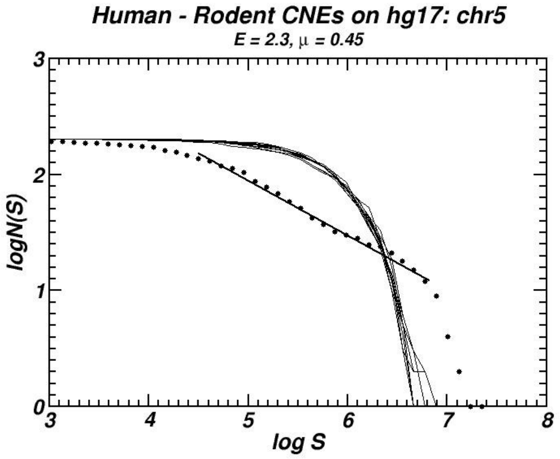
Human-Rodents CNEs (Dataset x)

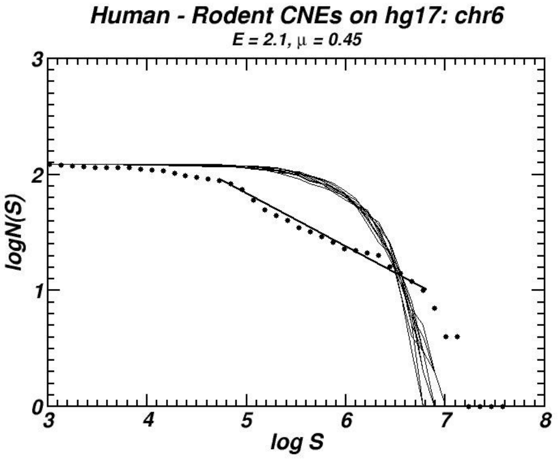


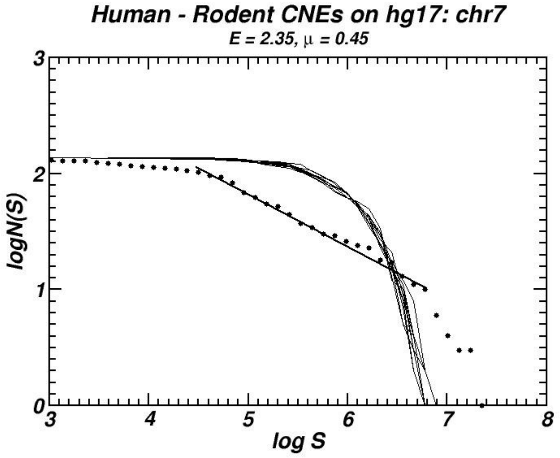




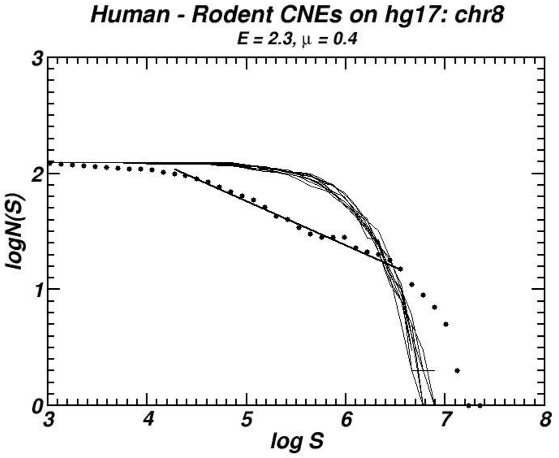




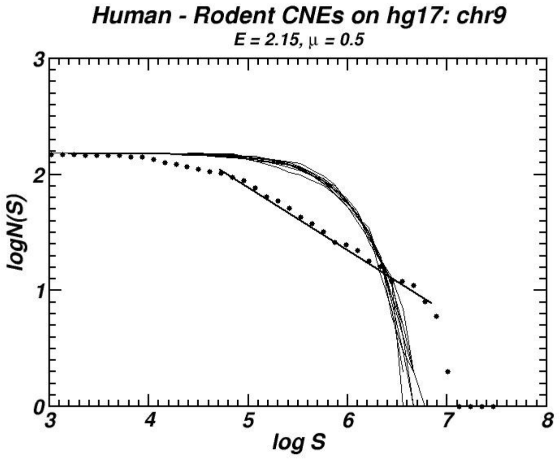



Human - Rodent CNEs on hg17: chr7

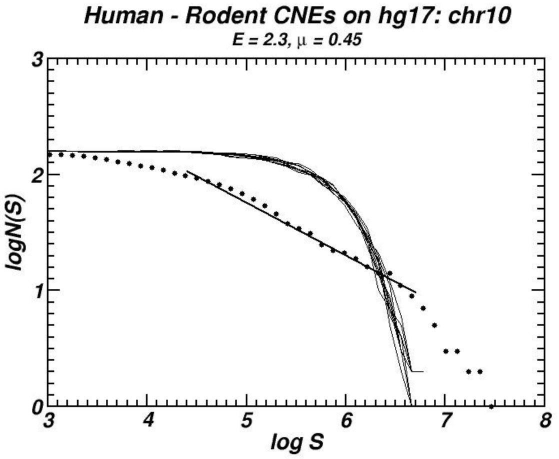
$E = 2.35$, $\mu = 0.45$


Human - Rodent CNEs on hg17: chr8

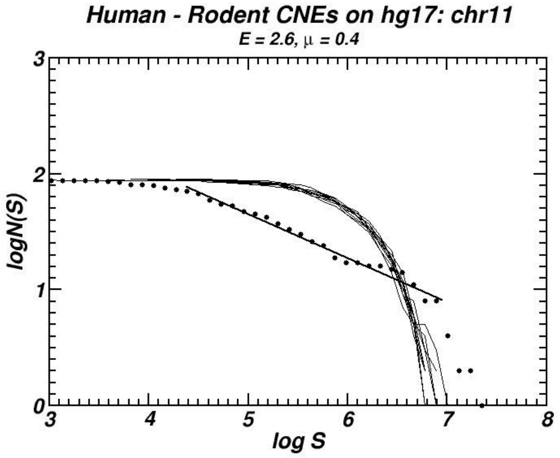
$E = 2.3$, $\mu = 0.4$


Human - Rodent CNEs on hg17: chr9

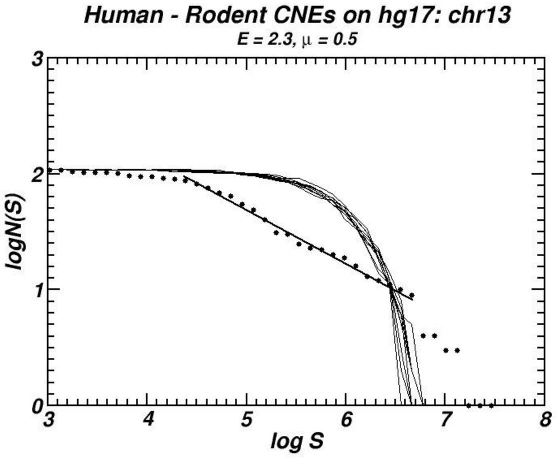
$E = 2.15$, $\mu = 0.5$


Human - Rodent CNEs on hg17: chr10

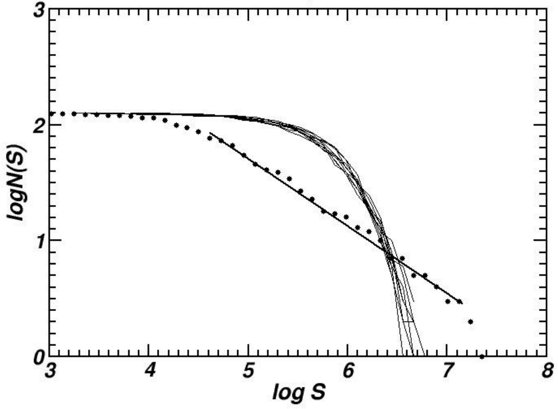
$E = 2.3$, $\mu = 0.45$


Human - Rodent CNEs on hg17: chr11

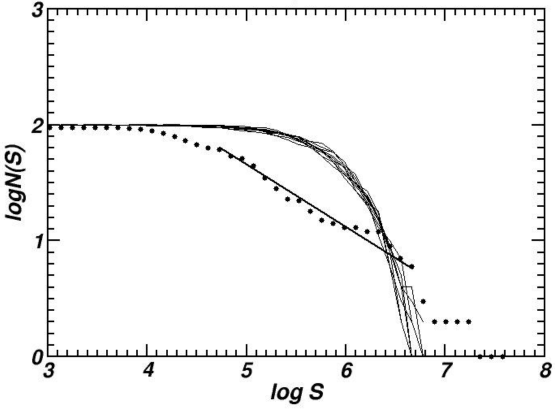
$E = 2.6$, $\mu = 0.4$


Human - Rodent CNEs on hg17: chr13

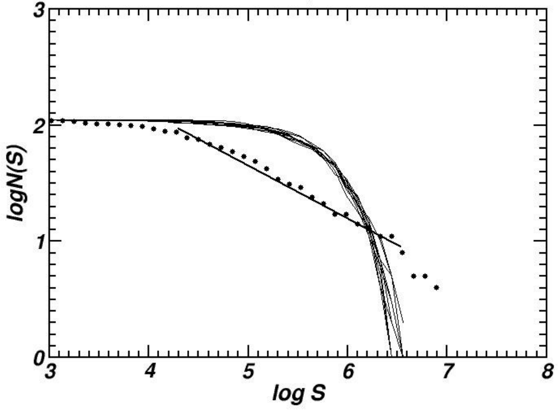
$E = 2.3$, $\mu = 0.5$


Human - Rodent CNEs on hg17: chr14

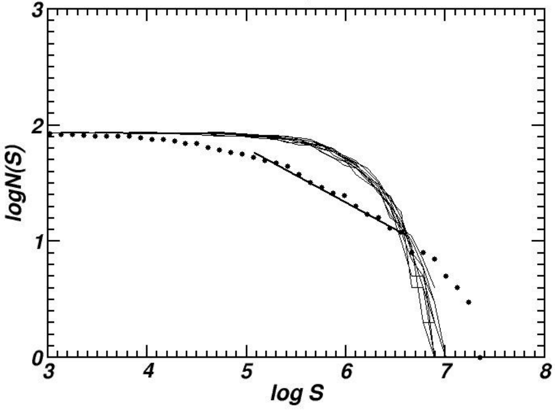
E = 2.55, μ = 0.6


Human - Rodent CNEs on hg17: chr15

E = 2, μ = 0.5

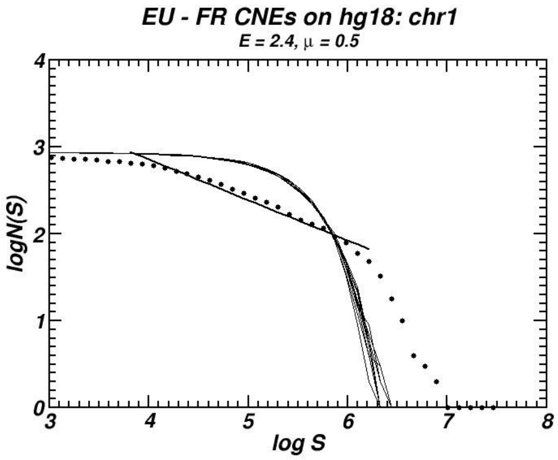

Human - Rodent CNEs on hg17: chr18

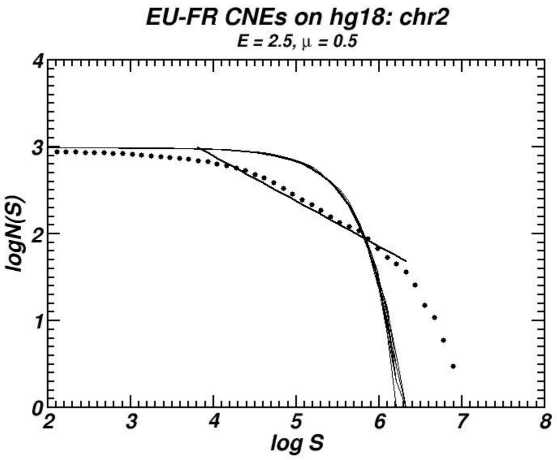
E = 2.25, μ = 0.6

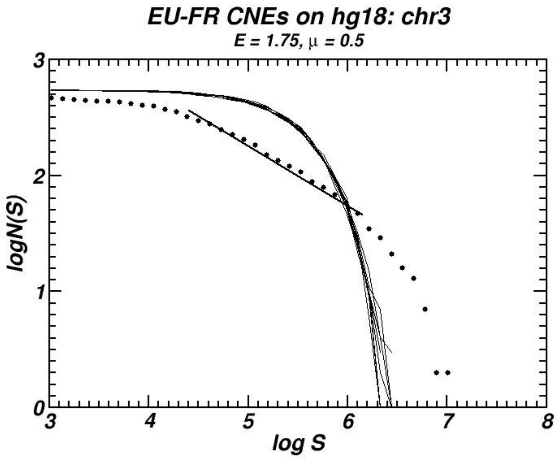

Human - Rodent CNEs on hg17: chrX

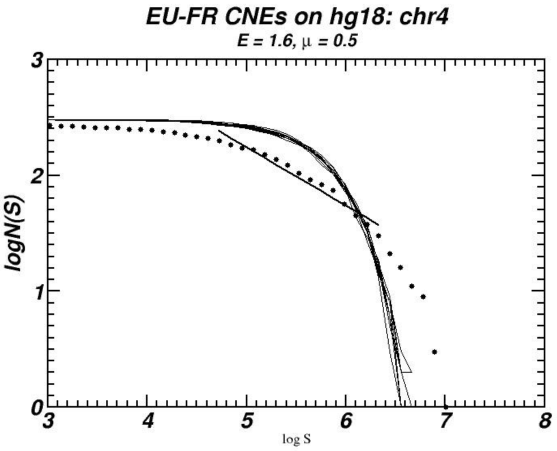
E = 1.55, μ = 0.5

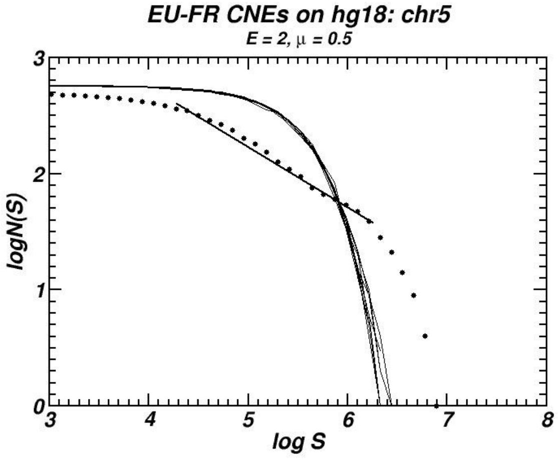
EU-FR CNEs (Dataset ia)

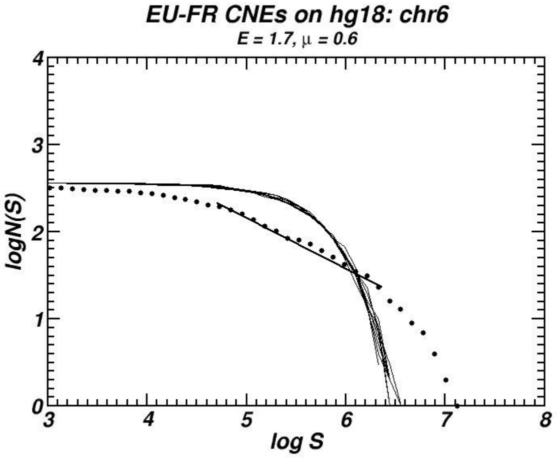


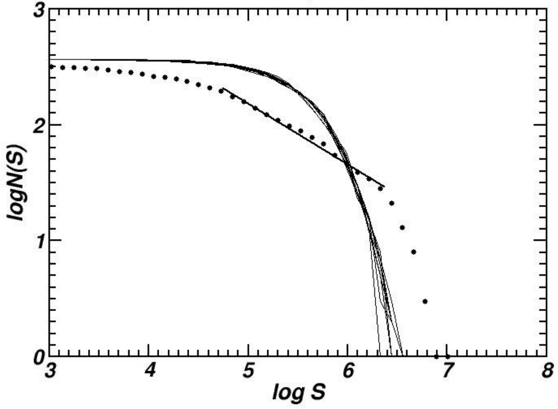






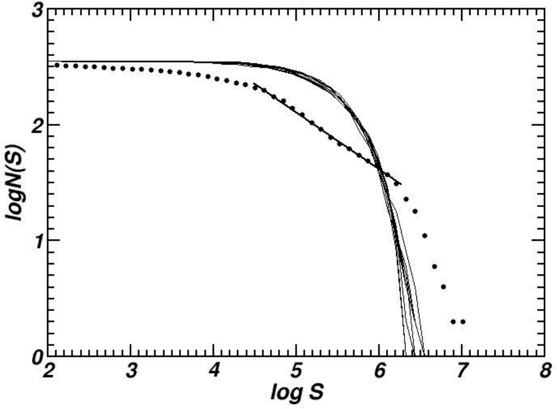






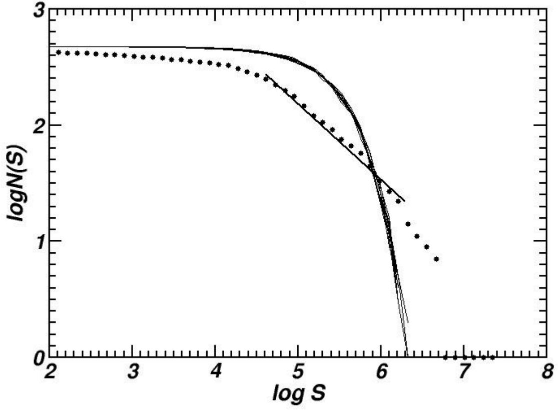
EU-FR CNEs on hg18: chr7

E = 1.65, μ = 0.5



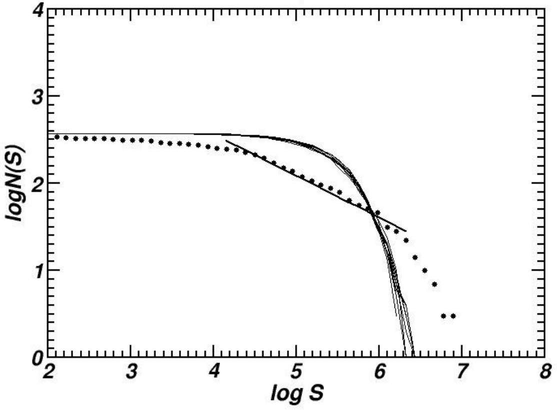
EU-FR CNEs on hg18: chr8

E = 1.8, μ = 0.5



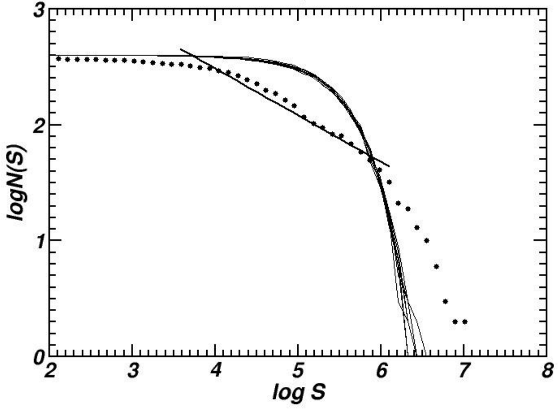
EU-FR CNEs on hg18: chr9

E = 1.7, μ = 0.65



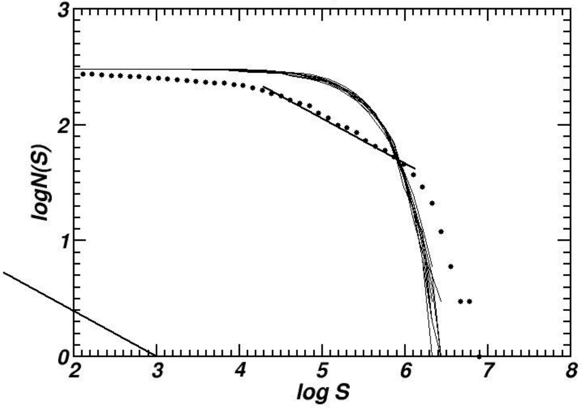
EU-FR CNEs on hg18: chr10

E = 2.15, μ = 0.47



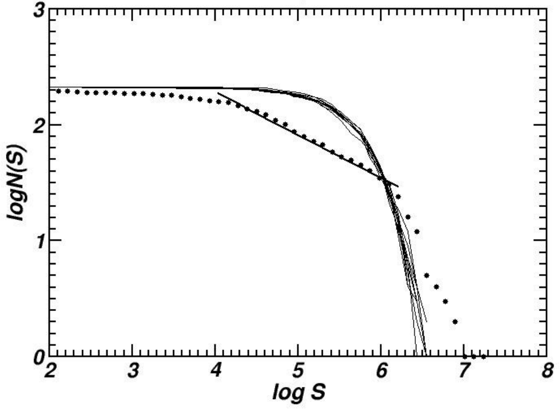
EU-FR CNEs on hg18: chr11

E = 2.5, μ = 0.4

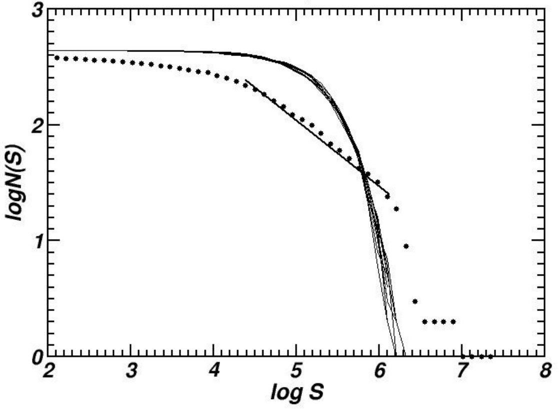


EU-FR CNEs on hg18: chr12

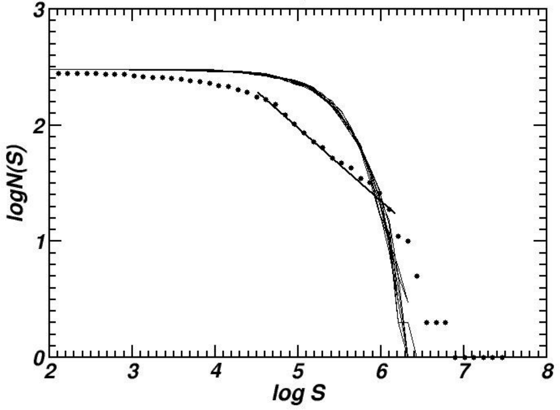
E = 1.85, μ = 0.4


EU-FR CNEs on hg18: chr13

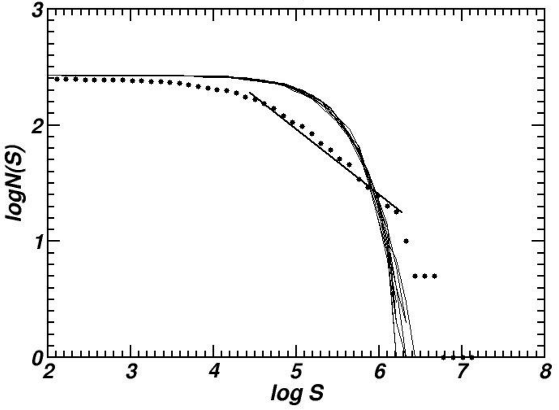
$E = 2.15$, $\mu = 0.37$


EU-FR CNEs on hg18: chr14

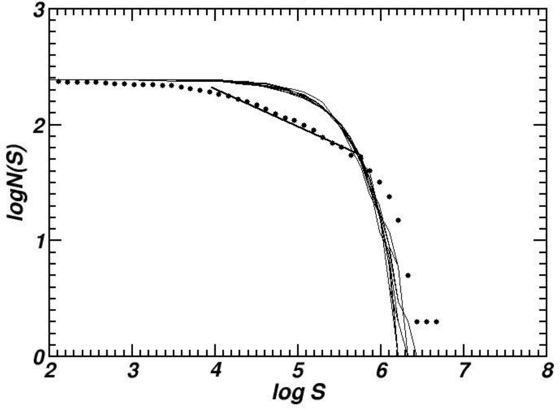
$E = 1.75$, $\mu = 0.6$


EU-FR CNEs on hg18: chr15

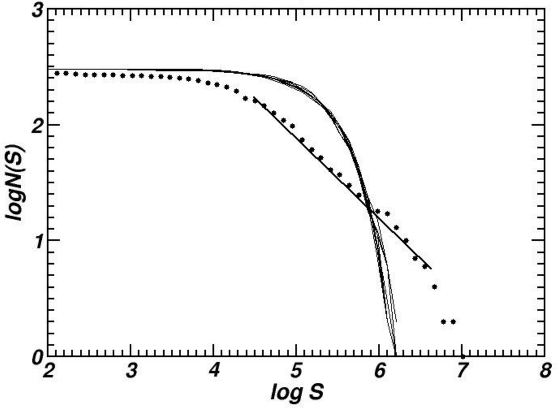
$E = 1.7$, $\mu = 0.6$


EU-FR CNEs on hg18: chr16

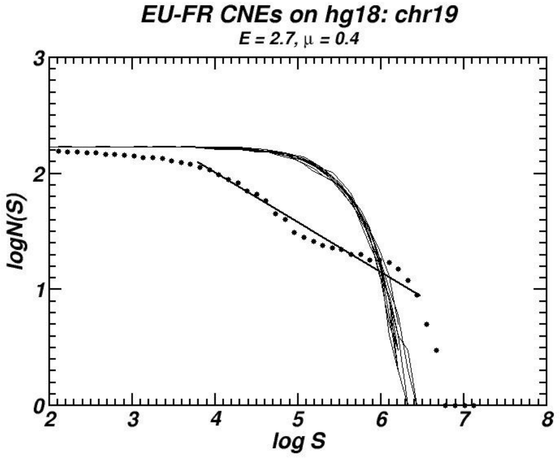
$E = 1.9$, $\mu = 0.6$


EU-FR CNEs on hg18: chr17

$E = 1.8$, $\mu = 0.3$

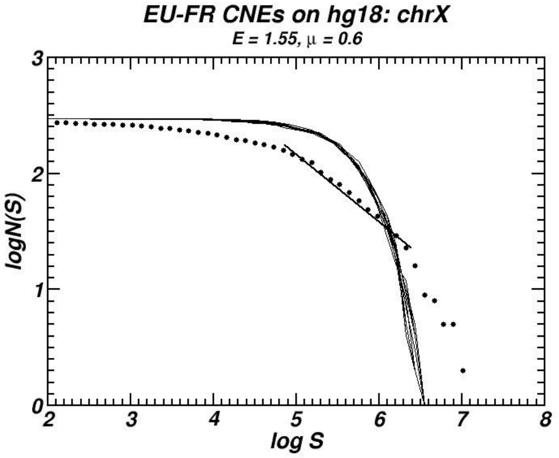

EU-FR CNEs on hg18: chr18

$E = 2.2$, $\mu = 0.7$



EU-FR CNEs on hg18: chr19

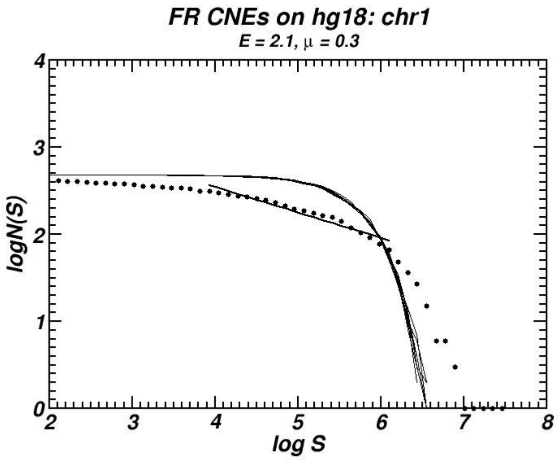
E = 2.7, μ = 0.4



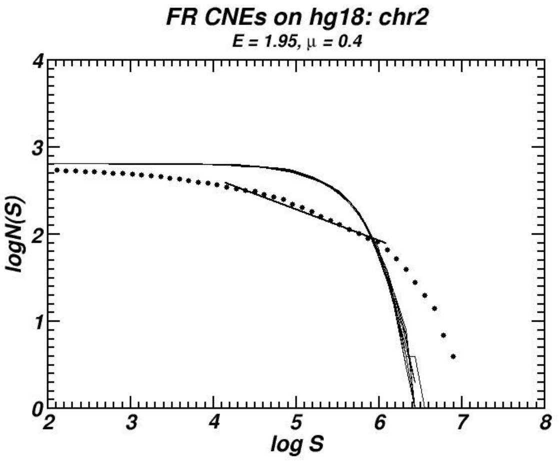
EU-FR CNEs on hg18: chrX

E = 1.55, μ = 0.6

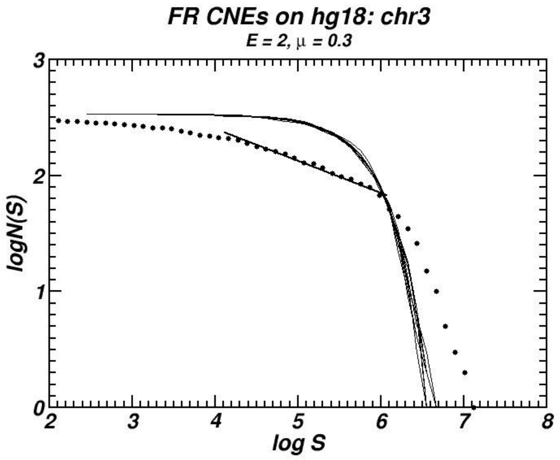
FR CNEs (Dataset ib)


FR CNEs on hg18: chr1

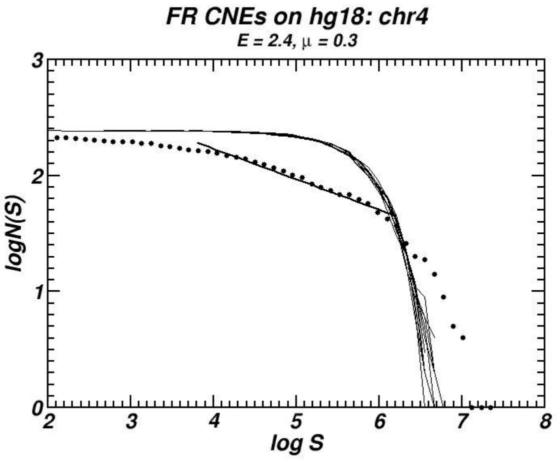
E = 2.1, μ = 0.3


FR CNEs on hg18: chr2

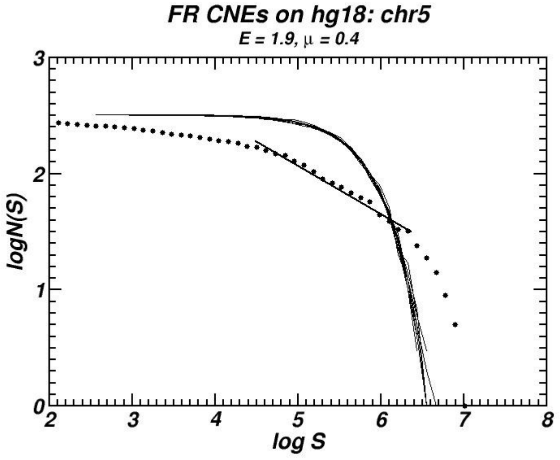
E = 1.95, μ = 0.4


FR CNEs on hg18: chr3

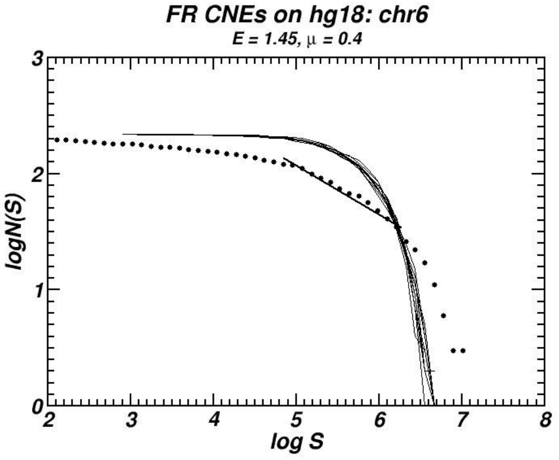
E = 2, μ = 0.3


FR CNEs on hg18: chr4

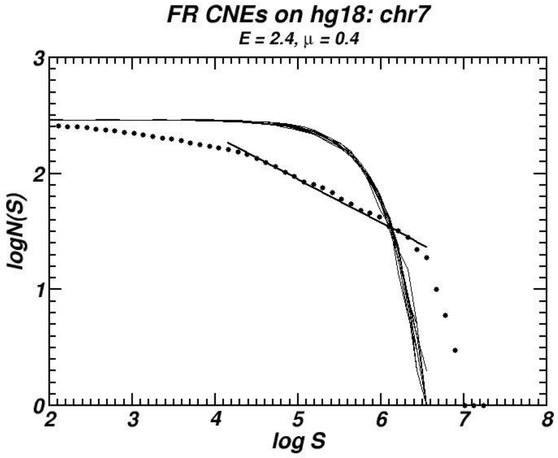
E = 2.4, μ = 0.3


FR CNEs on hg18: chr5

E = 1.9, μ = 0.4

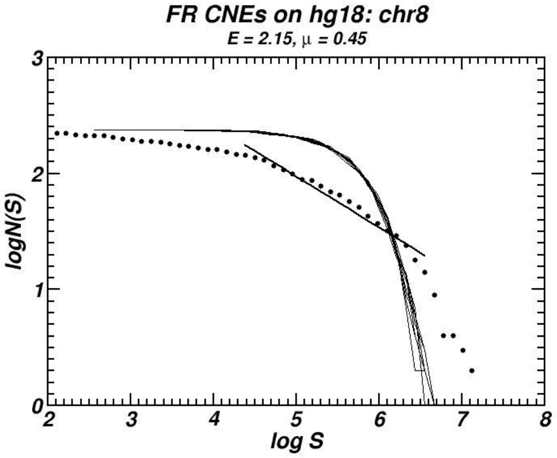

FR CNEs on hg18: chr6

E = 1.45, μ = 0.4



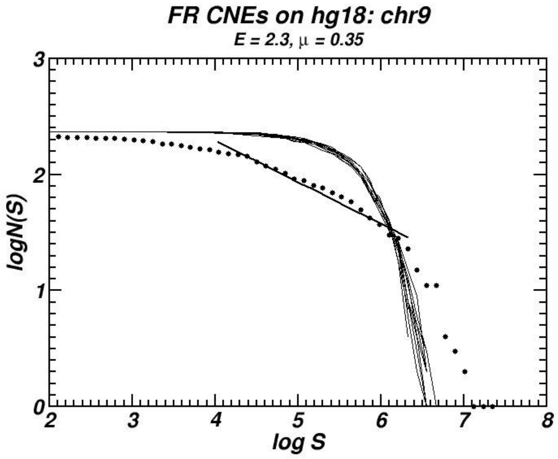
FR CNEs on hg18: chr7

$E = 2.4$, $\mu = 0.4$



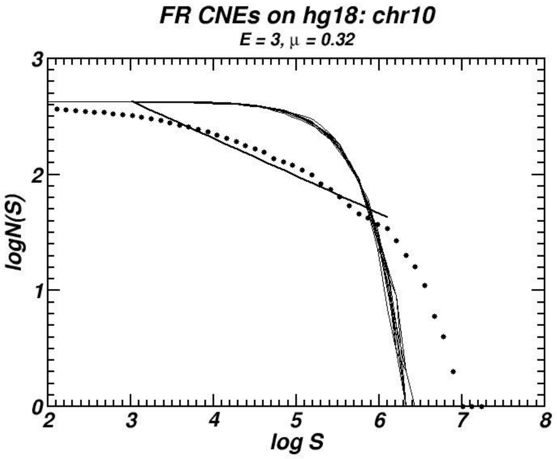
FR CNEs on hg18: chr8

$E = 2.15$, $\mu = 0.45$



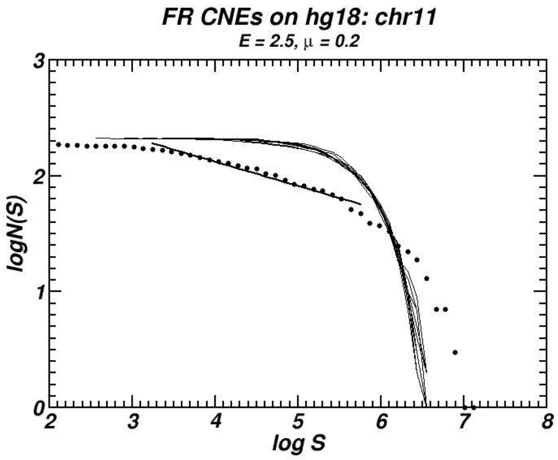
FR CNEs on hg18: chr9

$E = 2.3$, $\mu = 0.35$



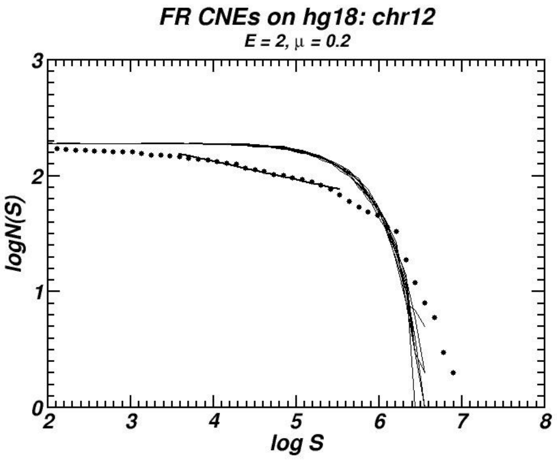
FR CNEs on hg18: chr10

$E = 3$, $\mu = 0.32$



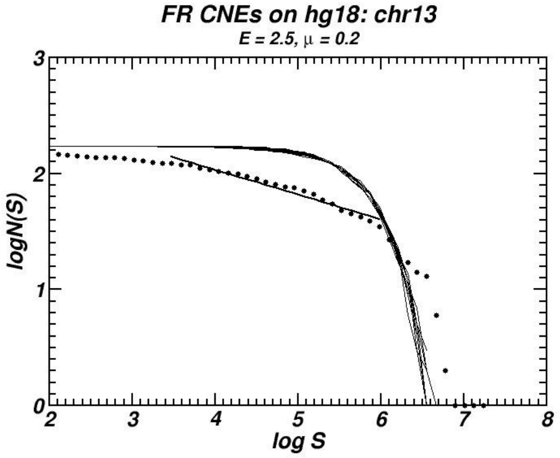
FR CNEs on hg18: chr11

$E = 2.5$, $\mu = 0.2$

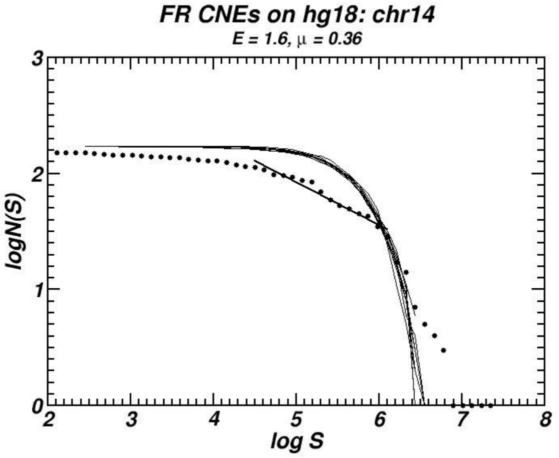


FR CNEs on hg18: chr12

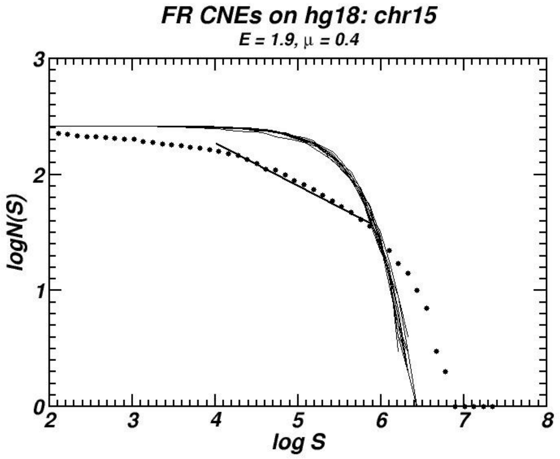
$E = 2$, $\mu = 0.2$


FR CNEs on hg18: chr13

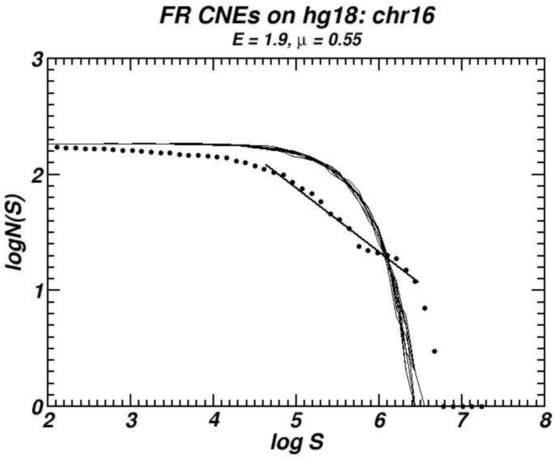
$E = 2.5, \mu = 0.2$


FR CNEs on hg18: chr14

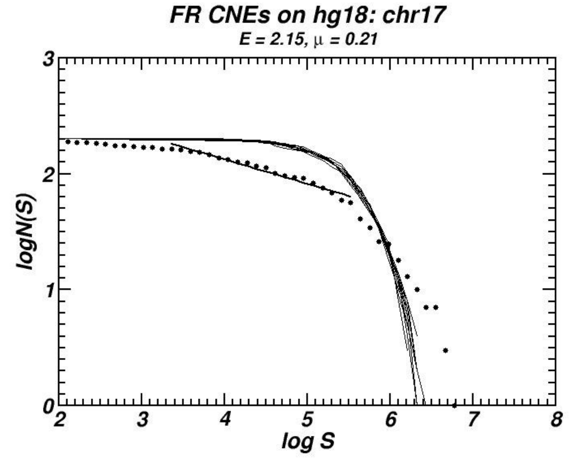
$E = 1.6, \mu = 0.36$


FR CNEs on hg18: chr15

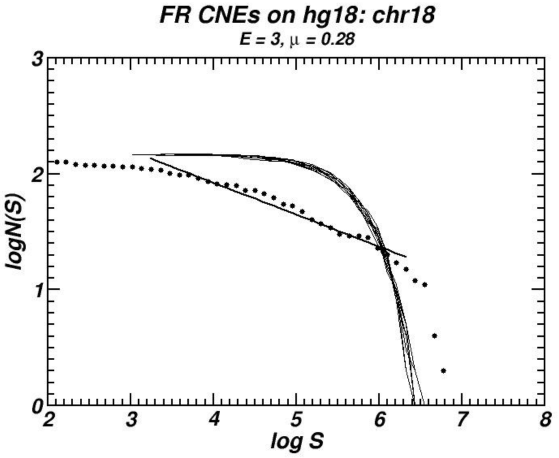
$E = 1.9, \mu = 0.4$


FR CNEs on hg18: chr16

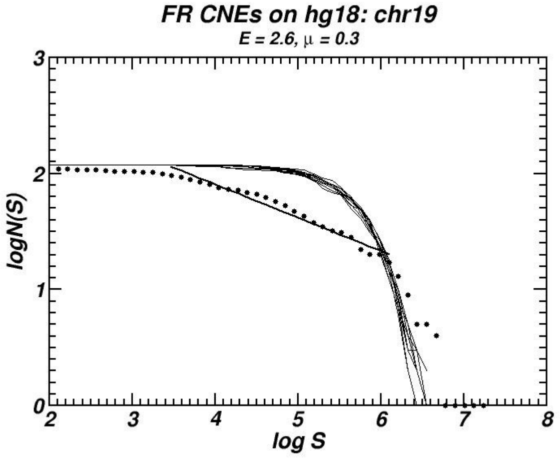
$E = 1.9, \mu = 0.55$

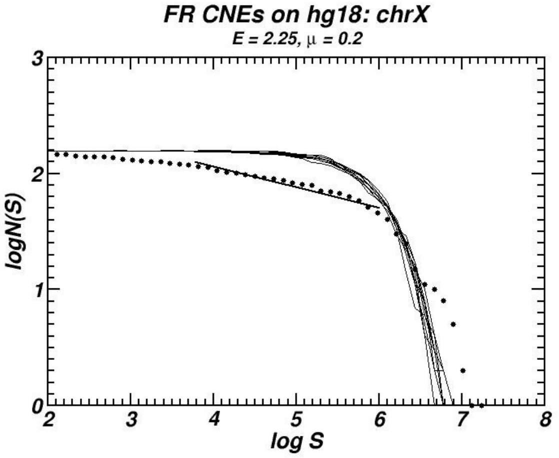

FR CNEs on hg18: chr17

$E = 2.15, \mu = 0.21$

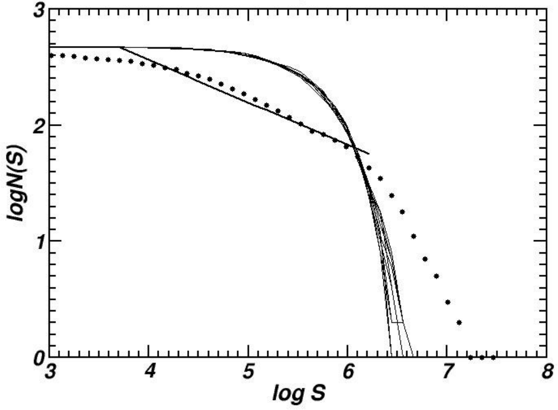

FR CNEs on hg18: chr18

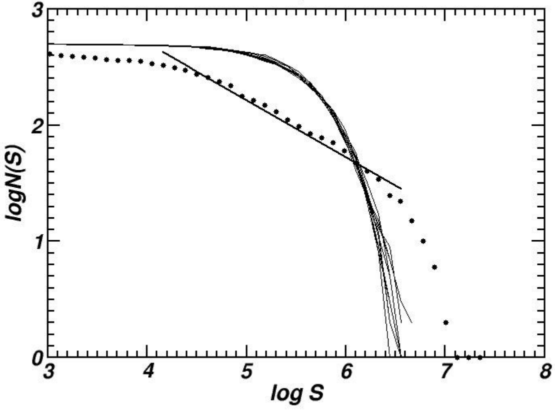
$E = 3, \mu = 0.28$

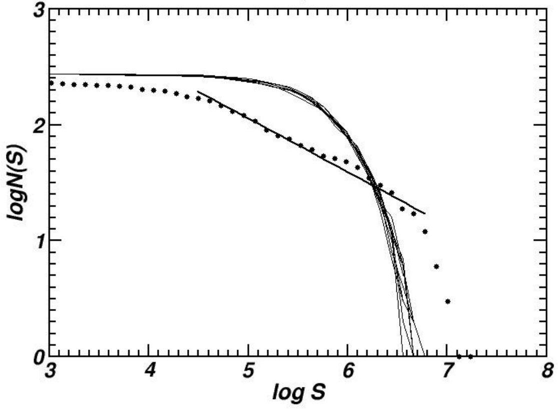

FR CNEs on hg18: chr19
E = 2.6, μ = 0.3
logN(S)
log S
0
1
2
3
2
3
4
5
6
7
8

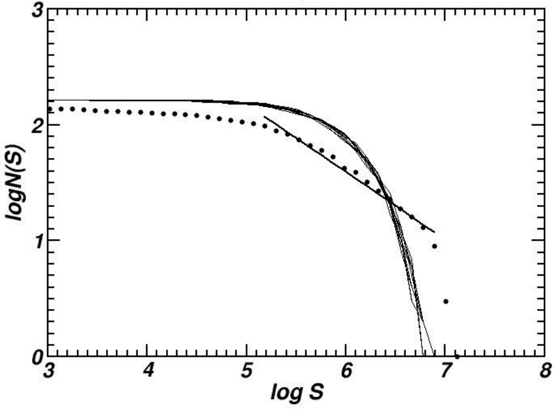

FR CNEs on hg18: chrX
E = 2.25, μ = 0.2
logN(S)
log S
0
1
2
3
2
3
4
5
6
7
8

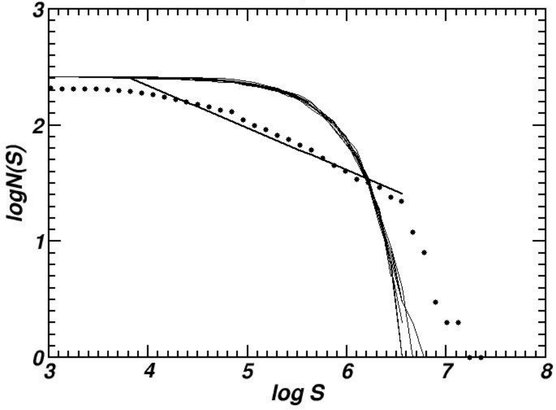
XT-FR CNEs (Dataset ic)


XT-FR CNEs on hg18: chr1
$E = 2.5$, $\mu = 0.36$

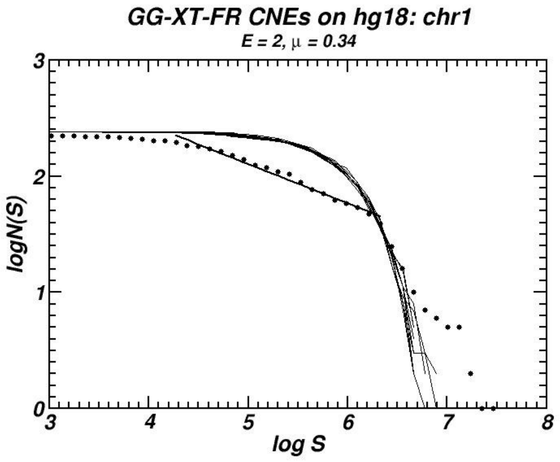

XT-FR CNEs on hg18: chr2
$E = 2.4$, $\mu = 0.5$

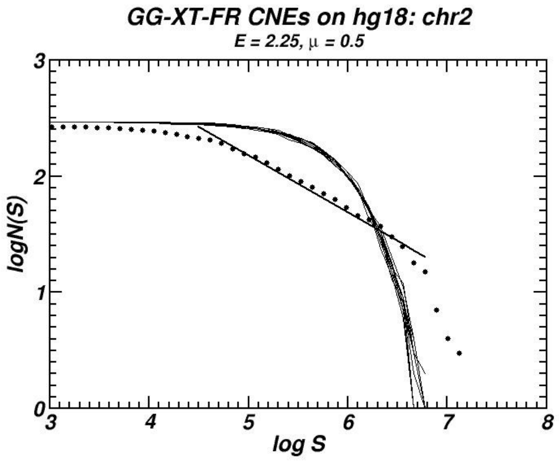

XTFR CNEs on hg18: chr3
$E = 2.25$, $\mu = 0.46$

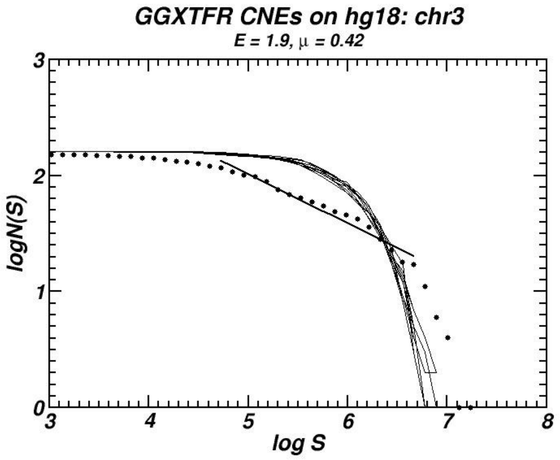

XTFR CNEs on hg18: chr4
$E = 1.7$, $\mu = 0.6$

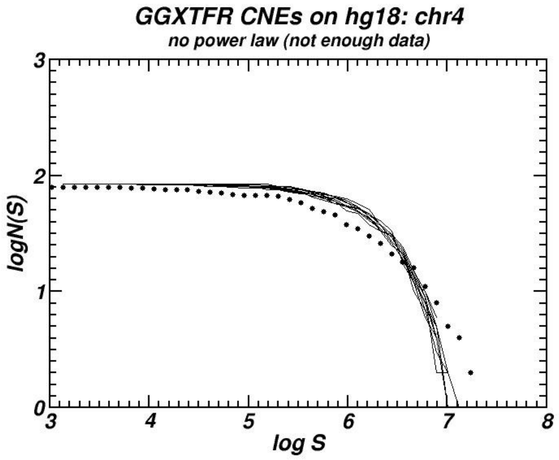

XTFR CNEs on hg18: chr5
$E = 2.75$, $\mu = 0.36$

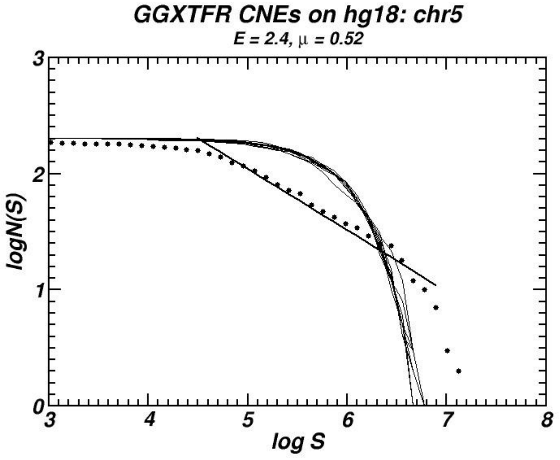
GG-XT-FR CNEs (Dataset id)



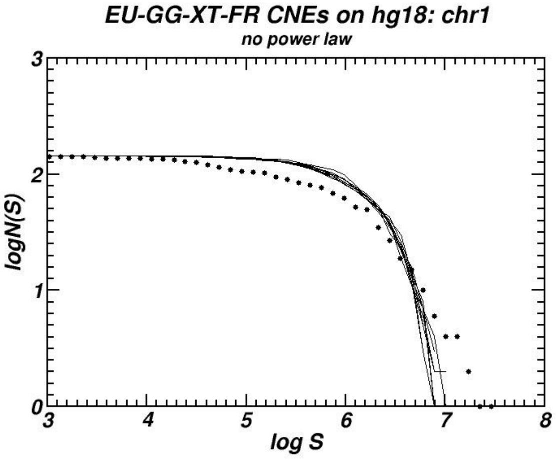




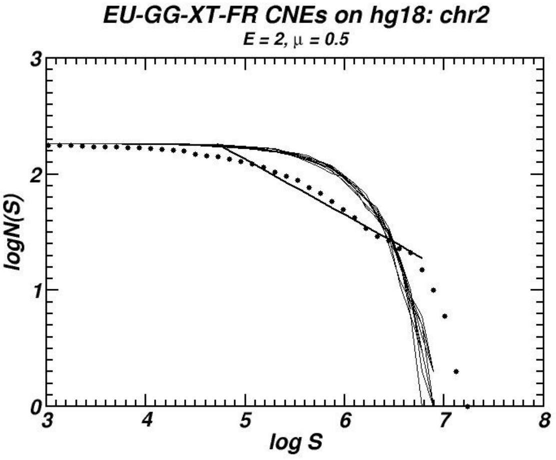




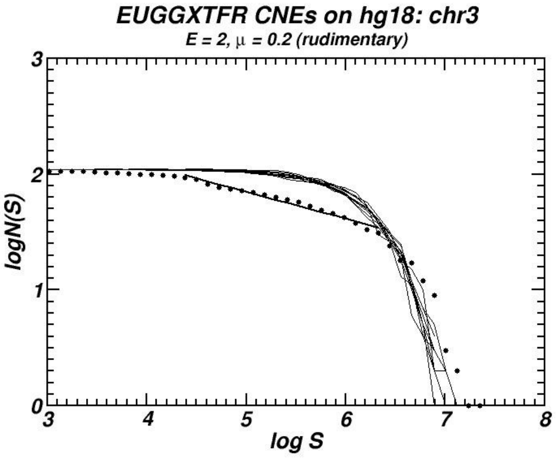
EU-GG-XT-FR CNEs (Dataset ie)


EU-GG-XT-FR CNEs on hg18: chr1

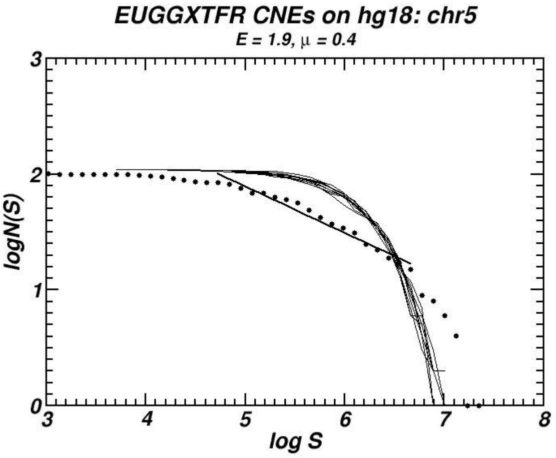
no power law


EU-GG-XT-FR CNEs on hg18: chr2

E = 2, μ = 0.5

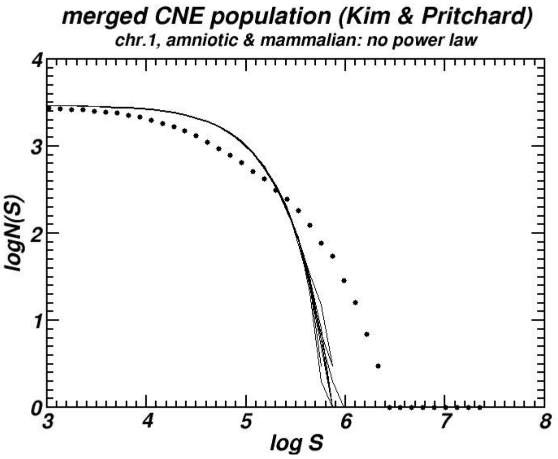

EUGGXTFR CNEs on hg18: chr3

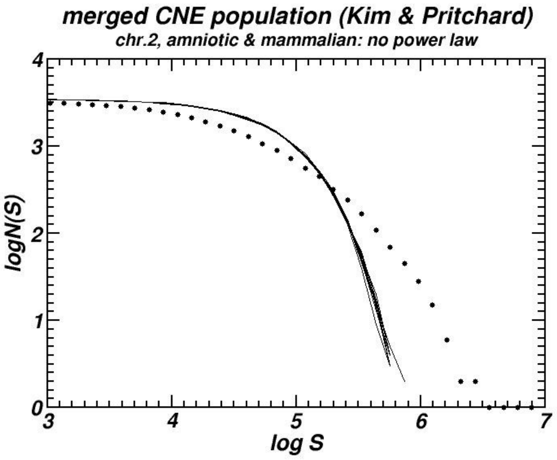
E = 2, μ = 0.2 (rudimentary)

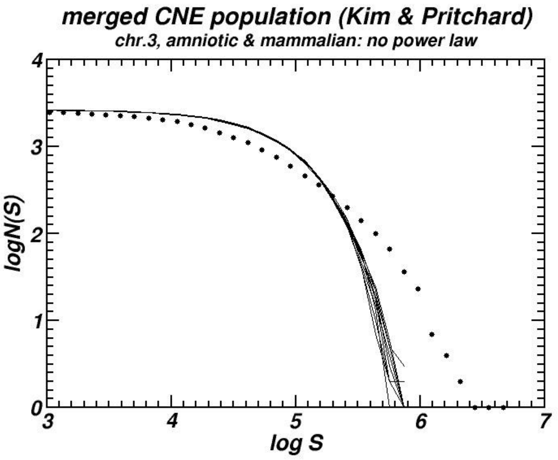

EUGGXTFR CNEs on hg18: chr5

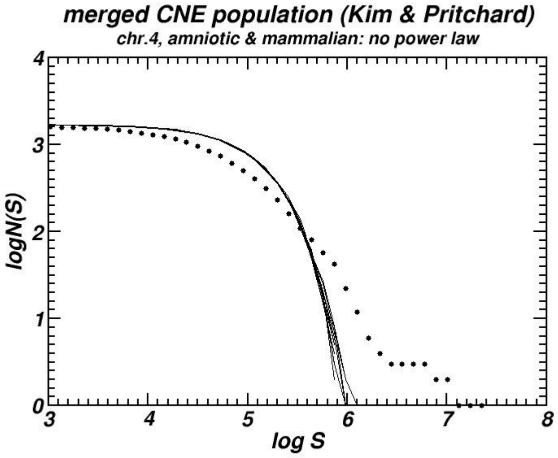
E = 1.9, μ = 0.4

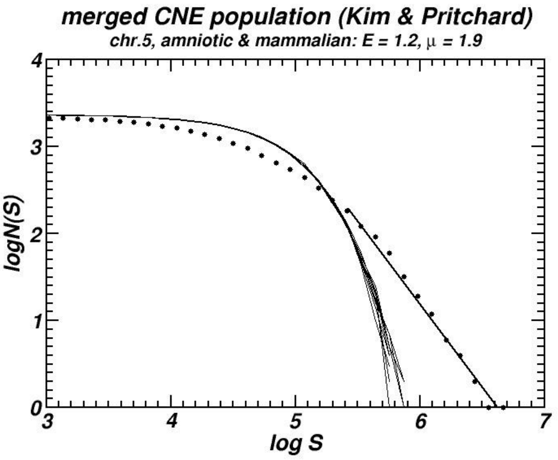
To obtain the figures from the merged and random datasets (adopted from Amniotic and Mammalian datasets as described in the text) shown below, we use the built-in function in R called sample (without replacement). Only the first five chromosomes are depicted :

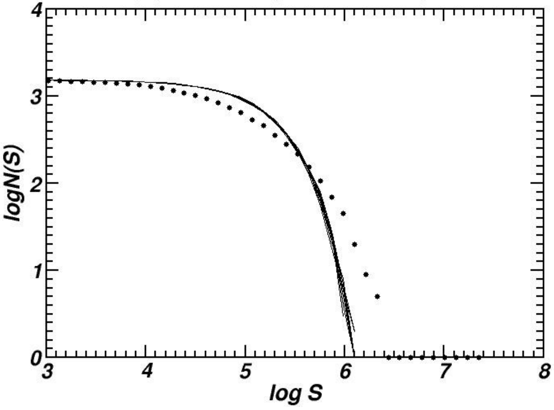

merged CNE population (Kim & Pritchard)
chr.1, amniotic & mammalian: no power law


merged CNE population (Kim & Pritchard)
chr.2, amniotic & mammalian: no power law

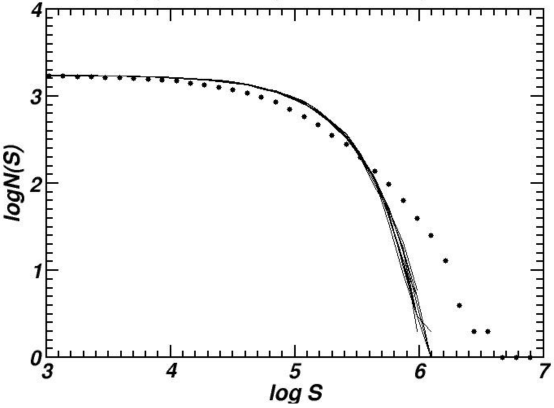

merged CNE population (Kim & Pritchard)
chr.3, amniotic & mammalian: no power law


merged CNE population (Kim & Pritchard)
chr.4, amniotic & mammalian: no power law

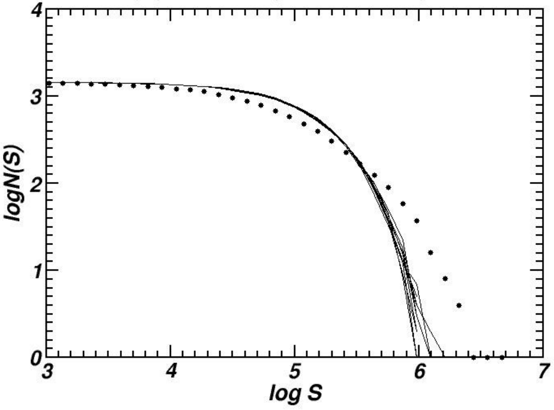

merged CNE population (Kim & Pritchard)
chr.5, amniotic & mammalian: $E = 1.2$, $\mu = 1.9$



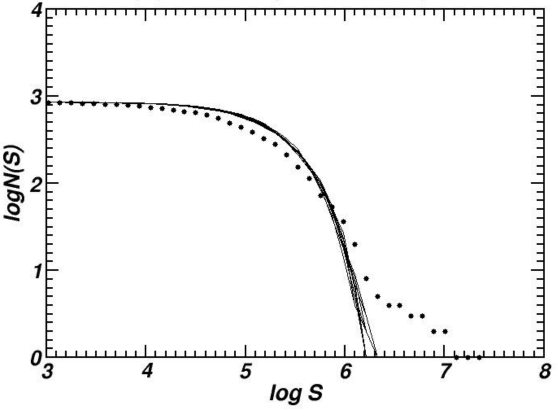
randomly selected mam. CNEs (Kim & Pritchard)
chr.1, population left eq. to amniotic: no power law



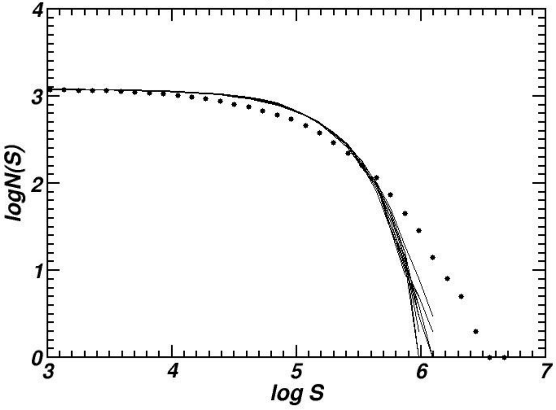
randomly selected mam. CNEs (Kim & Pritchard)
chr.2, population left eq. to amniotic: no power law



randomly selected mam. CNEs (Kim & Pritchard)
chr.3, population left eq. to amniotic: no power law



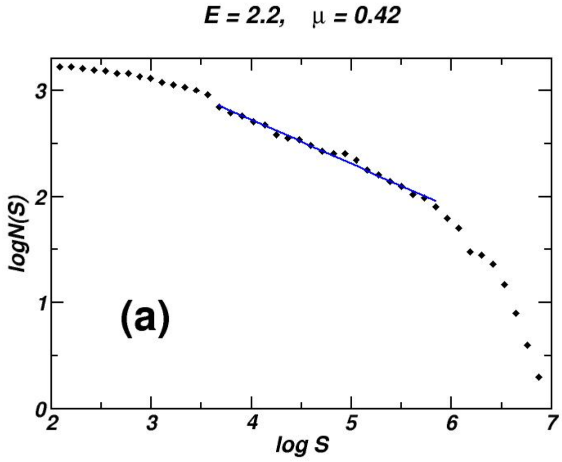
randomly selected mam. CNEs (Kim & Pritchard)
chr.4, population left eq. to amniotic: no power law

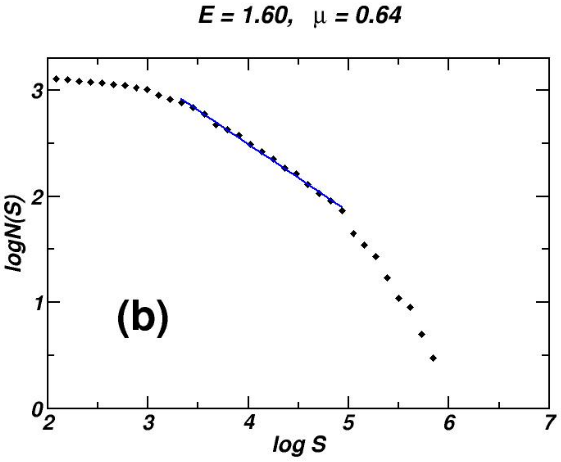


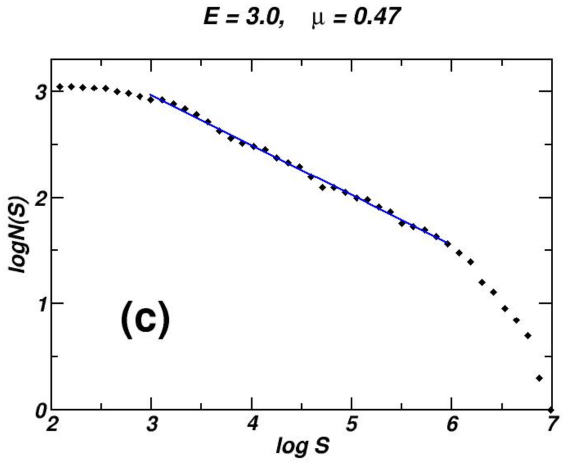
random mammalian CNEs on hg17: chr5
no power law

Appendix

Additional Simulations using the genomic duplications – CNE loss model


E = 2.2, μ = 0.42


E = 1.60, μ = 0.64


E = 3.0, μ = 0.47

Simulations' details

Examples of simulations additional to the ones given in Figure 3 are shown. Initially, 1000 markers (representing CNEs) are randomly inserted in a sequence 2Mnt long. Then, in **(a)**, 173 segmental duplication events occurred, with lengths sampled from a uniform distribution with maximum the 5% of the actual length of the simulated sequence. After each such event a number of CNEs equal to 90% of the number of the duplicated ones are eliminated. The length reached by the simulated chromosome was ~195 Mnt (steps ***i*** and ***ii*** of the model). In **(b)** the segmental duplications were 87 (~50% less) and the final sequence length ~22 Mnt. In **(c)** the number of segmental duplications is as in **(a)** and the finally reached length ~119Mnt. Here, 256 additional events of non-duplicated CNEs eliminations are also allowed (step ***iii*** of the model). These eliminations represent cases of loss of function of ancestral CNEs with a subsequent progressive decomposition. For genomic and for model-generated size distributions, circles and rhombs are used respectively, throughout.