## **Supplementary Tables**

The prediction results below are provided for two learning models, the KronRLS (see Methods section) and Random Forest (see Supplementary Methods). The averaged CV results are based on 5-fold CV in settings S1-S3, and 3x3 CV in S4 (Supplementary Tables 1-9). The pooled CV results were computed for KronRLS using smaller fold sizes, namely the LOO, LDO and LTO CV approaches in settings S1-S3, and 10x10 fold CV in setting S4 (Supplementary Tables 10-17). For the Random Forest, the fold sizes were the same as for the averaged CV experiments. All the experiments are based on nested CV strategy, where the inner CV rounds were used for the parameter selection, and the outer rounds for the performance evaluation.

Setting	2D	3D	ECFP4	$\delta$ <sup>a</sup>
<b>S</b> 1	88.3	89.1	89.4	86.7
S2	74.8	73.4	74.1	-
S2 $\delta^{b}$	72.7	73.4	73.8	-
<b>S</b> 3	86.1	87.9	88.2	88.1
S4	67.0	72.8	69.2	-

Supplementary Table 1: Concordance index, K<sub>d</sub> data, Kronecker RLS, averaged CV

Supplementary Table 2: Concordance index, K<sub>d</sub> data, Random Forest, averaged CV

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Setting	2D	3D	ECFP4	$oldsymbol{\delta}^{ ext{ a}}$	
<b>S</b> 1	88.5	88.3	88.8	88.2	
S2	67.0	68.7	67.5	-	
S2 $\delta^{b}$	65.6	66.5	66.8	-	
<b>S</b> 3	87.2	87.4	87.3	87.2	
S4	64.9	62.7	67.0	-	

Supplementary Table 3: AUC, Binarized K<sub>d</sub> data, Kronecker RLS, averaged CV

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Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$	
<b>S</b> 1	95.2	95.9	96.1	93.9	
S2	77.5	77.2	74.4	-	
S2 $\delta^{b}$	76.9	79.5	77.6	-	
<b>S</b> 3	93.6	94.8	94.9	94.3	
S4	70.0	74.2	69.1	-	

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Setting	2D	3D	ECFP4	$oldsymbol{\delta}^{ ext{ a}}$
<b>S</b> 1	95.5	95.1	95.7	91.5
S2	76.8	75.9	78.2	-
S2 $\delta^{b}$	75.3	76.2	76.9	-
<b>S</b> 3	94.4	94.7	94.5	92.1
<b>S</b> 4	73.3	73.1	73.8	-

Supplementary Table 4: AUC, Binarized K<sub>d</sub> data, Random Forest, averaged CV

Supplementary Table 5: AUC-PR, Binarized K<sub>d</sub> data, Kronecker RLS, averaged CV

Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$
<b>S</b> 1	67.0	68.4	69.2	64.9
S2	24.5	30.3	28.3	-
S2 $\delta^{b}$	26.7	31.2	29.9	-
S3	63.5	68.4	69.7	69.3
S4	17.2	25.9	23.7	-

Supplementary Table 6: AUC-PR, Binarized K<sub>d</sub> data, Random Forest, averaged CV

Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{a}$
S1	68.9	68.6	69.4	59.4
S2	24.9	23.3	24.1	-
S2 $\delta^{b}$	25.5	25.7	25.0	-
<b>S</b> 3	67.2	67.2	67.2	61.9
S4	22.2	22.8	22.0	-

**Supplementary Tables 1-6**. Prediction accuracy of Kronecker RLS and Random Forest algorithms on the  $K_d$  dataset of Davis et al. (2011). Concordance index (CI) results evaluate rank prediction of quantitative  $K_d$  labels, while the area under ROC curve (AUC) and area under precision-recall curve (AUC-PR) results are for the binarized  $K_d$  labels when using the cut-off threshold of  $K_d$ <30.00nM.

The rows indicate different evaluation settings, and the columns drug similarity measures. The  $\delta$  kernel indicates the use of the delta function kernel without any similarity information, that is, each drug<sup>a</sup> or target<sup>b</sup> is only similar to itself, resulting in the identity kernel matrix. The performance over the folds has been computed using averaging.

Setting	Enzyme	Ion Channel	GPCR	Nuclear Receptor
S1	96.0	96.4	92.7	86.1
S2	83.7	80.2	85.2	84.6
S2 $\delta^{b}$	83.2	80.2	86.5	82.8
S3	92.1	94.0	89.4	73.8
S3 $\delta^{a}$	91.9	93.3	85.9	56.7
S4	76.4	67.8	78.6	67.7

Supplementary Table 7: AUC, Yamanishi et al. (2008) data, Kronecker RLS, averaged CV

Supplementary Table 8: AUC-PR, Yamanishi et al. (2008), Kronecker RLS, averaged CV

Setting	Enzyme	Ion Channel	GPCR	Nuclear Receptor
S1	82.9	76.5	60.2	52.8
S2	36.1	25.8	37.8	49.3
S2 $\delta^{b}$	39.5	36.5	40.2	51.8
<b>S</b> 3	77.2	79.6	59.2	34.8
S3 $\delta^{a}$	78.6	81.1	58.6	34.9
S4	25.0	18.9	17.5	19.3

Supplementary Tables 7-8. Prediction accuracy of Kronecker RLS algorithm on the Yamanishi et al. (2008) data sets, evaluated using area under ROC curve (AUC) and area under precision-recall curve (AUC-PR). The rows represent different evaluation settings and the columns data sets. The  $\delta$  kernel indicates the use of the delta function kernel without any similarity information, that is, each drug<sup>a</sup> or target<sup>b</sup> is only similar to itself, resulting in the identity kernel matrix. The performance over the folds has been computed using averaging.

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Setting	CI	AUC	AUC-PR	_
S1	79.3	93.4	57.2	
S2	73.6	85.5	42.8	
S2 $\delta^{b}$	75.1	87.3	44.9	
S3	66.6	85.0	25.4	
S3 $\delta^{a}$	69.0	84.5	31.7	
<b>S</b> 4	59.2	74.9	16.2	

Supplementary Table 9: CI, AUC and AUC-PR, Ki data set, Kronecker RLS, averaged CV

Prediction accuracy of Kronecker RLS algorithm on the  $K_i$  dataset of Metz et al. (2011).

Concordance index (CI) evaluates the rank prediction of quantitative  $K_i$  labels, while the area under ROC curve (AUC) and area under precision-recall curve (AUC-PR) results are for the binarized  $K_i$  labels when using the cut-off threshold of  $K_i < 28.18$  m. The performance over the folds has been computed using averaging.

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Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$	
<b>S</b> 1	89.8	90.2	90.8	88.5	
S2	72.0	75.5	75.2§	-	
S2 $\delta^{b}$	72.2	76.0	75.1	-	
S3	86.7	88.2	88.4	88.5	
S4	70.0	72.8	72.0	-	

Supplementary Table 10: Concordance index, K<sub>d</sub> data, Kronecker RLS, pooled CV

Supplementary Table 11: Concordance index,  $K_d$  data, Random Forest, pooled CV

Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$
S1	88.5	88.3	88.8	88.2
S2	65.8	67.1	66.1	-
S2 $\delta^{b}$	64.7	64.9	64.4	-
<b>S</b> 3	87.2	87.4	87.2	87.2
S4	64.3	61.3	64.6	-

Supplementary Table 12: AUC, Binarized K<sub>d</sub> data, Kronecker RLS, pooled CV

Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$	
<b>S</b> 1	95.5	95.9	96.2	94.3	
S2	77.2	82.9	77.4	-	
S2 $\delta^{b}$	77.2	80.0	77.3	-	
<b>S</b> 3	94.7	95.5	95.1	94.3	
S4	73.9	80.8	74.8	-	

Supplementary Table 13: AUC, Binarized K<sub>d</sub> data, Random Forest, pooled CV

Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$	
<b>S</b> 1	95.5	95.1	95.7	91.5	
S2	73.8	72.9	74.3	-	
S2 $\delta^{b}$	72.2	72.5	72.2	-	
<b>S</b> 3	94.4	94.8	94.5	92.1	
S4	70.1	69.3	69.7	-	

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Setting	2D	3D	ECFP4	$\boldsymbol{\delta}^{\mathrm{a}}$	
<b>S</b> 1	71.3	72.1	74.2	71.3	
S2	20.8	36.2	27.5	-	
S2 $\delta^{b}$	23.9	34.7	28.7	-	
<b>S</b> 3	65.5	70.5	71.6	71.3	
<b>S</b> 4	17.8	33.9	24.9	-	

Supplementary Table 14: AUC-PR, Binarized K<sub>d</sub> data, Kronecker RLS, pooled CV

Supplementary Table 15: AUC-PR, Binarized K<sub>d</sub> data, Random Forest, pooled CV

Setting	2D	3D	ECFP4	$\delta^{a}$
S1	68.6	68.4	69.0	59.0
S2	19.9	20.0	20.3	-
S2 $\delta^{b}$	20.3	21.2	21.2	-
<b>S</b> 3	67.7	67.6	67.9	62.2
S4	18.2	18.2	17.9	-

**Supplementary Tables 10-15**. Prediction accuracy of Kronecker RLS and Random Forest algorithms on the  $K_d$  dataset of Davis et al. (2011). Concordance index (CI) results evaluate rank prediction of quantitative  $K_d$  labels, while the area under ROC curve (AUC) and area under precision-recall curve (AUC-PR) results are for the binarized  $K_d$  labels when using the cut-off threshold of  $K_d$ <30.00nM.

The rows indicate different evaluation settings, and the columns drug similarity measures. The  $\delta$  kernel indicates the use of the delta function kernel without any similarity information, that is, each drug<sup>a</sup> or target<sup>b</sup> is only similar to itself, resulting in the identity kernel matrix. The performance over the folds has been computed using pooling.

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Setting	Enzyme	Ion Channel	GPCR	Nuclear Receptor
S1	96.1	97.1	94.4	84.6
S2	81.3	75.4	84.4	83.3
S2 $\delta^{b}$	82.1	74.8	84.9	83.0
<b>S</b> 3	93.8	93.4	88.2	74.1
S3 $\delta^{a}$	93.7	93.6	86.2	64.3
S4	78.5	67.8	79.7	70.6

Supplementary Table 16: AUC, Yamanishi et al. (2008) data, Kronecker RLS, pooled CV

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Setting	Enzyme	Ion Channel	GPCR	Nuclear Receptor
S1	86.2	82.8	67.5	47.4
S2	22.1	27.9	35.2	38.9
S2 $\delta^{b}$	28.1	33.7	40.3	43.9
S3	82.0	79.3	60.3	26.1
S3 $\delta^{a}$	82.5	81.6	61.0	36.8
S4	20.8	16.7	18.3	13.3

Supplementary Table 17: AUC-PR, Yamanishi et al. (2008) data, Kronecker RLS, pooled CV

Supplementary Tables 16-17. Prediction accuracy of Kronecker RLS algorithm on the Yamanishi et al. (2008) data sets, evaluated using area under ROC curve (AUC) and area under precision-recall curve (AUC-PR). The rows represent different evaluation settings and the columns data sets. The  $\delta$  kernel indicates the use of the delta function kernel without any similarity information, that is, each drug<sup>a</sup> or target<sup>b</sup> is only similar to itself, resulting in the identity kernel matrix. The performance over the folds has been computed using pooling.