Statistical Applications of Over-fitting due to Trimmings

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(joint work with E. del Barrio, J.A. Cuesta-Albertos and C. Matrán)

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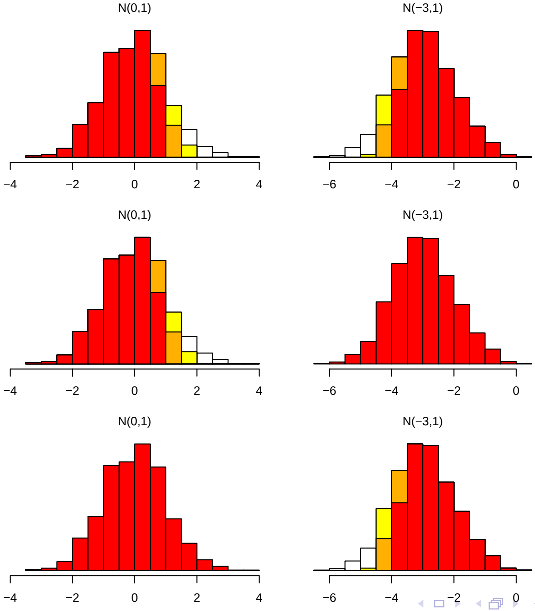
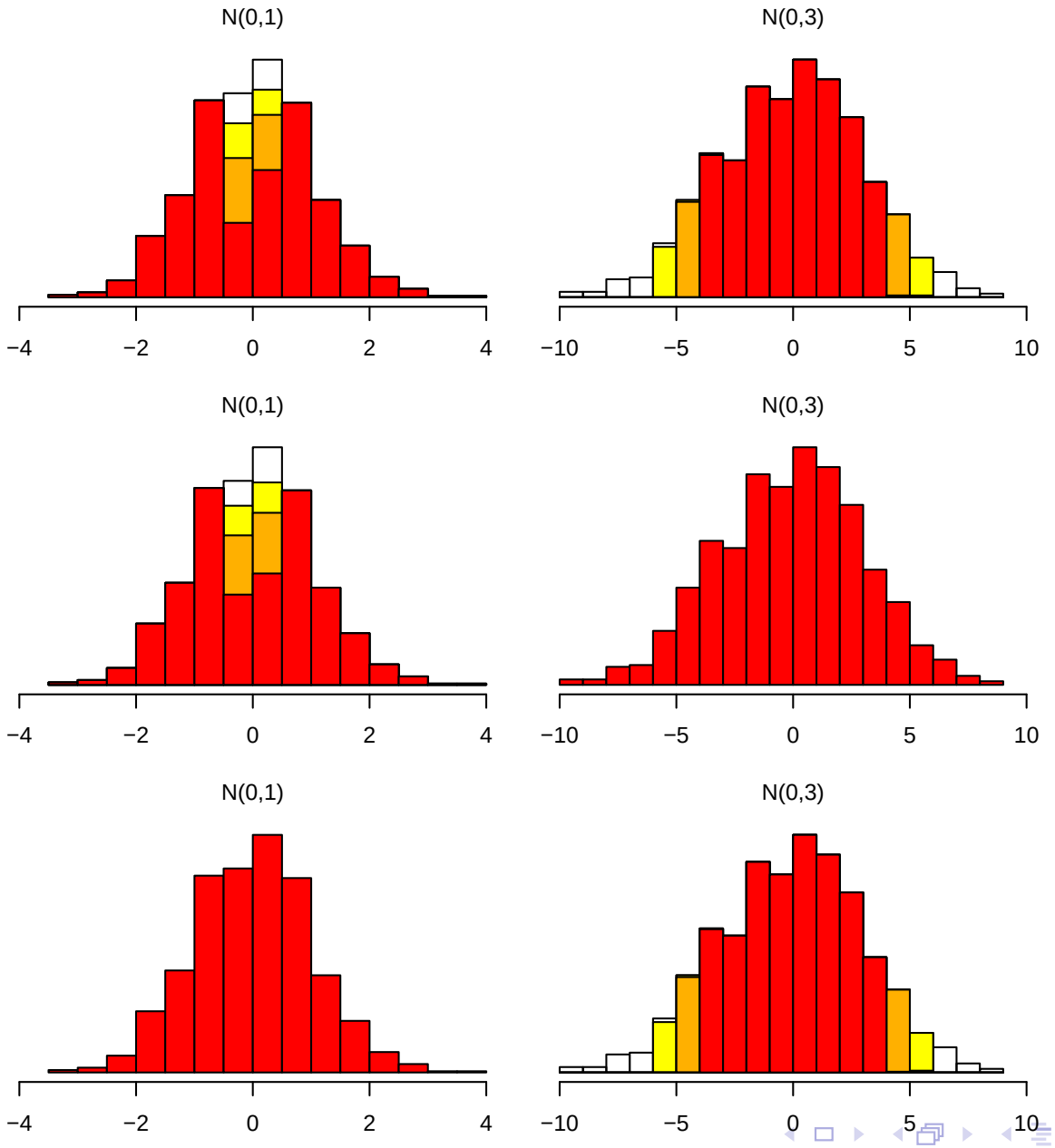
Outline

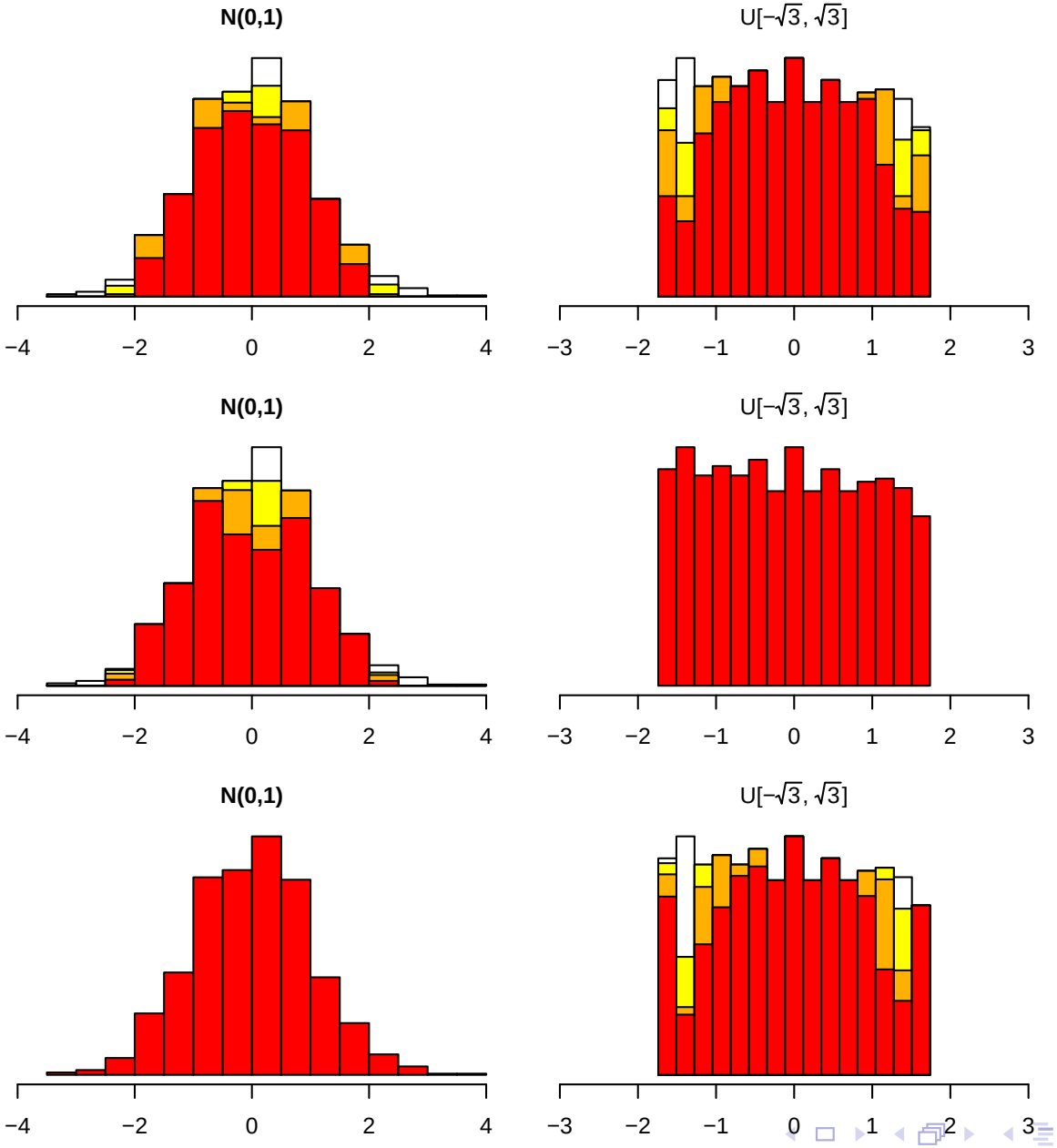
How impartial trimmings work?: N(0,1) vs N(-3,1)



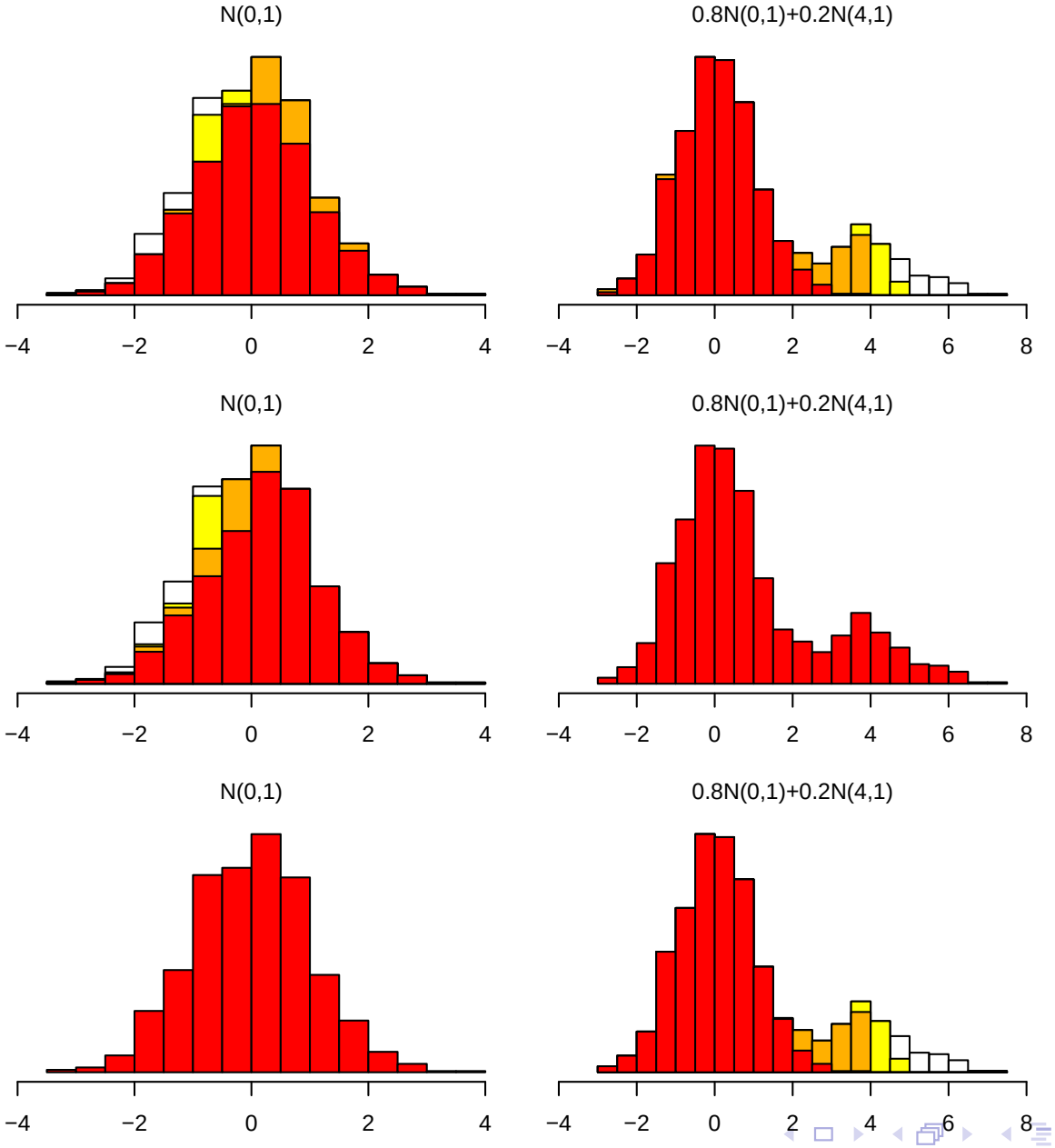
How impartial trimmings work?: N(0,1) vs N(0,3)



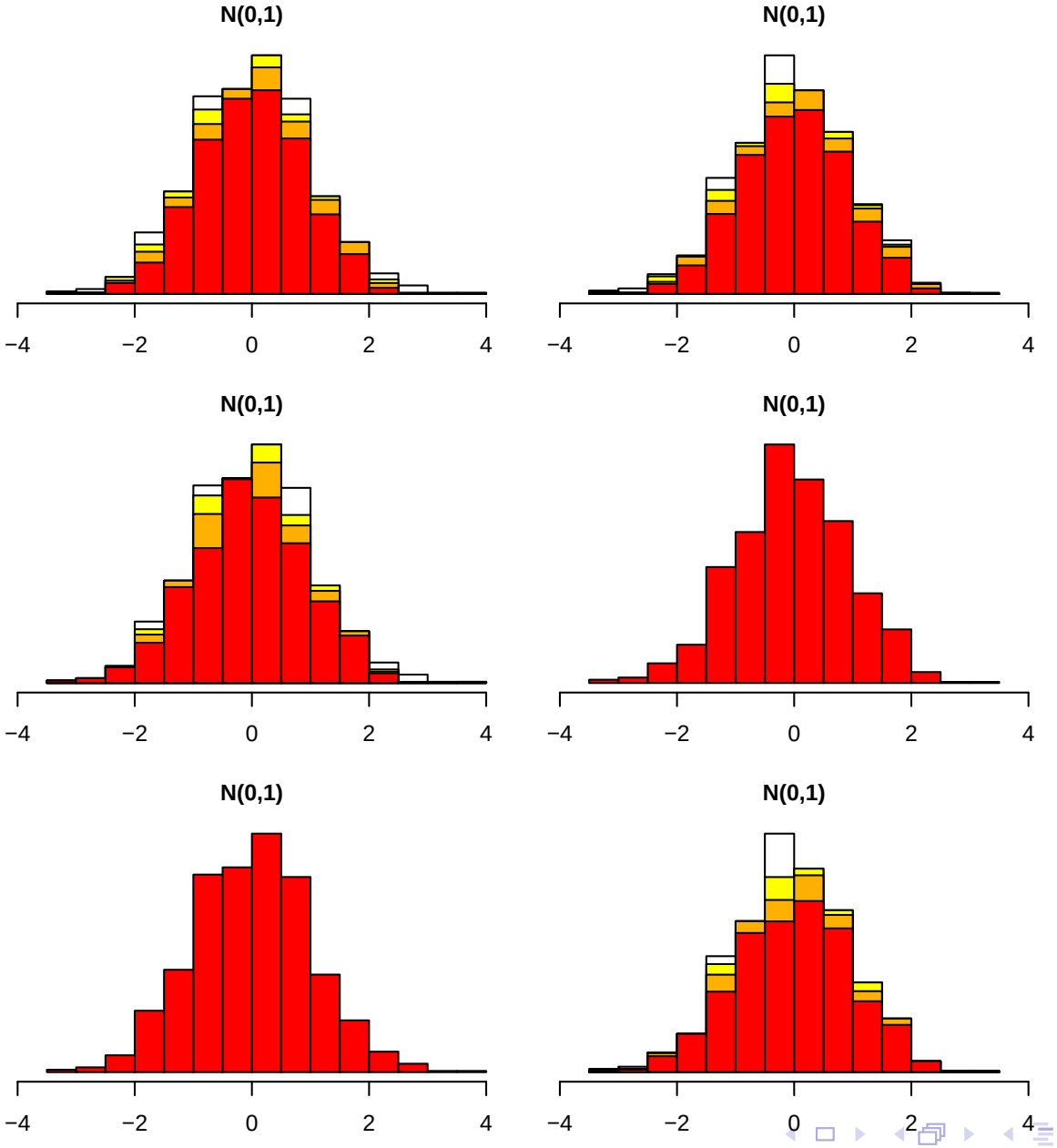
How impartial trimmings work?: N(0,1) vs U($-\sqrt{3},\sqrt{3}$)



How impartial .. work?: N(0,1) vs 0.8*N(0,1)+0.2*N(4,1)

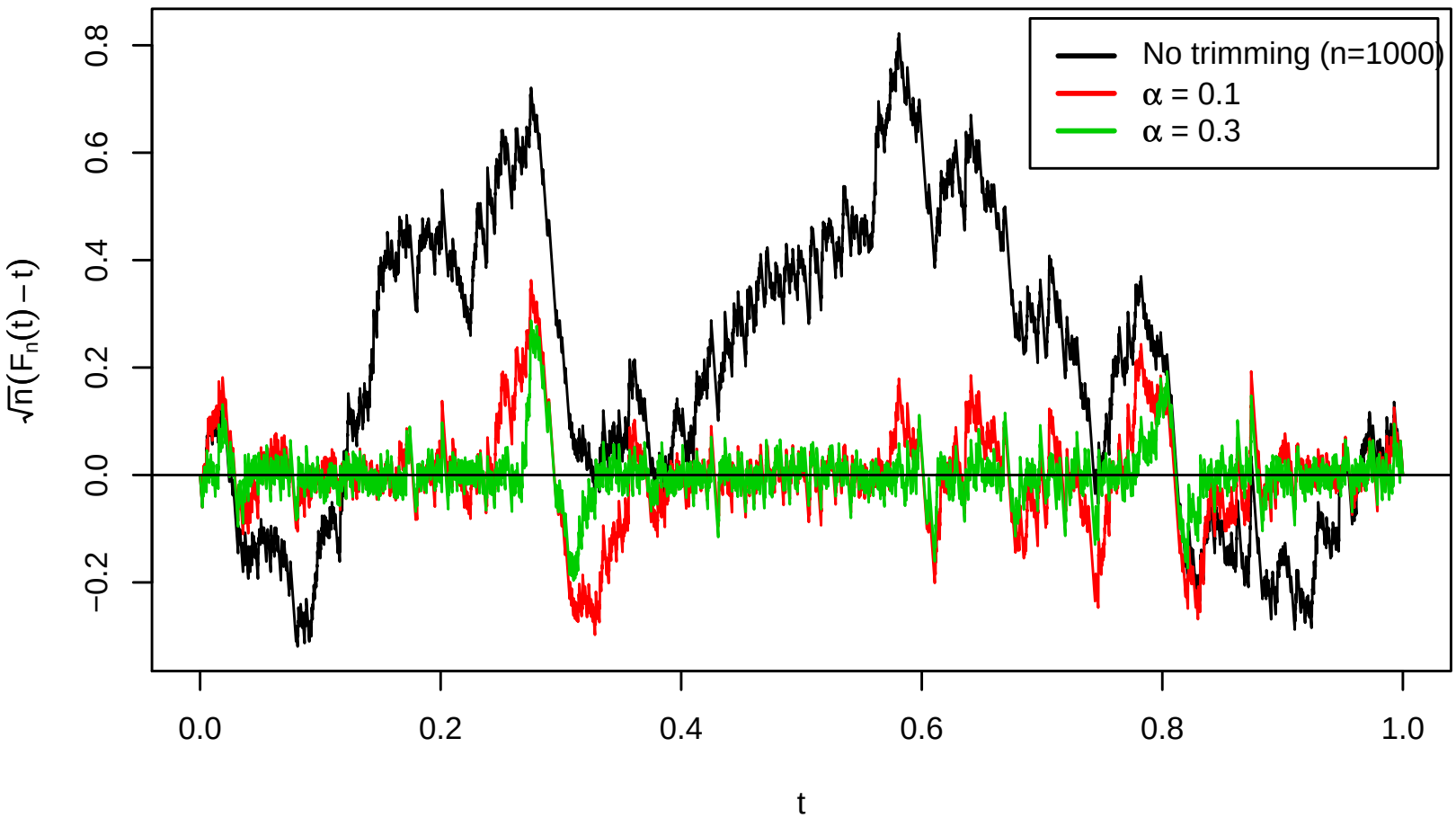


How impartial trimmings work?: N(0,1) vs N(0,1)



Overfitting.

Example(one sample problem): 1000 observations from U[0,1] vs U[0,1]



Overfitting.

Let $P \in \mathcal{P}_2(\mathbb{R})$, $P \ll \ell$, $X_1, X_2, \ldots, X_n$ and $Y_1, Y_2, \ldots, Y_n$ i.i.d $\sim P$. P_n and Q_n the respective empirical distributions,

	1 sample	
No trimming	$n\mathcal{W}_2^2(P_n, P) = O_P(1)$	
Trimming	$n\mathcal{W}_2^2(P_{n,\alpha}, P) = o_P(1)$	

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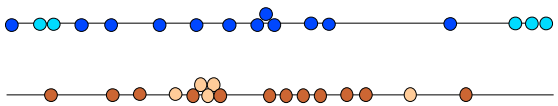
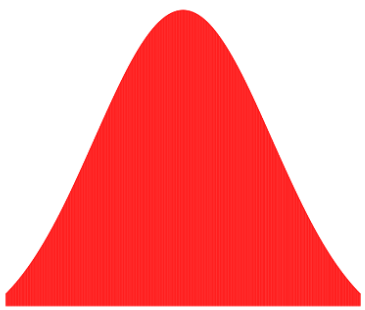
	1 sample	2 samples
No trimming	$n\mathcal{W}_2^2(P_n, P) = O_P(1)$	$n\mathcal{W}_2^2(P_n, Q_n) = O_P(1)$
Trimming	$n\mathcal{W}_2^2(P_{n,\alpha}, P) = o_P(1)$	$n\mathcal{W}_2^2(P_{n,\alpha}, Q_{n,\alpha}) = o_P(1)$

What does it mean? how we can take advantage of it?

$$\mathcal{W}_2(P_n, Q_n) > \mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})$$

Overfitting.





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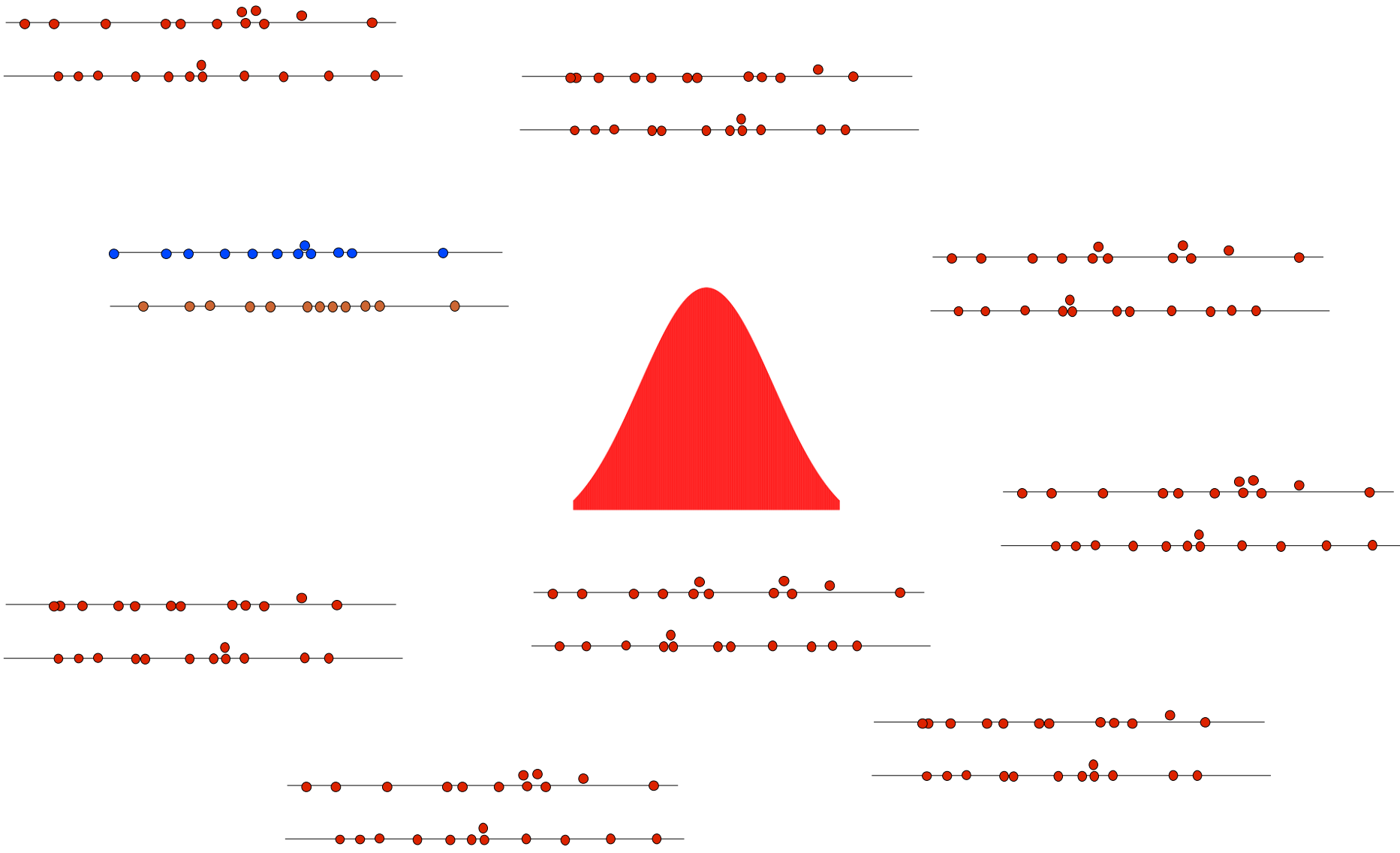

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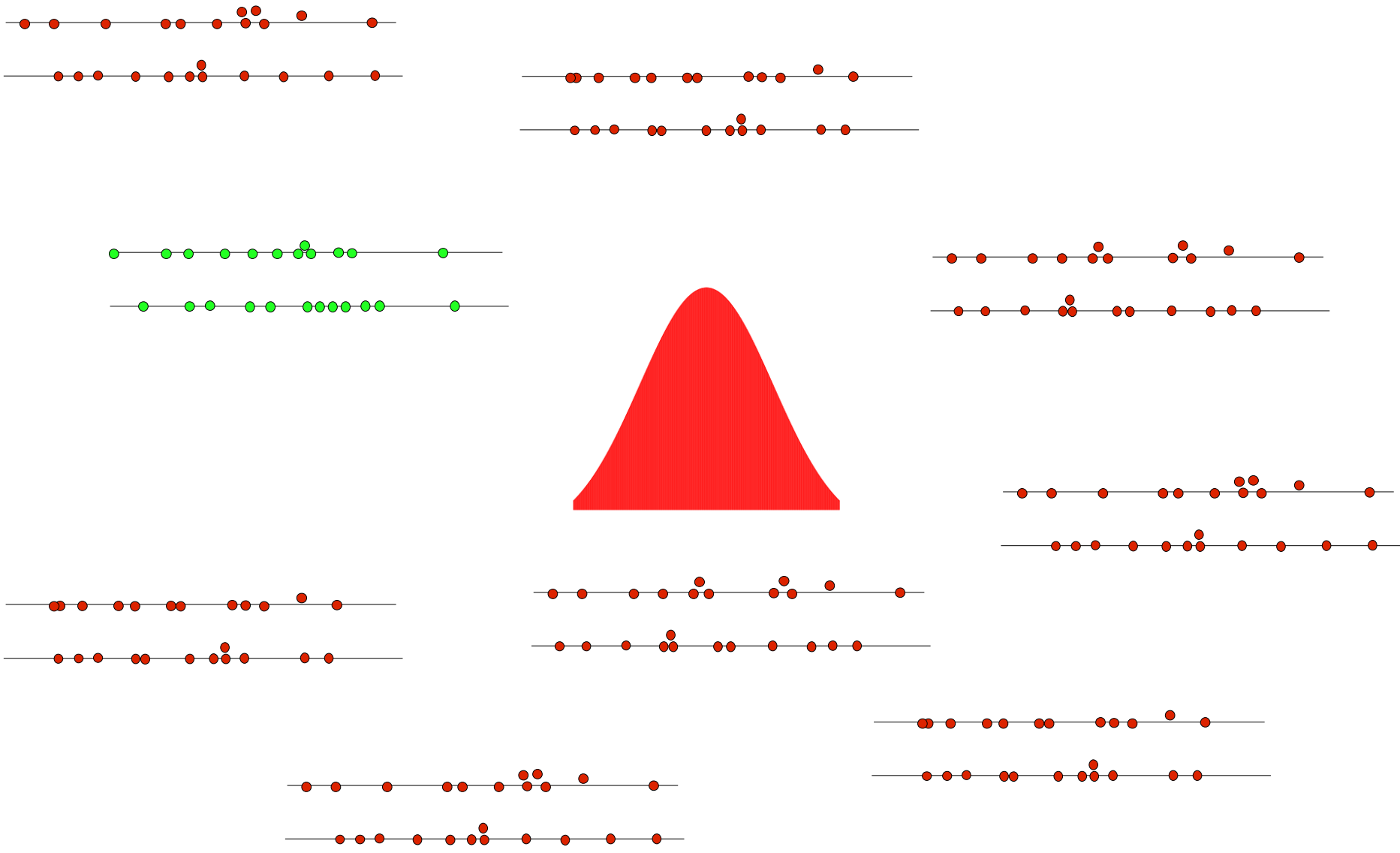

Overfitting: numerical example.

1. Generate two random samples from a $N(0,1)$ of size n, then trim them (α) and compute the $\mathcal{W}_2$ distance between the trimmed samples (of size $[n(1-\alpha)]$): $\mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})$.
2. Generate $R = 1000$ pairs of random samples from a $N(0,1)$ of size $m = [n(1-\alpha)]$ and compute $\mathcal{W}_2(P_m^i, Q_m^i)$, $i = 1, \ldots, 1000$.
3. Calculate the frequency of "$\mathcal{W}_2(P_m^i, Q_m^i) > \mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})$" (p-value).

(1): Pair of samples n.1 (n=100),

	trimming size							
	0%	1%	2%	3%	4%	5%	10%	15%
(1)	0.199	0.447	0.738	0.914	0.985	1	1	1

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(1): Pair of samples n.1 (n=100),
(2): Pair of samples n.2 (n=100),

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	0%	1%	2%	3%	4%	5%	10%	15%
(1)	0.199	0.447	0.738	0.914	0.985	1	1	1
(2)	0.020	0.030	0.062	0.109	0.235	0.383	0.978	1

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(3): Pair of samples n.3 (n=1000).

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(2)	0.020	0.030	0.062	0.109	0.235	0.383	0.978	1
(3)	0.364	0.918	1	1	1	1	1	1

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4. Repeat 1-3 100 times and compute the median p-value:

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n	0%	1%	2%	3%	4%	5%	10%	15%
100	0.433	0.703	0.850	0.932	0.976	0.993	1	1
300	0.513	0.880	0.977	0.997	1	1	1	1
1000	0.499	0.986	1	1	1	1	1	1

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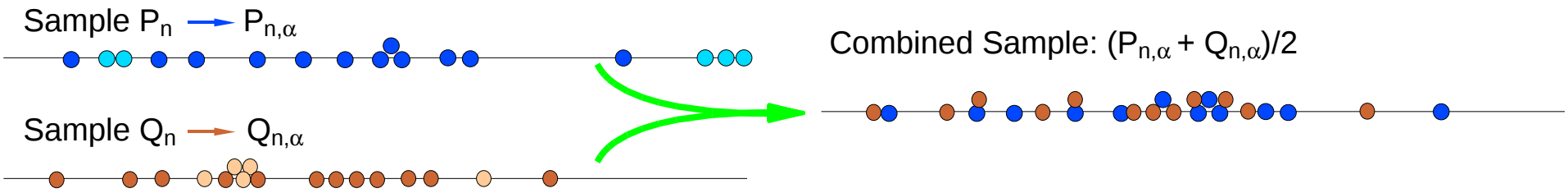
But, in practice we don't know the true model...

Overfitting and Bootstrap.



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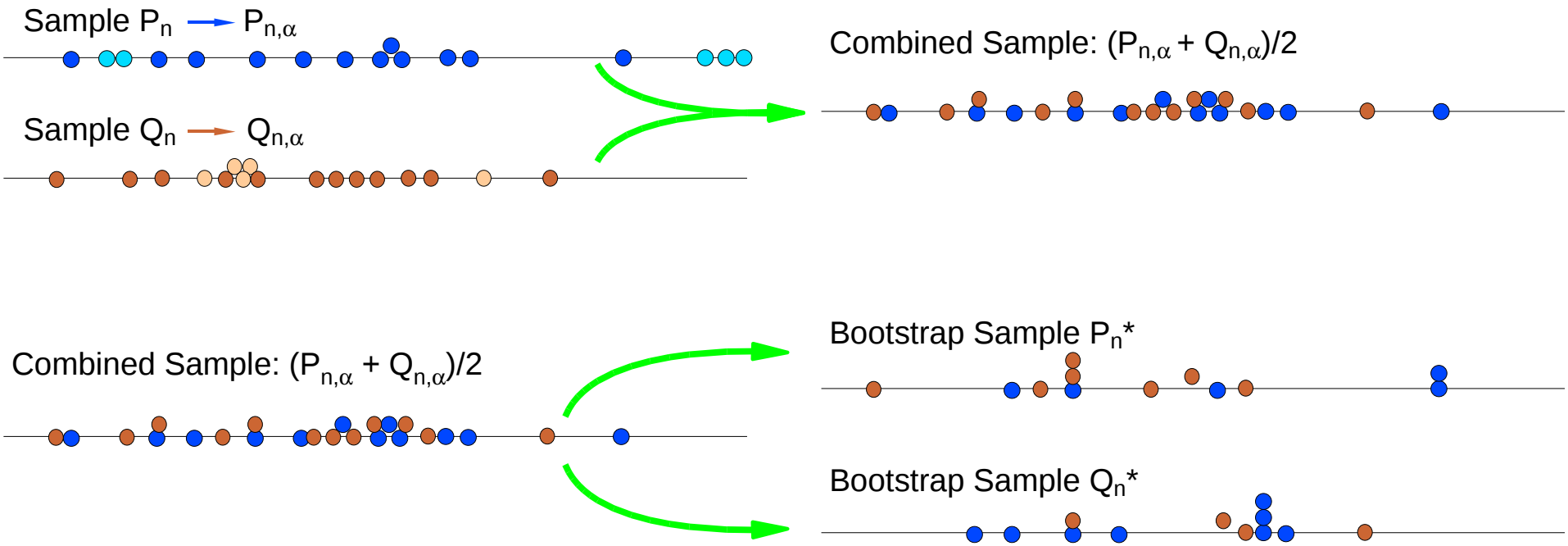

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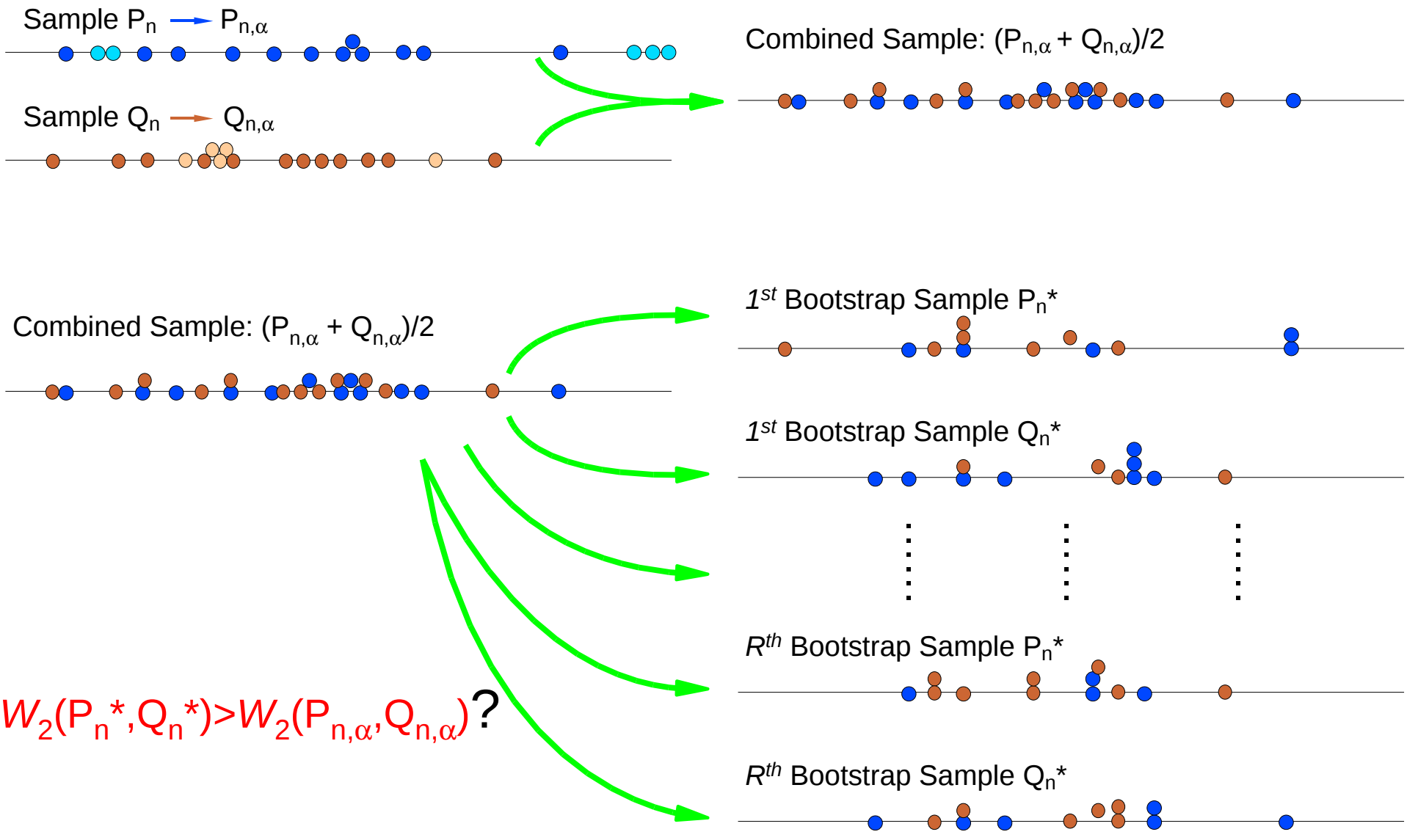

Bootstrap: revisiting the numerical example.

1. Compute the **bootstrap p-value** as the frequency of times:

$$\text{“}\mathcal{W}_2(P_m^*, Q_m^*) > \mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})\text{”}.$$

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2. Repeat the previous process for 100 pairs of N(0,1) samples of size n and compute the median p-value, then

	trimming size							
n	0%	1%	2%	3%	4%	5%	10%	15%
100	0.580	0.755	0.846	0.914	0.964	0.982	1	1
300	0.490	0.820	0.955	0.994	1	1	1	1
1000	0.577	0.973	1	1	1	1	1	1

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Are these results similar to those previous to the bootstrap procedure?

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Bootstrap.

Theorem

Let $\alpha > 0$ and $P, Q \in \mathcal{P}_{2+\delta}(\mathbb{R})$, for some $\delta > 0$. Let us suppose that P and Q have density functions f and g, with support in an interval (possibly non-bounded), with continuous derivatives,

(a) *If $\mathcal{W}_2(\mathcal{R}_{\alpha'}(P), \mathcal{R}_{\alpha'}(Q)) = 0$ for some $\alpha' \in (0, \alpha)$, then*

$$\mathbb{P}\left(\mathcal{W}_2(P_n^*, Q_n^*) > \mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})\right) \to 1.$$

(b) *If $\mathcal{W}_2(\mathcal{R}_{\alpha}(P), \mathcal{R}_{\alpha}(Q)) > 0$, then*

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$$\mathbb{P}\left(\mathcal{W}_2(P_n^*, Q_n^*) > \mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha})\right) \to 0.$$

- If $\mathcal{W}_2(\mathcal{R}_{\alpha}(P), \mathcal{R}_{\alpha}(Q)) > 0$:

$$n\mathcal{W}_2^2(P_n^*, Q_n^*) = O_P(1), \quad \text{and}$$

$$\mathcal{W}_2(P_{n,\alpha}, Q_{n,\alpha}) \to_{a.s} \mathcal{W}_2(\mathcal{R}_{\alpha}(P), \mathcal{R}_{\alpha}(Q)), \text{ then } n\mathcal{W}_2^2(P_{n,\alpha}, Q_{n,\alpha}) \to \infty.$$

Assessing the similarity of two distributions

- Given two distributions, P and Q, we say that they are similar at level α if $\mathcal{W}_2(\mathcal{R}_\alpha(P), \mathcal{R}_\alpha(Q)) = 0$.

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$$\mathcal{S}(P, Q) = \min_\alpha \{\alpha : \mathcal{W}_2(\mathcal{R}_\alpha(P), \mathcal{R}_\alpha(Q)) = 0\} \qquad (= d_{TV}(P, Q)).$$

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- Using the previous theorem, and given $\alpha \in (0, 1)$, we can assess whether

$$\mathcal{S}(P, Q) < \alpha \Leftrightarrow \exists \alpha' \in (0, \alpha) \text{ such that } \mathcal{W}_2(\mathcal{R}_{\alpha'}(P), \mathcal{R}_{\alpha'}(Q)) = 0,$$

$$\text{or } \mathcal{S}(P, Q) > \alpha \Leftrightarrow \mathcal{W}_2(\mathcal{R}_\alpha(P), \mathcal{R}_\alpha(Q)) > 0.$$

Comparison of two distributions

We have generated 5 random samples: A $\sim$ N(0,1), B $\sim$ N(0,1), C $\sim$ N(1,1), D $\sim$ N(1,2) and E $\sim$ N(2,1) for two sample sizes ($n = 30, 100$).

	0%	1%	5%	10%	20%	30%
A vs B	0.669	0.706	0.855	0.968	0.996	1.000
A vs C	0.002	0.000	0.004	0.011	0.146	0.897
A vs D	0.002	0.005	0.013	0.032	0.164	0.683
A vs E	0.000	0.000	0.000	0.000	0.000	0.000
C vs D	0.006	0.016	0.018	0.033	0.163	0.433

bootstrap p-values when $n = 30$.

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A vs B	0.964	0.974	0.998	1.000	1.000	1.000
A vs C	0.000	0.000	0.000	0.000	0.004	0.371
A vs D	0.000	0.000	0.000	0.000	0.091	1.000
A vs E	0.000	0.000	0.000	0.000	0.000	0.000
C vs D	0.000	0.000	0.000	0.001	0.134	0.905

bootstrap p-values when $n = 100$.

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bootstrap p-values when $n = 30$.

	0%	1%	5%	10%	20%	30%	$\mathcal{S}(P, Q)$
A vs B	0.964	0.974	0.998	1.000	1.000	1.000	0%
A vs C	0.000	0.000	0.000	0.000	0.004	0.371	38%
A vs D	0.000	0.000	0.000	0.000	0.091	1.000	39%
A vs E	0.000	0.000	0.000	0.000	0.000	0.000	68%
C vs D	0.000	0.000	0.000	0.001	0.134	0.905	32%

bootstrap p-values when $n = 100$.

Other examples

Generate 100 replicates of the bootstrap p-values:

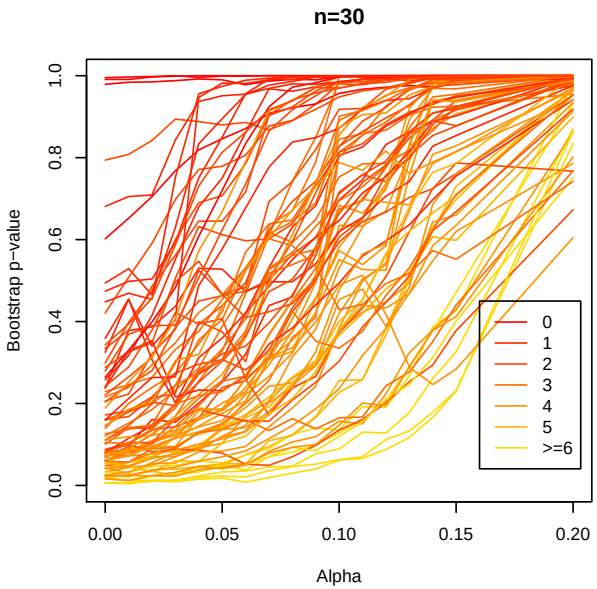
Case 1. $n = 100$. X's sample taken from $.90N(0,1) + .10N(5,1)$
Y's sample taken from $.90N(0,1) + .10N(-5,1)$
$\mathcal{S}(P,Q) = .1000$

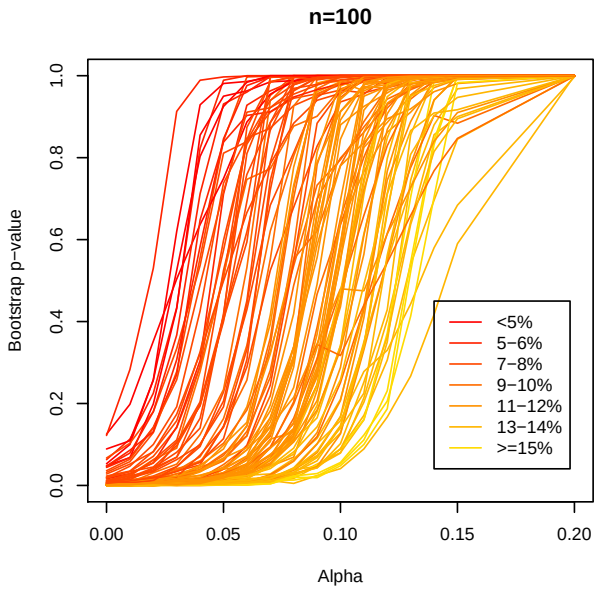
Case 2. $n = 100$. X's sample taken from $N(0,1)$
Y's sample taken from $.80N(0,1) + .20N(0,3)$
$\mathcal{S}(P,Q) = .0969$

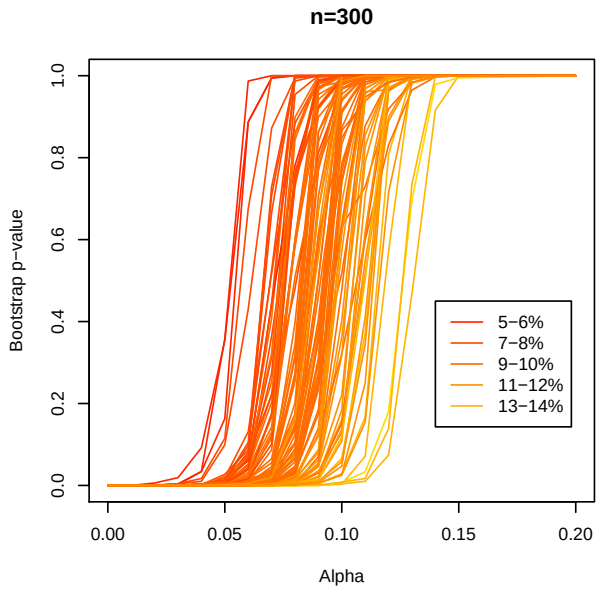
Medians of bootstrap p-values:

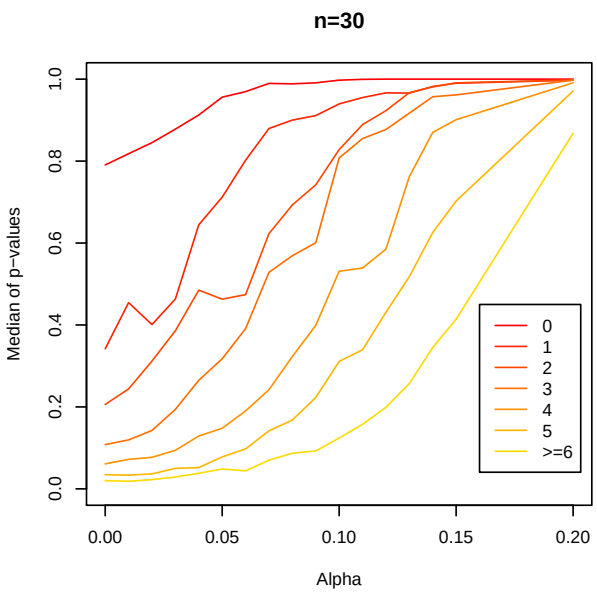
α	0	5	6	7	8	9	10	11	12	13	14	15
Case 1	0	.01	.03	.06	.12	.26	.47	.70	.87	.92	.97	.99
Case 2	.04	.46	.63	.80	.91	.98	.99	1	1	1	1	1

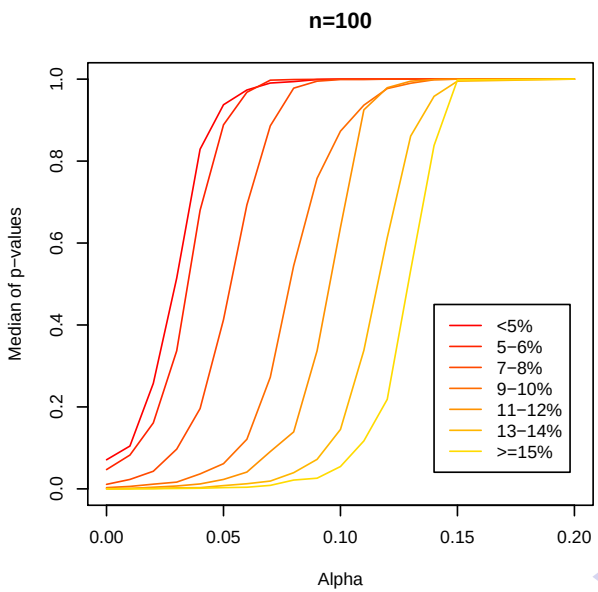
N(0,1) vs .9N(0,1)+.1N(5,1): 100 replicates

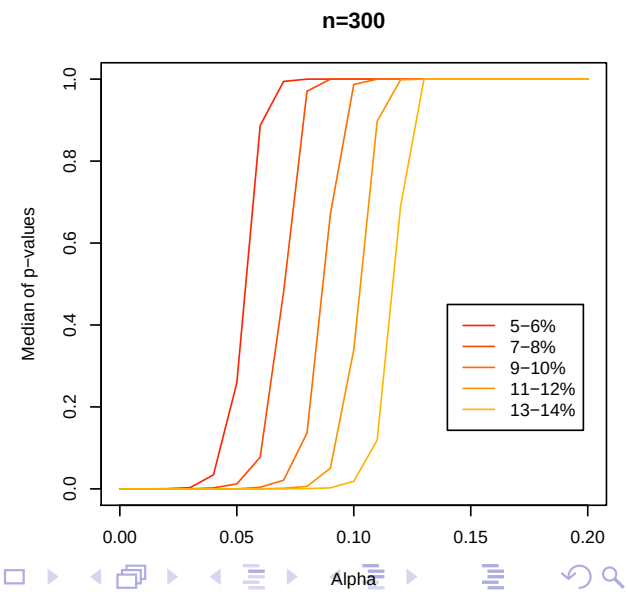












Conclusion

Test $H_0 : \mathcal{W}_2(\mathcal{R}_\alpha(P), \mathcal{R}_\alpha(Q)) = 0 \quad (\mathcal{S}(P, Q) \leq \alpha)$

Rejecting H_0 for small values of the bootstrap p-value.

This procedure is asymptotically error free.

Example: markers of *selectividad* exam

Marks of the access-to-university exam in the university district of Valladolid: 1550 exams of the same subject distributed between 10 markers.

Marker	1	2	3	4	5	6	7	8	9	10
N^o of exams	155	152	155	156	156	156	156	154	156	154

Do they mark in a homogeneous way? Do they use a common pattern to mark?

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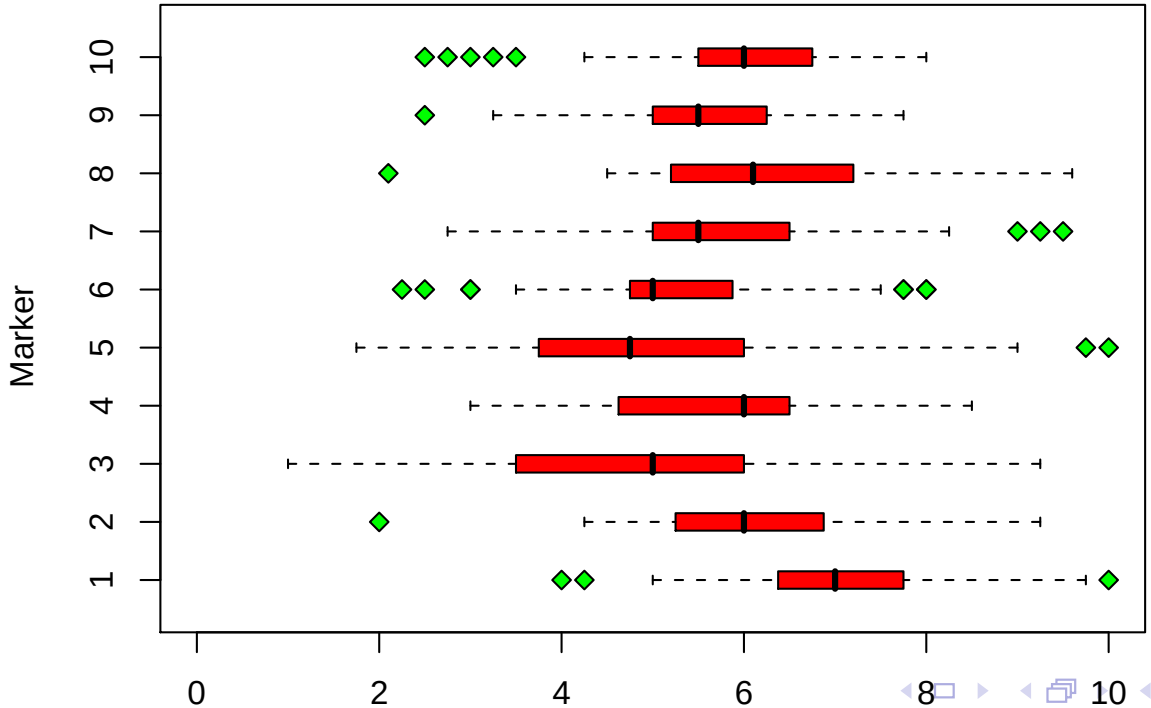

Looking for the "common pattern" of several distributions

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  4. Iterate steps 2-3 until none distribution leaves the group.

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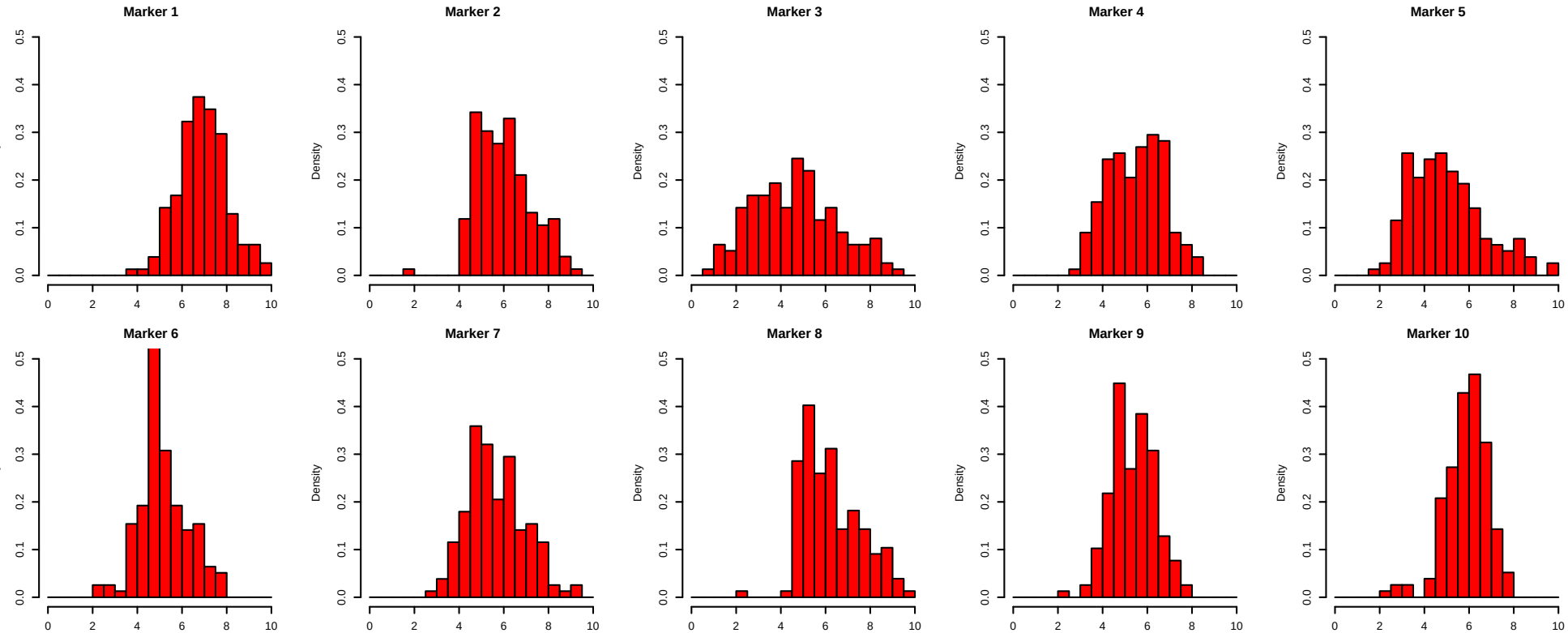
  4. Iterate steps 2-3 until none distribution leaves the group.
  5. Consider to recover the distributions out of the group.

Example: markers of *selectividad* exam



Example: sequential process

Step 0: All markers are in the group. Compute bootstrap p-values.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%	0.000	0.000	0.000	0.079	0.000	0.000	0.406	0.000	0.000	0.000
5%	0.000	0.134	0.000	0.497	0.000	0.000	0.997	0.000	0.001	0.000
10%	0.000	0.996	0.000	0.951	0.001	0.003	1.000	0.450	0.058	0.003
20%	0.000	1.000	0.036	1.000	0.572	0.642	1.000	1.000	1.000	0.591

Example: sequential process

Step 1: Marker 1 is the most *different* and goes out.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%	0.000	0.000	0.000	0.079	0.000	0.000	0.406	0.000	0.000	0.000
5%	0.000	0.134	0.000	0.497	0.000	0.000	0.997	0.000	0.001	0.000
10%	0.000	0.996	0.000	0.951	0.001	0.003	1.000	0.450	0.058	0.003
20%	0.000	1.000	0.036	1.000	0.572	0.642	1.000	1.000	1.000	0.591

Example: sequential process

Step 2: Recompute bootstrap p-values.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.000	0.000	0.083	0.000	0.000	0.254	0.000	0.000	0.000
5%		0.001	0.000	0.466	0.000	0.000	0.996	0.000	0.007	0.000
10%		0.740	0.000	0.949	0.006	0.031	1.000	0.036	0.399	0.000
20%		1.000	0.124	1.000	0.766	0.996	1.000	1.000	1.000	0.367

Example: sequential process

Step 2: Next marker that goes out is num. 3.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.000	0.000	0.083	0.000	0.000	0.254	0.000	0.000	0.000
5%		0.001	0.000	0.466	0.000	0.000	0.996	0.000	0.007	0.000
10%		0.740	0.000	0.949	0.006	0.031	1.000	0.036	0.399	0.000
20%		1.000	0.124	1.000	0.766	0.996	1.000	1.000	1.000	0.367

Example: sequential process

Step 3: Recompute bootstrap p-values.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.000		0.173	0.000	0.000	0.920	0.000	0.000	0.000
5%		0.089		0.518	0.000	0.000	0.999	0.000	0.055	0.000
10%		0.992		0.966	0.000	0.037	1.000	0.299	0.931	0.010
20%		1.000		1.000	0.146	0.993	1.000	1.000	1.000	0.652

Example: sequential process

Step 3: Marker 5 goes out.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.000		0.173	0.000	0.000	0.920	0.000	0.000	0.000
5%		0.089		0.518	0.000	0.000	0.999	0.000	0.055	0.000
10%		0.992		0.966	0.000	0.037	1.000	0.299	0.931	0.010
20%		1.000		1.000	0.146	0.993	1.000	1.000	1.000	0.652

Example: sequential process

Step 4: Recompute bootstrap p-values (1, 3 and 5 are out).

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.006		0.058		0.000	0.712	0.000	0.000	0.000
5%		0.619		0.349		0.000	0.998	0.005	0.056	0.001
10%		1.000		0.888		0.001	1.000	0.709	0.975	0.038
20%		1.000		1.000		0.769	1.000	1.000	1.000	0.879

Example: sequential process

Step 4: Marker 6 goes out (1, 3 and 5 are out).

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.006		0.058		0.000	0.712	0.000	0.000	0.000
5%		0.619		0.349		0.000	0.998	0.005	0.056	0.001
10%		1.000		0.888		0.001	1.000	0.709	0.975	0.038
20%		1.000		1.000		0.769	1.000	1.000	1.000	0.879

Example: sequential process

Step 5: Recompute bootstrap p-values of the markers in.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.067		0.013			0.322	0.001	0.000	0.000
5%		0.992		0.196			0.914	0.020	0.004	0.005
10%		1.000		0.825			1.000	0.865	0.338	0.120
20%		1.000		1.000			1.000	1.000	1.000	0.979

Example: sequential process

Step 5: Marker 10 goes out ($W_2(5\%)$ is 0.33 points and $W_2(10\%)$=0.25).

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.067		0.013			0.322	0.001	0.000	0.000
5%		0.992		0.196			0.914	0.020	0.004	0.005
10%		1.000		0.825			1.000	0.865	0.338	0.120
20%		1.000		1.000			1.000	1.000	1.000	0.979

Example: sequential process

Step 6: Recompute bootstrap p-values of the markers in.

	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.027		0.017			0.771	0.000	0.000	
5%		0.857		0.165			0.999	0.017	0.004	
10%		1.000		0.684			1.000	0.819	0.352	
20%		1.000		1.000			1.000	1.000	1.000	

Example: sequential process

Step 6: None of the markers out enters into the group.

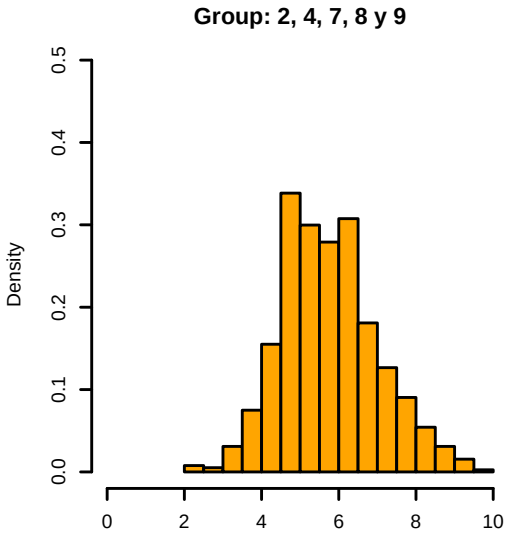
	Marker									
	1	2	3	4	5	6	7	8	9	10
1%	0.000	0.027	0.000	0.017	0.000	0.000	0.771	0.000	0.000	
5%	0.000	0.857	0.000	0.165	0.000	0.000	0.999	0.017	0.004	
10%	0.000	1.000	0.000	0.684	0.000	0.000	1.000	0.819	0.352	
20%	0.000	1.000	0.008	1.000	0.001	0.000	1.000	1.000	1.000	

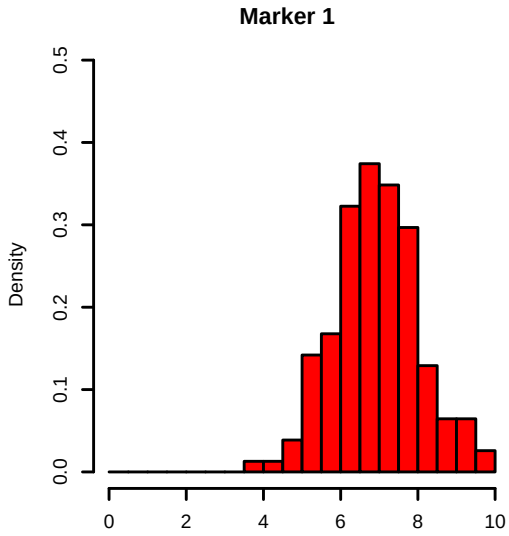
Example: sequential process

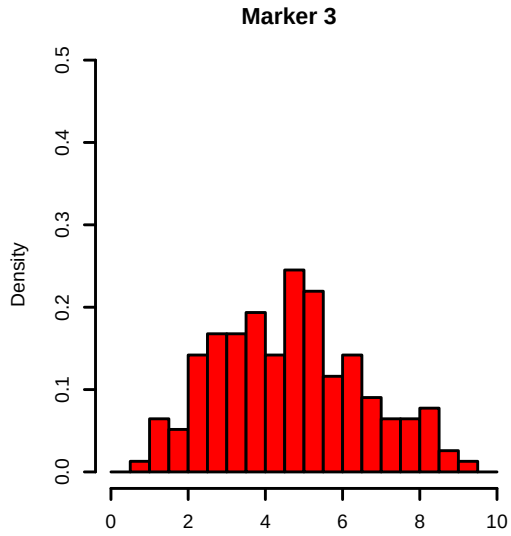
Step 6 (End): The group of markers that mark most similarly is 2, 4, 7, 8 and 9.

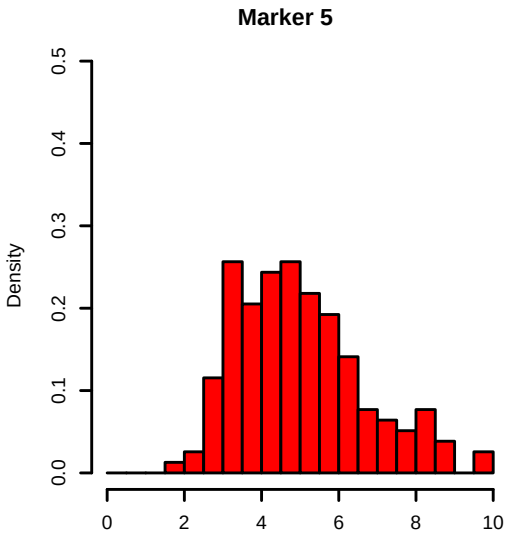
	Marker									
	1	2	3	4	5	6	7	8	9	10
1%		0.027		0.017			0.771	0.000	0.000	
5%		0.857		0.165			0.999	0.017	0.004	
10%		1.000		0.684			1.000	0.819	0.352	
20%		1.000		1.000			1.000	1.000	1.000	

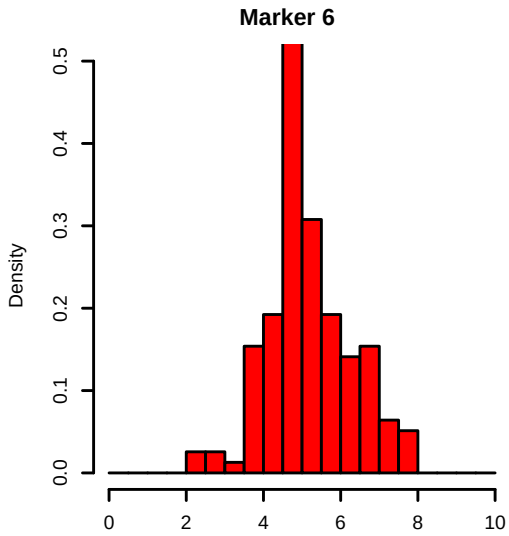
Example: markers of *selectividad* exam

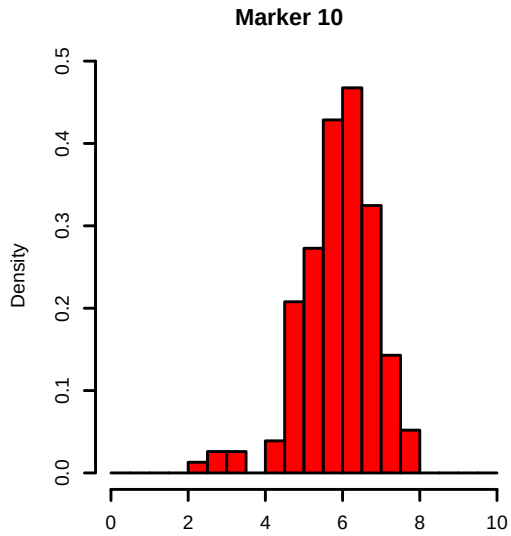












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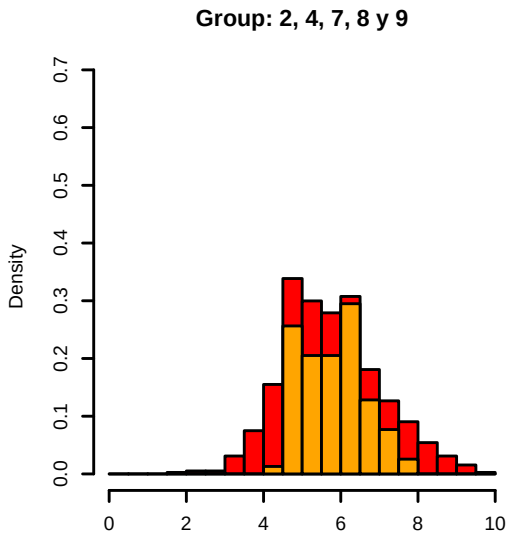

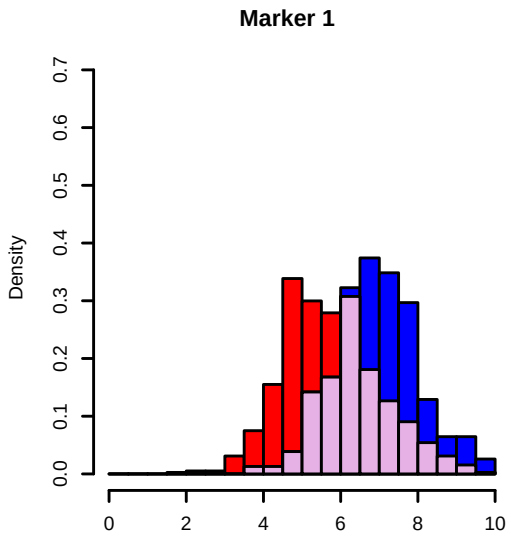

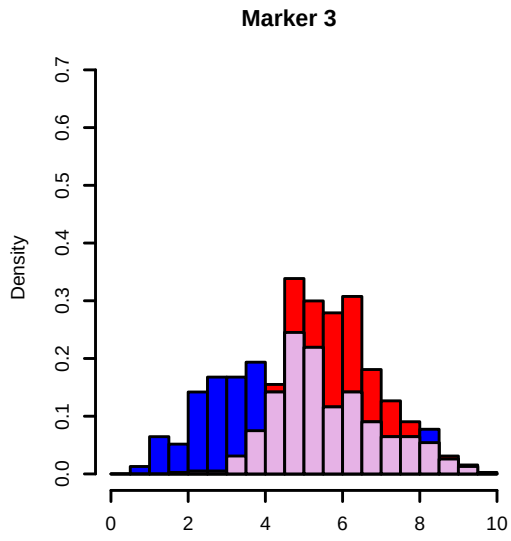

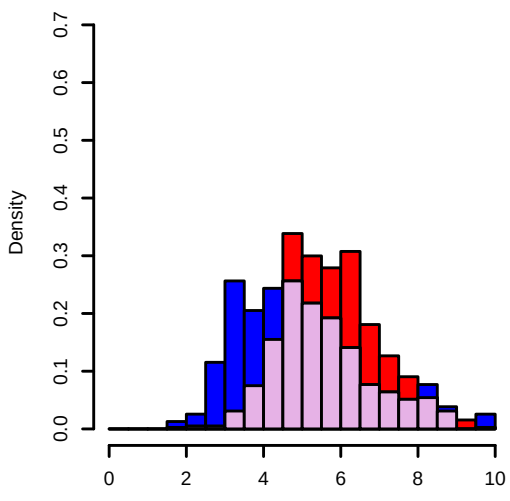

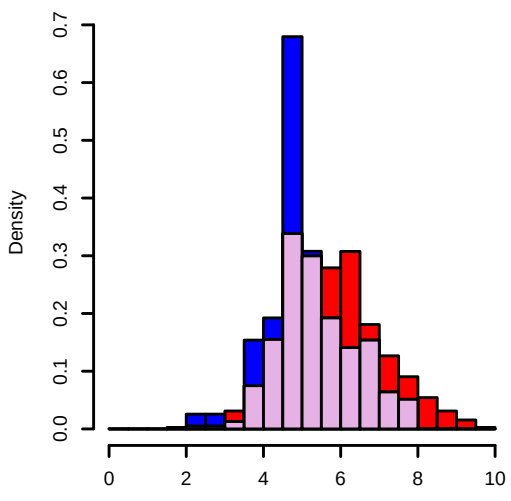

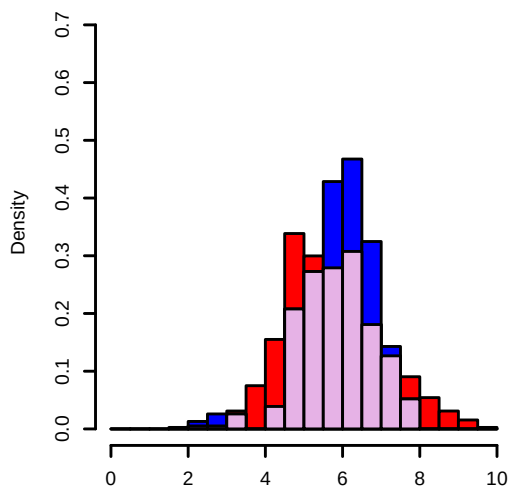

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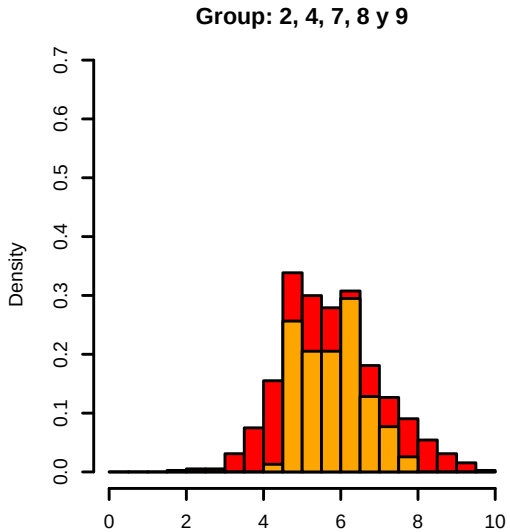
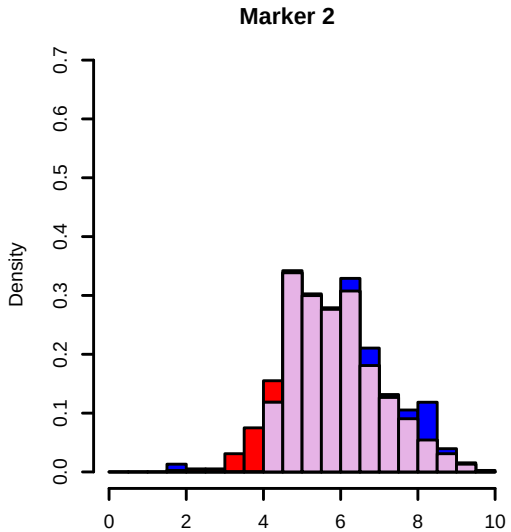
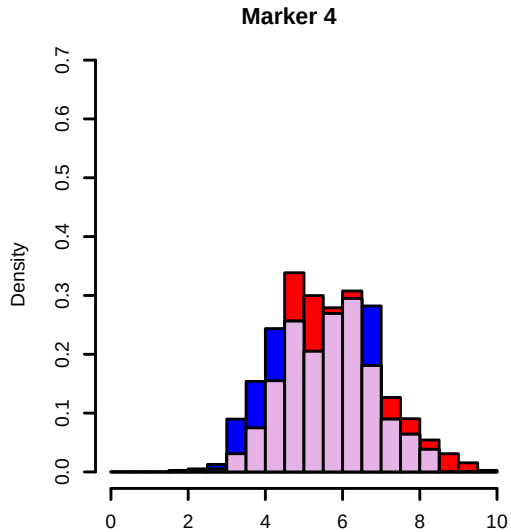
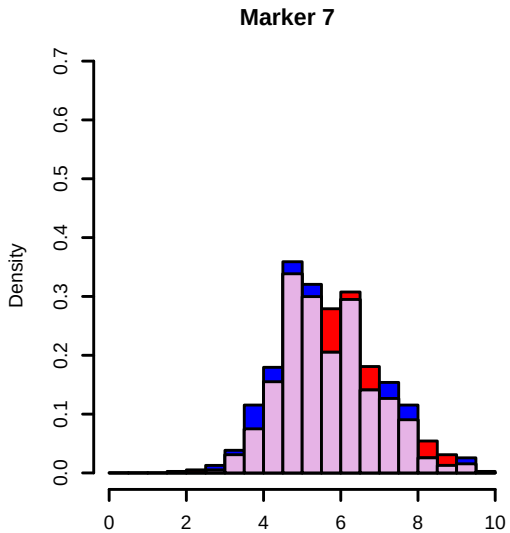
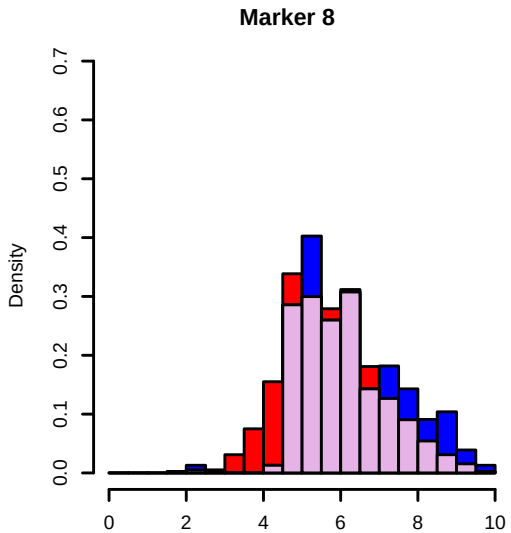
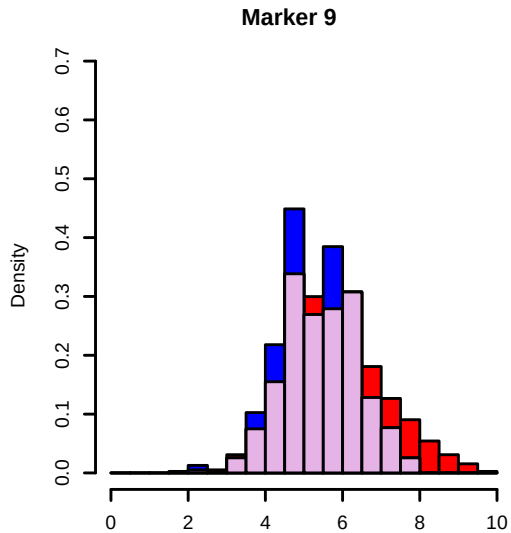




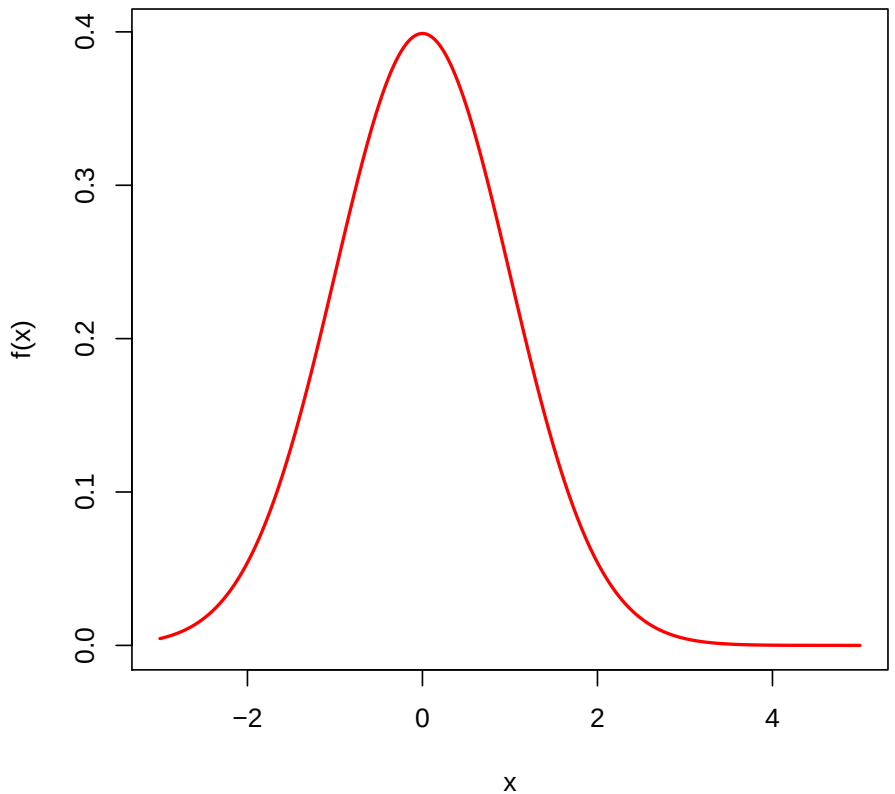








The 'Core' of several distributions



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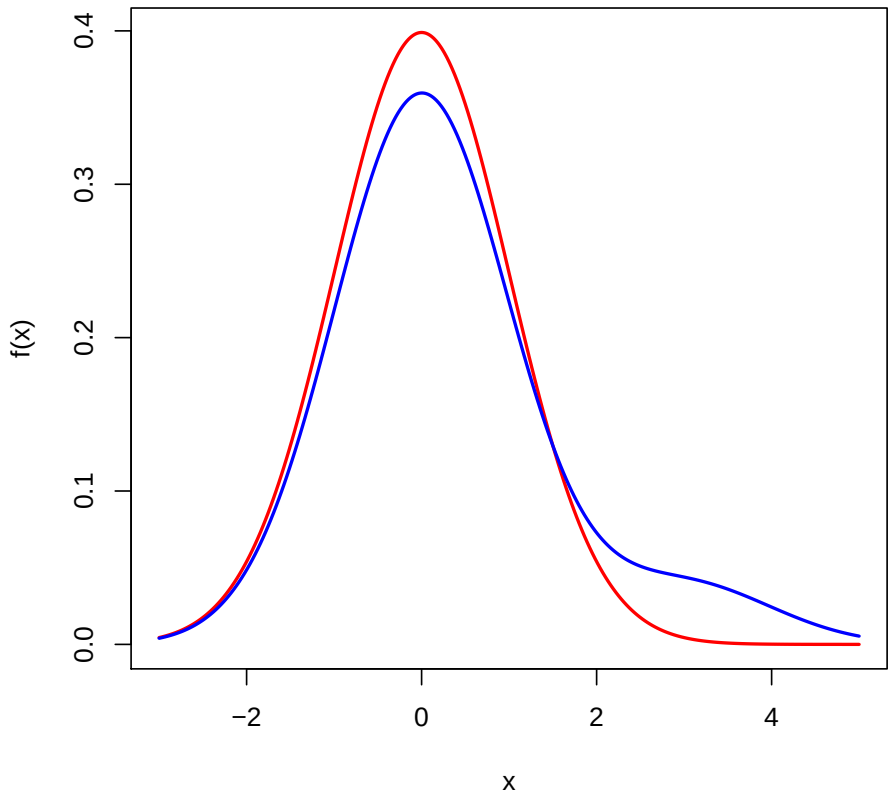

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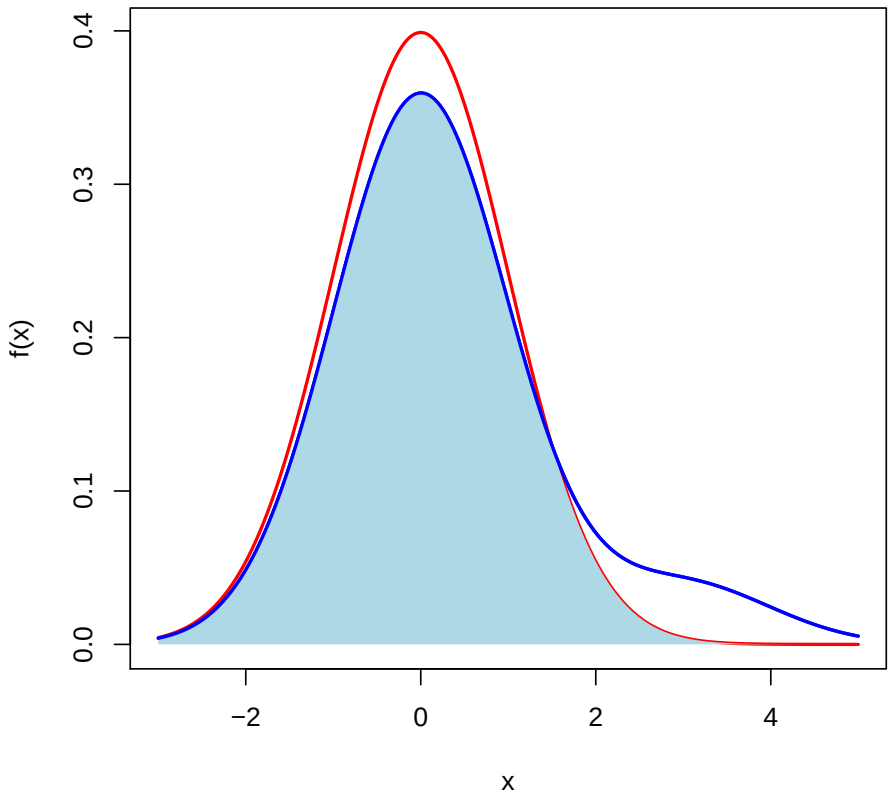

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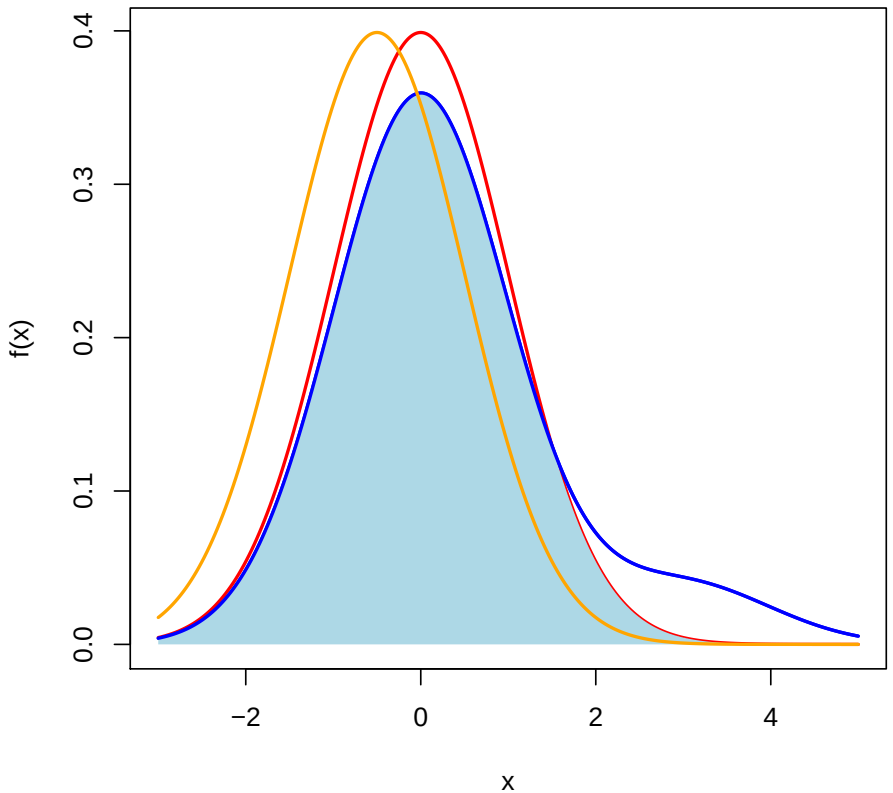

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