

# IMAGE INFORMATICS APPROACHES TO ADVANCE CANCER DRUG DISCOVERY

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## DECLARATION

This thesis presents my own work, and has not been submitted for any other degree or professional qualification. Wherever results were obtained in collaboration with others, I have clearly stated it in the text. Any information derived from the published work of others has been cited in the text, and a complete list of references can be found in the bibliography. Published papers arising from the work described in this thesis can be found in the appendices.

– Scott Warchal, 2018



*epigraph here*



## ACKNOWLEDGEMENTS

Acknowledgements here.



## ABSTRACT

High content image-based screening assays utilise cell based models to extract and quantify morphological phenotypes induced by small molecules. The rich datasets produced can be used to identify lead compounds in drug discovery efforts, infer compound mechanism of action, or aid biological understanding with the use of tool compounds. Here I present my work developing and applying high-content image based screens of small molecules across a panel of eight genetically and morphologically distinct breast cancer cell lines.

I implemented machine learning models to predict compound mechanism of action from morphological data and assessed how well these models transfer to unseen cell lines, comparing the use of numeric morphological features extracted using computer vision techniques against more modern convolutional neural networks acting on raw image data.

The application of cell line panels have been widely used in pharmacogenomics in order to compare the sensitivity between genetically distinct cell lines to drug treatments and identify molecular biomarkers that predict response. I applied dimensional reduction techniques and distance metrics to develop a measure of differential morphological response between cell lines to small molecule treatment, which controls for the inherent morphological differences between untreated cell lines.

These methods were then applied to a screen of 13,000 lead-like small molecules across the eight cell lines to identify compounds which produced distinct phenotypic responses between cell lines. Putative hits were then validated in a three-dimensional tumour spheroid assay to determine the functional effect of these compounds in more complex models, as well as proteomics to determine the responsible pathways.

Using data generated from the compound screen, I carried out work towards integrating knowledge of chemical structures with morphological data to infer mechanistic information of the unannotated compounds, and assess structure activity relationships from cell-based imaging data.



## LAY SUMMARY

Drugs act by altering the behaviour of cells, usually by disrupting the internal cellular machinery necessary for normal function, or in the case of diseases, by trying to reverse dysfunctional cellular processes responsible for disease initiation and progression back towards a normal state. Subtle changes in cellular functions can be detected visually through microscopy and fluorescent labels which bind to subcellular components such as DNA. Using automated image analysis methods it is possible to analyse these microscope images of cells and create a detailed description of each individual cell, represented as a series of measurements describing various attributes such as the cell's size, location and concentration of various biomolecules, this can be thought of as the cell's "fingerprint". Using these cellular fingerprints it is possible to test drugs in an effort to find those that convert a disease-like fingerprint into a healthy looking one, or to compare the fingerprints produced by unknown drugs to ones produced by molecules whose function is already known.

My work focuses on how to generate and exploit compound fingerprints across a number of different cells which represent different types of breast cancer. A significant challenge in studying distinct cancer cell types is that each cell has its own unique fingerprint regardless of drug treatment, which makes comparisons between cells more difficult. In addition, I investigate how more advanced computational tools alongside this varied dataset can aid predicting how novel compounds work.

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## LIST OF ACRONYMS

**2D** Two-dimensional

**3D** Three-dimensional

**ABL** Abelson murine leukemia viral oncogene homologue

**BCR** Breakpoint Cluster Region

**ANN** Artificial Neural Network

**BSA** Bovine Serum Albumin

**CCLE** Cancer Cell Line Encyclopedia

**CCM** Cerebral Cavernous Malformation

**CNN** Convolutional Neural Network

**DMEM** Dulbecco's Modified Eagle Medium

**DMSO** Dimethyl sulfoxide

**EMA** European Medicines Agency

**FDA** U.S Food and Drug Administration

**GDSC** Genomics of Drug Sensitivity in Cancer

**GPU** Graphics processing Unit

**HCS** High Content Screening

**HTS** High Throughput Screening

**MCL** Markov Clustering Algorithm

**MoA** Mechanism of Action

**MOI** Multiplicity Of Infection

**mRMR** Minimum-Redundancy-Maximum-Relevancy

**PBS** Phosphate Buffered Saline

**PCA** Principal Component Analysis

**PDD** Phenotypic Drug Discovery

**RGB** Red Green Blue

**SAR** Structure Activity Relationship

**STS** Staurosporine

**TCCS** Theta Comparative Cell Scoring

# 1 | INTRODUCTION

## 1.1 Eroom's Law: The increasing cost of drug discovery

Throughout the last 70 years the cost of developing a new drug has steadily increased, a study by Scannel *et al.* noted the cost has approximately doubled every 9 years,<sup>1</sup> this observation has been dubbed “Eroom’s law” in a homage to Moore’s law.<sup>i</sup> The cost of bringing a new drug to market is now approaching £1 billion, taking 10 years from initial concept through to regulatory approval, the reasons behind this ever-increasing cost are still under debate although it is clear the issue is multi-faceted. One explanation may be that the low-hanging fruits of drug discovery have already been taken; for example the most effective traditional remedies have been studied and their active ingredients commercialised, natural products screened to identify the most potent bioactive molecules, many single gene disorders and eminently druggable oncogene-driven homogeneous tumours have been cured, leaving us to tackle the more complex diseases and pharmacological targets. This pessimism has led to the ever present idea that drug discovery is undergoing a productivity crisis,<sup>2</sup> and that the investments made in early stage research do not translate into actionable pharmacology which can be used to develop effective therapies for patients, and has led to a renewed interest in alternative drug discovery paradigms.

## 1.2 The drug discovery process

### 1.2.1 Target-based screening

Over the past 30 years the majority of drug discovery programmes have seized upon technological advances in robotics and automation to screen ever expansive compound libraries against pre-defined protein targets. It would be difficult to argue that this target-based high-throughput screening (HTS) approach has not been fruitful, yielding many successful therapeutics across a range of disease areas, largely attributed to an increased understanding of the genomic basis of many diseases. However, despite numerous clinical and commercial success stories, HTS is not a panacea, with a high attrition rate of lead compounds once they enter clinical trials.<sup>3</sup> A large majority of these clinical trial failures are not due to toxicity, but rather a lack of efficacy which can often be traced back to limited validation of the hypothesised target in the face of complex disease aetiology.<sup>4</sup>

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<sup>i</sup>The well-known observation that the number of transistors in microprocessors approximately doubles every 2 years.

### 1.2.2 Phenotypic screening

Phenotypic screening differs from target-based screening in that it does not rely on prior knowledge of a specific target, but instead interrogates a biologically relevant assay to identify compounds which alter the phenotype in a biologically desirable way. This target-agnostic approach can prove useful in diseases with poorly understood mechanisms or those with no obvious druggable protein targets. Phenotypic screening is not a new approach in small molecule drug discovery, it was the primary method for many decades before the genomics revolution made target hypothesis more tractable.<sup>5</sup>

Many concerns related to phenotypic screening are centred on the lack of mechanistic information for a given lead compound. Whilst the lack of a known target presents challenges and may cause concerns within a commercial drug discovery programme, regulatory bodies such as the Food and Drug Adminstration validation of the hypothesised target Agency (EMA) do not require a known target for drug approval, only that the drug is safe and efficacious. Metformin is a first-line therapy for type 2 diabetes and is on the World Health Organisation's list of essential medicines, it decreases liver glucose production and has an insulin sensitising effect on many tissues. Despite approval since 1957 and widespread clinical use, the molecular mechanism of metformin remained unknown for 43 years.<sup>6</sup> Although knowledge of the molecular target is not necessary to get a drug into the clinic, target deconvolution is still an important part of most phenotypic drug discovery programmes, without knowing the protein or proteins a compound is binding to lead optimisation via structure activity relationship (SAR) studies becomes extremely difficult. In addition, knowledge of the molecular target of a lead compound generated by a phenotypic screen can be used as a basis for instigating a conventional high-throughput hypothesis-driven screen on a novel target, this is why many view phenotypic screening as a complimentary method to target based screening rather than a competing approach or proposed replacement.<sup>7</sup>

### 1.3 High content imaging

High content imaging is a technique utilising high-throughput microscopes and automated image analysis, commonly used in phenotypic screening as a method for gathering multivariate datasets from images of biological specimens and has proven useful in a wide variety of phenotypic assays, ranging from 2D mammalian cells,<sup>8,9</sup> *in vivo* studies in zebrafish<sup>10</sup> and even plants and crops.<sup>11</sup>

High content screens – screening studies carried out with high content imaging – are particularly useful in phenotypic drug discovery for several reasons. High content imaging provides spatial resolution enabling the use of more complex assays including co-culture and 3D models, which might better represent the biological complexity of disease relative to 2D reductionist models. However, these complex assays often have phenotypes which are more difficult to quantify, which a single univariate readout may fail to accurately recapitulate, therefore the multivariate datasets produced by high content screening enables a more in-depth view into the endpoints which should be measured in a complex assay. A second benefit is the multivariate data generated by high content screening offers a more unbiased method for detecting hits in a phenotypic assay, as predicting which variable to measure beforehand may lead to missed biologically interesting phenotypes. With the advent

of more complex datasets generated from high-content imaging, the process of image-analysis and computational methods for data processing has given rise to the term “high-content analysis”.

### 1.3.1 Image analysis

Image analysis is the process in which raw image data from a high-content screen is transformed into measurements which can be used to describe the observed morphology of the biological specimen exposed to a perturbagen. Here I will focus on cell-based assays for small-molecule screening, though the same methods apply for most other assays (spheroids/organoids etc) and perturbagens (siRNA, CRISPR etc).

The standard approach to extracting numerical features from cell morphologies is through segmenting cells and sub-cellular structures into “objects”, and then computing image-based measurements on those objects. Typically each cell within an image is identified by first segmenting nuclei from the background. A number of well-established image thresholding algorithms can be used for segmenting nuclei from background, most automatically calculate an intensity threshold to binarise an image based on histograms of pixel intensities.<sup>12,13</sup> The segmented nuclei can then be used as seeds to detect cell boundaries, either through edge detection in a channel containing a cytoplasmic marker, or more crudely by expanding a number of pixels from the nuclei centre to approximate cell size. There are also less commonly used methods which utilise machine learning based on trained parameters to segment cells,<sup>14</sup> or forgo segmentation entirely to measure morphological features from the raw images.<sup>15,16</sup>

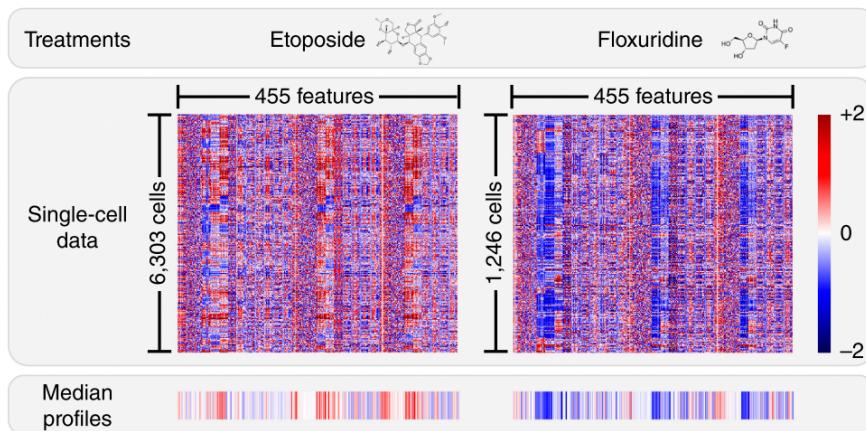
After cells and sub-subcellular objects have been segmented morphological characteristics are measured for each object, these measurements can cover a wide variety of morphologies depending on the aims of the assay, although can be grouped into 4 main classes:

**Shape.** Calculated on the properties of the object masks, e.g. area, perimeter, eccentricity. Shape features are commonly used as they are interpretable, robust, and quick to calculate.

**Intensity.** These features are based on the pixel intensity values within the object boundaries. They can be calculated for multiple channels and include measurements such as average intensity, integrated intensity, and radial distribution of intensity values. Great care has to be taken when using intensity values as they are susceptible to batch effects and microscope artefacts such as vignetting.<sup>17</sup>

**Texture.** Measures of patterns of intensities within objects, typically derived from grey level co-occurrence matrices.<sup>18</sup> This can be used to quantify morphologies such as small speckles or stripes within an image. Texture measurements are often computationally expensive and difficult to interpret although can be useful for measuring subtle morphological changes.

**Spatial context.** These are typically relationships between objects, such as the number of neighbouring cells or nuclei, percentage of a cell boundary in contact with neighbouring cells. This class can also include the simple measure of cell or nuclei count within a field of view.



**Figure 1.1:** Single cell data aggregation to a median profile. Two matrices representing single cell morphology data for a treatment, with columns displaying multiple measured morphological features for each cell represented as a row. (*Figure re-used from Caicedo et al. Nat Methods, 2017*)

### 1.3.2 Data analysis

Measuring morphological features produces an  $m \times n$  dataset per object class, where  $m$  is the number of objects and  $n$  is the number of morphological features measure for that object. Commonly single object level data is aggregated to population level, where the population can be a field of view, microtitre-well, or treatment level (see figure 1.1); with the most popular aggregation method being a simple median average.<sup>19</sup> Once the object-level data has been aggregated to a common population level such as per well data, the features from each object class can be combined into a dataset represented by a single  $p \times q$  matrix, where  $p$  is the number of wells (or other level of aggregation), and  $q$  is the total number of combined features from all object classes. It is then useful to view each row of this matrix as a feature vector, or morphological profile which summarises the morphology induced by a treatment.

There are a number of fairly standard data pre-processing steps involved in high content analysis, consisting of: quality-control checks and outlier removal, batch correction, normalisation, standardising feature values, and dimensional reduction or feature selection.<sup>19</sup>

**Quality control.** Errors are usually introduced at the imaging or segmentation phase of high-content assays, either through poor image quality caused by out-of-focus wells or debris, or poorly chosen segmentation parameters causing artefacts with otherwise acceptable images and subsequent outlier morphological features. As assays often generate thousands if not millions of images, it is not practical to manually check each image and segmentation mask for quality, therefore a number of automated methods have been developed to flag potential image artefacts and extreme feature values.

Image artefacts can be detected through measures of image intensity, as out-of-focus images tend to have shallow intensity gradients across the image and lose high-frequency intensity changes,<sup>20</sup> whereas images containing debris such as dust and fibres contain a large percentage of saturated

pixels. Segmentation errors usually create extreme values for most feature measurements which can be highlighted using typical outlier detection methods such as Hampel filtering<sup>21</sup> and local outlier factor.<sup>22</sup>

**Batch correction.** Batch effects are accumulations of multiple sources of technical variation such as equipment, liquid-handling error, reagents and environmental conditions which can influence measurements and mislead researchers, and are particularly prevalent in high-throughput experiments. They are normally identified by visually through boxplots of features, with plates or weeks on the x-axis, or through comparing correlations, within plates, between plates of the same batch and across batches. If batch effects are apparent they can be corrected, the simplest method is to standardise each batch separately, other methods include 2-way ANOVA<sup>23</sup> or canonical correlation analysis.<sup>24</sup>

**Standardisation.** When many morphological features are measured from an image, they are unlikely to share the same scale/units or have similar variance – e.g. cell-area measured in pixels which may range from zero to several thousand and cell-eccentricity which is constrained between zero and one. It is therefore useful to standardise all feature values to be mean centred and have comparable variance. This aids in many downstream data analysis methods which assume standardised feature values.

**Dimensional reduction and feature selection.** As with any high-dimensional data a large number of features can cause issues with analysis and interpretation, this is commonly known as the “curse of dimensionality”.<sup>25</sup> Another issue is that many of the measured features may not contribute information, either as they have little or no variation between samples, or are redundant due to high correlation with existing features. Dimensional reduction and feature selection methods are both commonly used in other biological fields such as genomics and proteomics, and are now routinely used in high-content imaging analysis. A widely used technique is principal component analysis (PCA), which is an unsupervised approach to maximise variation through a linear combination of orthogonal features. PCA can be used to reduce the number of features by selecting a subset of principal components which explain a specified proportion of variance in the data. Loss of interpretability can be an issue when using PCA, and is why some researchers favour feature selection methods which aim to retain original feature labels whilst still reducing dimensionality by removing uninformative features. Many of the feature selection methods are supervised, which may not fit in with unbiased analyses, although Peng *et al.* developed an unsupervised minimum-redundancy-maximum-relevancy (mRMR) feature selection method which has found use in high-content analyses.<sup>26</sup>

Following data pre-processing, downstream analysis is typically focused on one of two tasks: identifying hit compounds in a screen, or comparing the similarity of morphology profiles created by treatments – both of which use distance as a metric, either comparing hits against a negative control, or treatments against one another respectively.

### 1.3.3 Image based screening

Phenotypic and image-based screens can be used in traditional drug discovery roles whereby a compound library is screened in a biologically relevant cell-based assay in order to identify compounds which produce a favourable phenotype and hits or lead compounds identified from a high throughput biochemical assay are evaluated in a more complex image-based cell assay to determine their quality. These assays typically rely on either a positive control compound which is known to elicit the phenotype of interest in order to optimise and validate the assay has appropriate signal-to-noise attributes for testing multiple compounds. Or alternatively, a carefully designed assay in which a disease model utilising abnormal patient-derived or genetically engineered cells is used to identify compounds which revert the disease associated phenotype towards a healthy or wild-type phenotype. An example of this is demonstrated by Gibson *et al.*,<sup>27</sup> whereby they modelled cerebral cavernous malformation (CCM) using siRNA knockdown of the *CCM2* gene in human primary cells, and screened small molecules to identify candidates which rescued the siRNA induced phenotype using fluorescent markers of the nucleus, actin filaments, and VE-cadherin cell-cell junctions. Candidate compounds were then validated in an *in vivo* mouse model, which lead to the ongoing pre-clinical development of 4-Hydroxy-TEMPO as a novel therapeutic for CCM. This is an elegant demonstration that combining good disease models with target agnostic phenotypic screens can effectively yield promising therapeutic candidates without complex bioinformatics techniques.

### 1.3.4 Image based profiling

In contrast to screening studies which are mainly interested in looking for a defined phenotype, profiling is used to create phenotypic “fingerprints” of perturbagens analogous to transcriptional profiles, which can be used for clustering, inference and prediction. One of the main uses of phenotypic profiling is to compare the similarity of morphological profiles allowing clustering and machine learning methods to build rules in order to classify new or blinded treatments according to similar annotated neighbouring treatments.

One of the landmark papers of high-content profiling was published in 2004 when Perlman *et al.*<sup>28</sup> first demonstrated that morphological profiles between drugs could be clustered according to compound mechanism-of-action using a custom similarity metric and hierarchical clustering. Most studies utilising morphological profiling use unsupervised hierarchical clustering in order to group treatments into bins which produce similar cellular phenotypes,<sup>29,30</sup> although other clustering algorithms such as graph-based Markov clustering algorithm (MCL),<sup>31,32</sup> and spanning trees<sup>33</sup> are sometimes used.

## 1.4 Phenotypic screening in cancer drug discovery

Cancer drug discovery programmes of past decades seized upon uncontrolled proliferation as a clinically relevant phenotype to use in screening studies, giving rise to a number of anti-proliferative and cytotoxic compounds, which are still used in the clinic but often renowned for their severe side-effects. Many modern day oncology drug discovery programmes still retain anti-proliferation

as a key predictor for pre-clinical success, although increased understanding of cancer's molecular underpinnings has driven many oncology programmes towards a more target-directed approach. The prototypical success story of target-driven drug discovery in oncology is imatinib, a tyrosine kinase inhibitor targeting the BCR-ABL fusion protein in chronic myeloid leukemia. However, despite imatinib's exceptional success, unfortunately in most cases targeting a single driver in a complex signalling network results in compensatory signalling, activation of redundant pathways and unpredicted feedback mechanisms, all of which diminish efficacy *in vivo*.

In a review of 48 small molecule drugs approved for use in oncology between 1999 and 2013, 31/48 were discovered through target based screens, whereas 17/48 were based on leads from target-agnostic phenotypic screens,<sup>7</sup> of those compounds discovered through target directed screening programmes the vast majority (75%) were kinase inhibitors. However, phenotypically derived compounds did not live up to the hypothesis that target-agnostic screening should be more likely to identify compounds with novel MoAs,<sup>34</sup> with only 5/17 being first in class molecules. An explanation for this sparsity of novel mechanisms is that phenotypic assays which use cytotoxicity readouts are likely to find low-hanging fruit such as targeting microtubule stabilisation and DNA replication dynamics.<sup>7</sup> One option to combat this narrow attention on a select few targets – caused by either hypothesis-driven or simplistic phenotypic screens – is to utilise the more detailed mechanistic information offered by high-content imaging to explore novel biological mechanism and this broader areas of therapeutic target space rather than relying on cellular death as catch-all phenotypic readout.

In addition to high-content imaging screens with cells grown in 2D monolayers, more complex phenotypic models such as 3D tumour spheroids are being increasingly adopted in pre-clinical oncology. 3D tumour spheroids are multi-cellular aggregates thought to better recapitulate environment and biology of real tumours compared to cells grown in 2D monolayers on tissue culture plastic. There is mounting evidence that spheroids offer a more predictive model of *in vivo* compound efficacy than their 2D counterparts,<sup>35,36,37</sup> this is thought to be caused by the hypoxic environment in the centre of the spheroid, increased cell-cell contact and greater presence of extracellular matrix components which better represents conditions found *in vivo*. Three-dimensional spheroid models lend themselves well to phenotypic and image-based screening projects, with compound efficacy determined through use of fluorescent markers of cell-viability,<sup>37</sup> cell-cycle dynamics,<sup>38</sup> or by analysis of spheroid morphology which can also incorporate 3D volumetric measurements.<sup>39</sup>

#### 1.4.1 Cancer cell line panels

Panels of multiple cancer cell lines such as the NCI-60, Cancer Cell Line Encyclopedia (CCLE)<sup>40</sup> and Genomics of Drug Sensitivity in Cancer (GDSC)<sup>41</sup> have been widely used to facilitate high-throughput screening and increase certainty in hit selection / disease-specificity,<sup>42,43</sup> and as a research tool to study pharmacogenomics.<sup>44,45,46</sup> The use of cancer cell line panels can also benefit phenotypic screens by mirroring the heterogeneity found in patient populations, as well as heterogeneous cell populations found in tumours.<sup>47</sup> Throughout this body of work I have used a panel of eight breast cancer cell lines (table 1.1), these cell lines were chosen based on a number of criteria:

Cell line	Molecular subclass	Mutational status	
		PTEN	PI3K
MCF7	ER	WT	E545K
T47D	ER	WT	H1047R
MDA-MB-231	TN	WT	WT
MDA-MB-157	TN	WT	WT
HCC1569	HER2	WT	WT
SKBR3	HER2	WT	WT
HCC1954	HER2	*	H1047R
KPL4	HER2	*	H1047R

**Table 1.1:** Panel of breast cancer cell lines chosen for study. PI3K:Phosphoinositide-3-kinase, PTEN:Phosphatase and tensin homolog, ER:Estrogen receptor, TN:triple-negative, HER2:human epidermal growth factor, WT:wild-type, \*:lack of consensus regarding the mutational status.

1. Relatively fast growth to allow compound screening to be performed in weekly batches.
2. Adherent to tissue culture plastic to enable 2D imaging.
3. Form a monolayer when grown in 2D – overlapping cells cause difficulties for most image segmentation methods.
4. Amenable for morphometric imaging – larger and/or flatter cells allow for better discrimination of sub-cellular features.
5. Distinct morphologies to evaluate the robustness of morphological profiling methods.
6. A collection which represents a range of molecular sub-classes of breast cancer.

#### 1.4.2 Breast cancer

The cell lines used in this work are all immortalised human cancer cell lines originating from breast cancer patients. Breast cancer cell lines were chosen as the disease has been the focus of many years of research resulting in many well characterised cell lines with freely available genomic, proteomic and imaging datasets. Breast cancer is sub-divided into several subclasses defined by the molecular components which drive disease progression. The three main drivers of breast cancer are oestrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). Aberrant signalling in one of more of these pathways is responsible for approximately 80-85% cases of breast cancer. The remaining 15-20% of cases are classified as triple negative (TN). Molecular subclasses are used clinically to stratify patients based on immunohistochemically stained tumour sections examined by pathologists to inform therapeutic and surgical options. In addition to these simple subtypes, there are alternative and more complex methods of stratifying patients based histopathological phenotype, response to endocrine and (neo)adjuvant therapy, and copy number alterations.<sup>48</sup>

## 1.5 Thesis structure

The following chapters focus on selected topics from my PhD, some of which has been published (see appendix). Chapter 2 contains general methods which are used throughout and apply to multiple chapters. Chapter 3 is an analysis of machine learning methods to classify compound MoA from high content imaging data, with a focus on how well classifiers transfer across to new data from morphologically distinct cell lines. Chapter 4 describes the development and application of a novel analytical method to detect and quantify differential phenotypic responses between morphologically distinct cell lines when treated with small molecules. Chapter 5 describes a high content screen of 13,000 small molecules in order to identify compounds which produced distinct phenotypic responses between cell lines, functional assays to validate hits and proteomics to investigate potential pathways responsible. Chapter 6 describes work towards developing methods which combine cheminformatics of compound chemical structure with high content morphological data in order to infer MoA of unannotated compounds, as well as assess the correlation of chemical similarity and phenotypic similarity. Chapter 7 presents general conclusions from the my PhD and future directions.



# 2 | GENERAL METHODS

These methods are used throughout the work in this thesis and are listed here to reduce repetition. Each subsequent chapter will have a separate methods section which refers to methods unique to that particular chapter, or how they differ from the general methods described here.

## 2.1 Cell culture

The cell-lines were all grown in DMEM (# CATNO MANUFACTURER) and supplemented with 10% foetal bovine serum and 2 mM L-glutamine, incubated at 37°C, humidified and 5% CO<sub>2</sub>.

## 2.2 Generation of GFP labelled cell lines

Stable GFP expressing cell lines were created from the eight breast cancer cell lines in order to aid with spheroid image segmentation. Cells were seeded at approximately 35,000 cells per well of a 6-well plate in 3 mL of DMEM and incubated for 24 hours (37°C) to achieve 20% confluence. After 24 hours of incubation, 35 µL of IncyCyte NucLight Green Lentivirus (#4624 Essen) was added to each well at an MOI of 1 with 1.5 µL of polybrene (1:2000). Plates were then incubated for an additional 24 hours followed by a media change, and another 24 hour incubation. Media was then changed for selection media consisting of 1 µg/mL puromycin and complete DMEM, followed by another 24 hour incubation. Following selection of puromycin resistant cells, cells were trypsinised and placed in a T75 tissue culture flask for further growth. GFP labelled cells and parental cell-lines were compared to ensure growth characteristics remained the same. This was achieved by measuring confluence in 6 well plates seeded with 10,000 cells per well and confluence measured with the Incucyte ZOOM. Following successfull transduction, GFP labelled cells were maintained in 0.5 µg/mL puromycin complete DMEM.

### 2.2.1 Culturing cells in 96-well plates

### 2.2.2 Culturing cells in 384-well plates

## 2.3 Compound handling

### 2.3.1 24 compound validation set

Compounds (table 2.1) were diluted in DMSO at a stock concentration of 10 mM. Compounds plates were made in v-bottomed 96-well plates (#CATNO MANUFACTURER), at 1000-fold

Compound	MoA class	Supplier	Catalog no.
Paclitaxel	Microtubule disrupting	Sigma	T7402
Epothilone B	Microtubule disrupting	Selleckchem	S1364
Colchicine	Microtubule disrupting	Sigma	C9754
Nocodazole	Microtubule disrupting	Sigma	M1404
Monastrol	Microtubule disrupting	Sigma	M1404
ARQ621	Microtubule disrupting	Selleckchem	S7355
Barasertib	Aurora B inhibitor	Selleckchem	S1147
ZM447439	Aurora B inhibitor	Selleckchem	S1103
Cytochalasin D	Actin disrupting	Sigma	C8273
Cytochalasin B	Actin disrupting	Sigma	C6762
Jaskplakinolide	Actin disrupting	Tocris	2792
Latrunculin B	Actin disrupting	Sigma	L5288
MG132	Protein degradation	Selleckchem	S2619
Lactacystin	Protein degradation	Tocris	2267
ALLN	Protein degradation	Sigma	A6165
ALLM	Protein degradation	Sigma	A6060
Emetine	Protein synthesis	Sigma	E2375
Cycloheximide	Protein synthesis	Sigma	1810
Dasatinib	Kinase inhibitor	Selleckchem	S1021
Saracatinib	Kinase inhibitor	Selleckchem	S1006
Lovastatin	Statin	Sigma	PHR1285
Simvastatin	Statin	Sigma	PHR1438
Camptothecin	DNA damaging agent	Selleckchem	S1288
SN38	DNA damaging agent	Selleckchem	S4908

**Table 2.1:** Annotated compounds and their associated mechanism-of-action label used in the classification tasks.

concentration in 100% DMSO by serial dilutions ranging from 10 mM to 0.3  $\mu$ M in semi-log concentrations. Compounds were added to assay plates containing cells after 24 hours of incubation by first making a 1:50 dilution in media to create an intermediate plate, followed by a 1:20 dilution from intermediate plate to the assay plate, with an overall dilution of 1:1000 from the stock compound plate to the assay plate.

## 2.4 Cell painting staining protocol

In order to capture a broad view of morphological changes within a cell using fluorescent microscopy, a choice has to be made which cellular structures to label. This choice is limited by the availability of the fluorescent filter sets fitted to the microscope, reagent costs, and the scalability of the protocol when used in a large screen. Fortunately, this problem was already addressed by another group who published a protocol – named “cell painting” – for labelling 7 cellular structures, using 6 non-antibody stains imaged in the same 5 fluorescent channels available with our microscopy setup.<sup>29,49</sup>

The cell-painting protocol was initially optimised by Gustafsdottir *et al.* for use in the U2OS osteosarcoma cell line, and briefly tested in a few other commonly used cell-lines. However, when tested on the panel of 8 breast cancer cell lines, the staining protocol was observed to induce morphological changes on certain cell lines, in the absence of compounds. It was found that changing the media, and adding the MitoTracker DeepRed stain to live MDA-MB-231 cells produced a

Stain	Labeled Structure	Wavelength (ex/em [nm])	Concentration	Catalog no.; Supplier
Hoechst 33342	Nuclei	387/447 ±20	2 µg/mL	#H1399; Mol. Probes
SYTO14	Nucleoli	531/593 ±20	3 µM	#S7576; Invitrogen
Phalloidin 594	F-actin	562/624 ±20	0.85 U/mL	#A12381; Invitrogen
Wheat germ agglutinin 594	Golgi and plasma membrane	562/624 ±20	8 µg/mL	#W11262; Invitrogen
Concanavalin A 488	Endoplasmic reticulum	462/520 ±20	11 µM	#C11252; Invitrogen
MitoTracker DeepRed	Mitochondria	628/692 ±20	0.6 µM	#M22426; Invitrogen

**Table 2.2:** Reagents used in the cell painting protocol and the excitation/emission wavelengths of the filters used in imaging, ex: excitation, em: emission

rounded morphology, which was not observed in the other cell lines. As any morphological changes introduced by the staining protocol would mask those caused by small-molecules, the protocol was adapted by removing the media change step, and moving the addition of wheat germ agglutinin and MitoTracker DeepRed until after fixation. As the cells were now fixed immediately in their existing media this prevented any alterations to the morphology and improved the wheat germ agglutinin staining, although as the MitoTracker stain relies on membrane potential of the mitochondria, the selectivity of the MitoTracker stain was reduced when used on fixed cells, though it still produced selective enough labelling to capture large changes in mitochondrial morphology.

To stain cells in a 96 or 384 well plates, the cells are first fixed by adding an equal volume of 8% paraformaldehyde (#CATNO MANUFACTURER) to the existing media resulting in a final paraformaldehyde concentration of 4%, and left to incubate for 30 minutes at room temperature. The plates are then washed with PBS (100 µL for a 96 well plate, 50 µL for a 384 well plate) and permeabilised with (50 µL 96-well, 30 µL 384-well) 0.1% Triton-X100 solution for 20 minutes at room temperature. A solution of cell painting reagents was made up in 1% bovine serum albumin (BSA) solution (see table 2.2). Cell painting solution was added to plates (30 µL 96-well, 20 µL 384-well) and left to incubate for 30 minutes at room temperature in a dark place. Plates were then washed with PBS (100 µL 96-well, 50 µL 384) three times, before the final aspiration plates were sealed with a transparent plate seal (#CATNO MANUFACTURER).

## 2.5 Imaging

### 2.5.1 ImageXpress

Imaging was carried out on an ImageXpress micro XL (Molecular Devices, USA) a multi-wavelength wide-field fluorescent microscope equipped with a robotic plate loader (Scara4, PAA, UK).

## 2.5.2 Cell painting image capture

Images were captured in 5 fluorescent channels at 20x magnification, exposure times were kept constant between plates and batches as to not influence intensity values.

## 2.6 Image analysis

### 2.6.1 Cellprofiler

Images were analysed using Cellprofiler v2.1.1 to extract morphological features. Briefly, cell nuclei were segmented in the Hoechst stained image based on intensity, clumped nuclei were separated based on shape. Nuclei objects were used as seeds to detect and segment cell-bodies in the cytoplasmic stains of the additional channels. Subcellular structures such as nucleoli and Golgi apparatus were segmented and assigned to parent objects (cells). Using these masks marking the boundary of cellular objects, morphological features are measured for multiple image channels returning per object measurements.

## 2.7 Data analysis

### 2.7.1 Preprocessing

Out of focus and low-quality images were detected through saturation and focus measurements and removed from the dataset. Image averages of single object (cell) measurements were aggregated by taking the median of each measured feature per image. Features were standardised on a plate-by-plate basis by dividing each feature by the median DMSO response for that feature and scaled by a z-score ( $z$ ) to a zero mean and unit variance by

$$z = \frac{x - \mu}{\sigma} \quad (2.1)$$

where  $\mu$  is the mean and  $\sigma$  is the standard deviation.

Feature selection was performed by calculating pair-wise correlations of features and removing one of a pair of features that have correlation greater than 0.9, and removing features with very low or zero variance.

# 3

## CELL MORPHOLOGY CAN BE USED TO PREDICT COMPOUND MECHANISM-OF-ACTION

### 3.1 Introduction

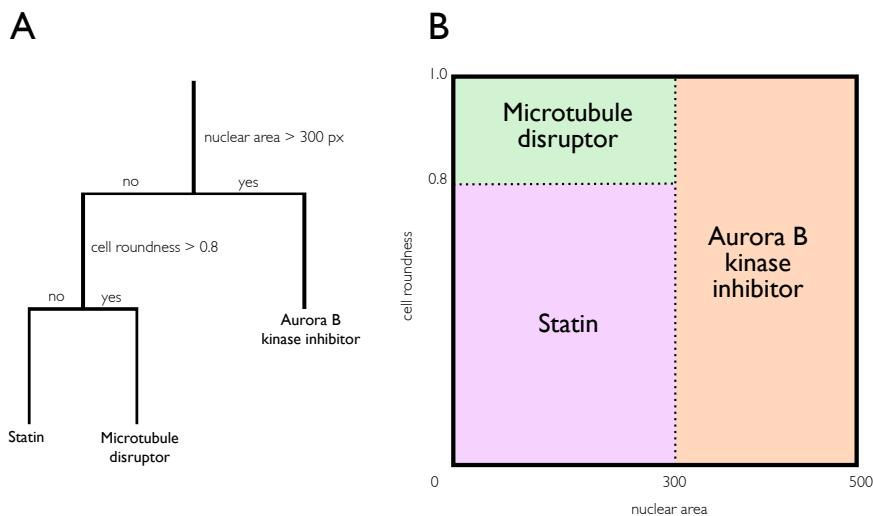
Cellular morphology is influenced by multiple intrinsic and extrinsic factors acting on a cell, and striking changes in morphology are observed when cells are exposed to biologically active small molecules. This compound-induced alteration in morphology is a manifestation of various perturbed cellular processes, and we can hypothesise that compounds with similar MoA which act upon the same signalling pathways will produce comparable phenotypes, and that cell morphology can, in turn, be used to predict compound MoA.

In 2010 Caie *et al.* generated, as part of a larger study, an image dataset consisting of MCF7 breast cancer cells treated with 113 small molecules grouped into 12 mechanistic classes, these cells were then fixed, labelled and imaged in three fluorescent channels<sup>47</sup>. This dataset (also known as BBBC021) has become widely used as a benchmark in the field for MoA classification tasks, with multiple publications using the images to compare machine learning and data pre-processing approaches.<sup>50,51,52,53</sup> Whilst this is important work, it has led to the situation whereby the vast majority of studies in this field have based their work on a single dataset generated with a one cell-line.

One of the issues associated with phenotypic screening when used in a drug discovery setting is target deconvolution. Once a compound has been identified which results in a desirable phenotype in a disease-relevant assay it is common to want to know which molecular pathways the hit compound is acting upon. While target deconvolution is a complex and difficult task, image-based morphological profiling represents one option similar to transcriptional profiling that can match an unknown compound to the nearest similar annotated compound in a dataset, while at the same time being far cheaper than the transcriptional methods such as LINCS1000<sup>54</sup>.

#### 3.1.1 Machine learning methods to classify compound MoA

Predicting compound MoA from phenotypic data is a classification task. This type of machine learning problem is well researched, and there are several models appropriate for our labelled data. As the raw data is in the form of images, it can be approached as an image classification task, a problem in the field receiving lots of attention due to recent theoretical and technological breakthroughs. Whereas a more classical approach would be to extract morphological information from the images, generating a multivariate dataset from the images, and training a classifier on these morphological



**Figure 3.1:** (A) An example of a simple mock decision tree to classify compound mechanism of action based on morphological features. (B) Depiction of decision space as divided by the decision tree model. Shaded areas show how new input data will be classified based on the decision rules (dotted lines).

features.

To develop and validate a machine learning model the dataset has to be split into training, validation and test sets. This is because overfitting is a common problem in machine learning, whereby the model is trained and accurately predicts labels on one dataset, but performs poorly when applied to new data on which it was not trained. Most classification models will overfit to some degree, typically performing better on the training dataset than any other subsequent examples, but the challenge is to limit this overfitting, and also to ensure that the data used to report accuracy measures has not been used in any way to train or validate the model.

### 3.1.2 Ensemble of decision trees trained on extracted morphological features

A decision tree is a very simple method that can be used for both regression and classification. The method works by repeatedly dividing the decision space using binary rules on the feature values until a terminal node containing a classification label is reached (figure 3.1). Simple decision trees like those shown in figure 3.1 perform relatively poorly on all but the simplest of classification problems. However, by aggregating many decision trees and their predictions we can create more accurate and robust models in a practice known as ensemble learning.<sup>55</sup> Bagging<sup>56</sup> and Boosting<sup>57</sup> are two popular methods for constructing ensembles of decision trees. As combining the output of several decision trees is useful only if there is a disagreement among them, these two methods both attempt to solve the same problem of generating a set of correct decision trees, that still disagree with one another as much as possible on incorrect predictions.

Decision tree methods work best with multivariate tabular data, with well defined features describing each observation, this is in contrast to image data which consists of 2D arrays of pixel intensities. Therefore, in order to train such a model, cellular morphology needs to be quantified by measuring cellular features. This is a common task with multiple software packages available, which follow two main steps: (1) Segment objects from the background. Objects may be

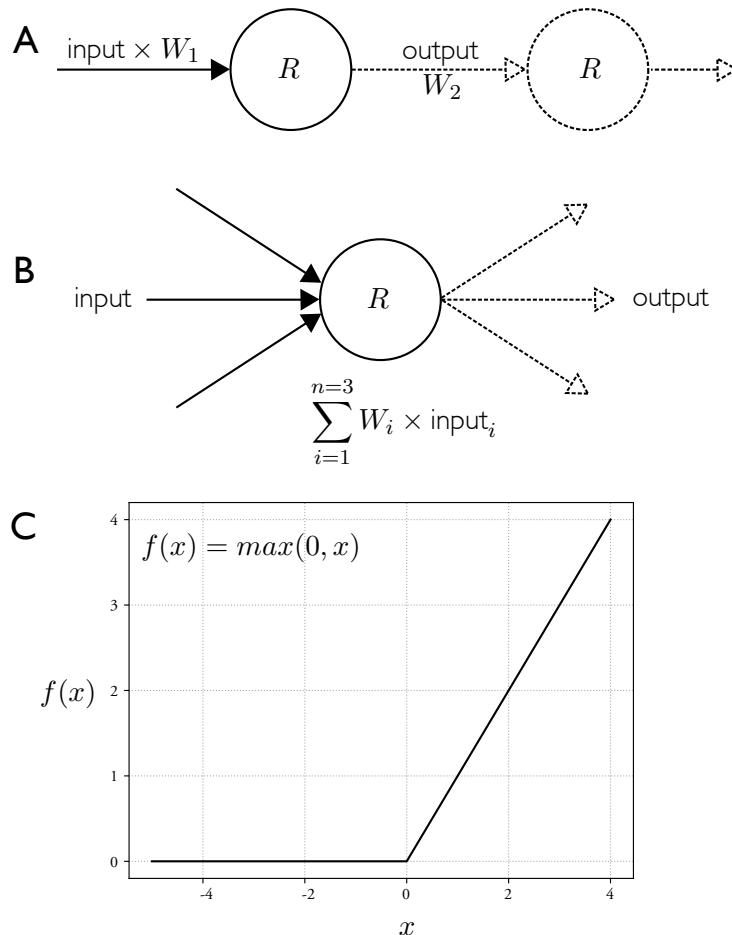
sub-cellular structures or whole-cell masks (2) Measure various attributes from the object, this is typically based on size, shape and intensity. Cellprofiler<sup>58</sup> was chosen primarily due to the high configurability and the permissive license enabling large-scale distributed processing on compute clusters in order to reduce the image analysis time. The images captured on the ImageXpress were analysed using Cellprofiler, quantifying approximately 400 morphological features. The datasets produced by the Cellprofiler analysis contained morphological measurements on an individual cell level. Although we can train a model on single cell data we are not interesting in classifying morphologies of single cells, but rather classifying an image or a collection of images that represent a compound treatment, this therefore allows several approaches to structuring the training data:

1. Train and test on median profiles.
2. Train on single cell data, test on image or well median profiles.
3. Train on single cell data, test on single cell data and classify the parent image as the most commonly predicted class of cell in that image.
4. Train on median profiles of bootstrapped single cell samples within an image, and test on median profiles.

### 3.1.3 Convolutional neural networks trained on pixel data

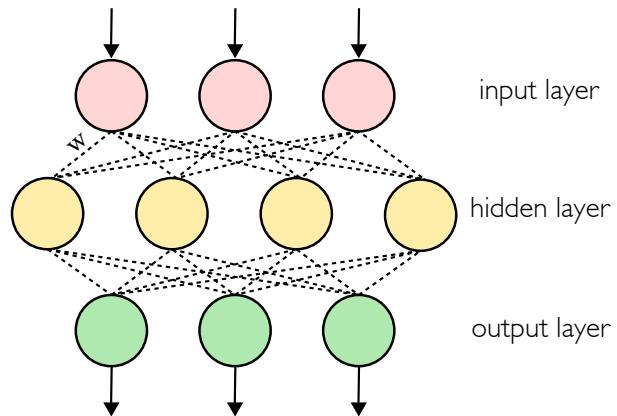
Artificial neural networks (ANNs) are becoming increasingly common in a wide range of machine learning tasks. Although many of the theories underpinning ANNs are decades old,<sup>59</sup> they have only recently achieved widespread practical use due to improved methods for training<sup>60</sup> and the availability of more computing power allowing the use of more complex models. ANNs are (very) loosely inspired by the structure of biological brains, with interconnected neurons passing signals through layers onto subsequent neurons forming a chain with the output of one neuron becoming the input for the next neuron. In between neurons, the signals can be altered by multiplying the value by a weight ( $W$ ), it is through adjusting these individual weights that ANNs optimise their performance for a particular task, similar to how long-term potentiation is used to strengthen synaptic connections in biological brains. When a signal reaches a neuron, it is combined via a weighted sum with all the other inputs from other connected neurons and passed through an activation function. This activation function – similar to an action potential in neurons – determines the output of the neuron for the given aggregated input, which is then passed as new inputs onto subsequent neurons and so on, however, in contrast to an all-or-nothing output of an action potential there are several types of activation functions used in ANNs, most of which have a graded output (figure 3.2B).

The neurons in an ANN are typically arranged in several layers: an input layer; one or more hidden layers; and a final output layer (figure 3.3). With each layer, the network transforms the data into a new representation, through training the network these representations make the data easier to classify. In the final layer, the data is ultimately represented in a way which makes a single output neuron activate more strongly than the other neurons in that layer, and so the data



**Figure 3.2:** (A) A representation of a single connected neuron in an ANN, the input value to the neuron is multiplied by the weight ( $W_1$ ), before being passed through the activation function  $R$ , the output of which is then multiplied by  $W_2$ , and passed as the input to the next neuron. (B) A neuron with multiple inputs and outputs, typical of those in a hidden layer. The activation function acts on the weighted sum of all inputs, and returns a single output value which is then directed to all connected neurons in the next layer. Where  $W_i$  is the weight of  $\text{input}_i$ . (C) A common activation function also known as a rectifier, in this example a rectified linear unit (ReLU), in the inputs ( $x$ ) is transformed and passed as output. So  $f(x)$  can be viewed as the output for a given value of  $x$ .

**Figure 3.3** Representation of a simple 3-layer ANN with a single fully connected hidden layer, three input neurons and three output neurons.  $W$  denotes a weighted connection between an input neuron and a hidden-layer neuron, with all connections between neurons having an associated adjustable weight. A network such as this would take a vector of three numbers as input, and would be capable of predicting three classes from the output layer of three neurons depending on the activation strengths of the neurons in the final output layer.



is ultimately transformed into a single value – the index of the active neuron which corresponds to a particular class. A new ANN is initialised with random weights, to train a neural network these weights are adjusted by feeding in labelled data and adjusting weights in order to minimise classification errors through a process known as backpropagation.<sup>60</sup>

The convolution aspect of convolutional neural networks plays an important role when working with image data. Two-dimensional convolutions are widely used in image processing – blurring, sharpening and edge detection are all common operations which use this operation. They work by mapping a kernel – a smaller matrix of values – across a larger matrix, thereby using information from a small region of pixels in their transformation of each individual pixel. This lends itself well to ANNs, as a pixel value in isolation is less informative than a pixel value in the context of the neighbouring values. Depending on the size and the values within the kernel, the transformations highlight different features within an image. Two dimensional convolutions are used in ANNs by starting with many randomly initialised kernels, and updating the kernel values through training in order to best highlight features which prove useful for accurately predicting classes. Using a single convolutional layer highlights simple features in an image such as edges and speckles, by combining several convolutional layers more complex features are highlighted through combinations of these simple features. These convolved images are then flattened into a one-dimensional vector which is used as an input in a fully connected ANN such as that depicted in figure 3.3.

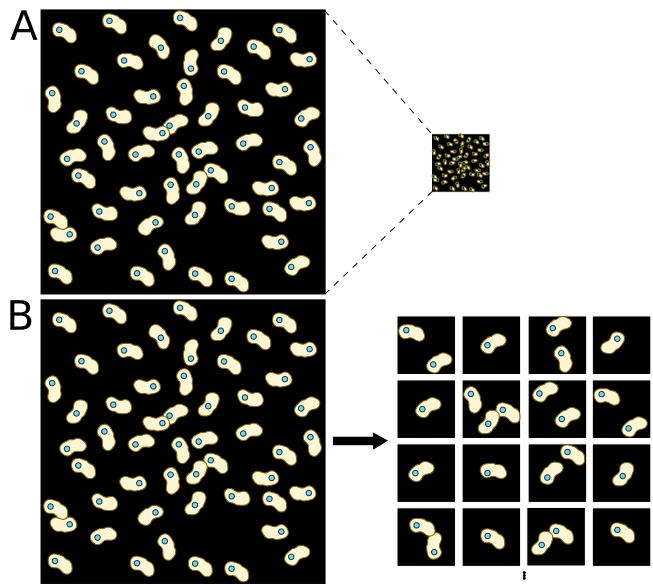
TODO: need some intro into the tasks, the mechanistic classes.

TODO: aims of the chapter

## 3.2 Results

### 3.2.1 CNN predictions are improved using sub-images

The images generated by the ImageXpress microscope with zero binning are  $2160 \times 2160$  pixel tiff files, with a bit-depth of 16, whilst these image properties are common in microscopy, they are extreme for current CNN implementations. Most image classification tasks involving CNN's use 8-bit images in the region of 300 by 300 pixels, relatively small images are used as the convolutional layers of deep CNN's generate many thousands of matrices, and using smaller input images drastically reduces the computing resources and time required to train such classifiers.

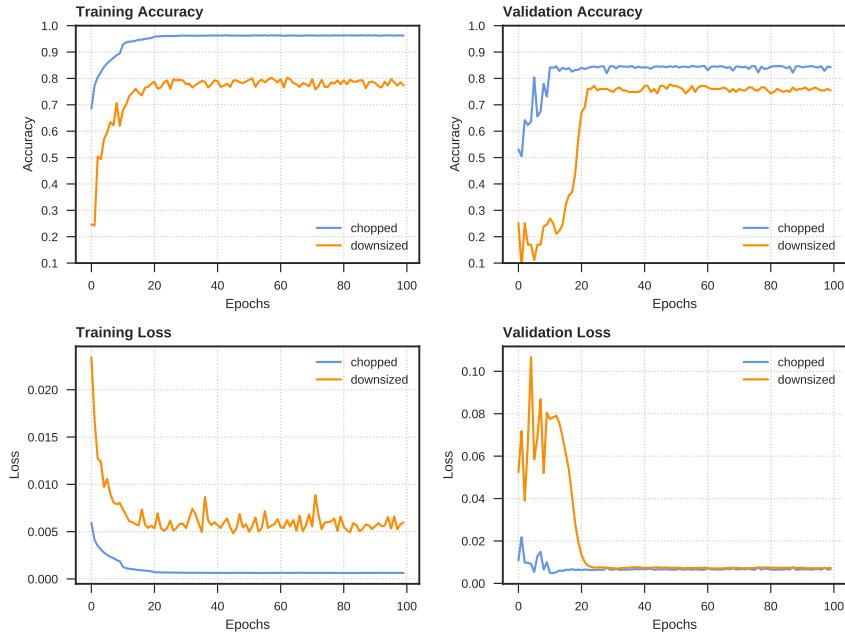


**Figure 3.4:** Two options for adapting large microscope images to work with the smaller input size of typical CNNs. **(A)** Full-sized images are downsized to the desired dimensions via bilinear or bicubic interpolation. **(B)** Images are chopped into smaller sub-images, cell detection can be carried out beforehand to ensure images contain at least one cell.

This presents the issue of how to reduce the  $2160 \times 2160$  images into small images, one option is to downscale the entire image using bi-linear or bi-cubic interpolation, while a second option is to chop the original image up into smaller sub-images (figure 3.4). Downsizing the original image by simple scaling has a few potential problems which make it unsuitable for this particular task: many of the finer-grained cell morphologies such as mitochondria and endoplasmic reticulum distribution will be lost due to the reduction in image resolution; in addition, it was found that whole well images are susceptible to over-fitting as the classifier learned biologically irrelevant features such as the locations of cells within an image, which although should be random might have some spurious association with particular class labels. When chopping images into sub-images the most simple and commonly used method is to chop each image into an evenly spaced grid, whilst this is unbiased and easy to implement, it has the downside of potentially returning many images that do not contain any cells. A more nuanced approach is to first detect the  $x,y$  co-ordinates of each cell in the image, and creating a  $300 \times 300$  bounding-box around the centre of each cell. This method returns an image per cell, negating the issue of empty images; it does however require detecting cell locations and handling cells located next to the image border.

To compare the performance of using either downsized whole images or cropped sub-images, a pair of ResNet18 models were trained using either one of the datasets. It was evident during training that using sub-images resulted in a higher final validation accuracy (0.847) compared to whole-images (0.778), as well as converging much faster than the whole-image-trained model (figure 3.5).

It should be noted that the validation accuracy reported from the sub-image trained model is for classifying individual sub-images. One way to better use these individual sub-image classifications is to predict the parent image class based on a consensus of the predicted classes of the child sub-



**Figure 3.5:** Comparison of training ResNet18 model on chopped sub-images vs down-sized images from the MDA-MB-231 cell line. Chopped images were  $300 \times 300$  crops centered on nuclei. Whole images were  $2160 \times 2160$  images downsized to  $300 \times 300$  pixels.

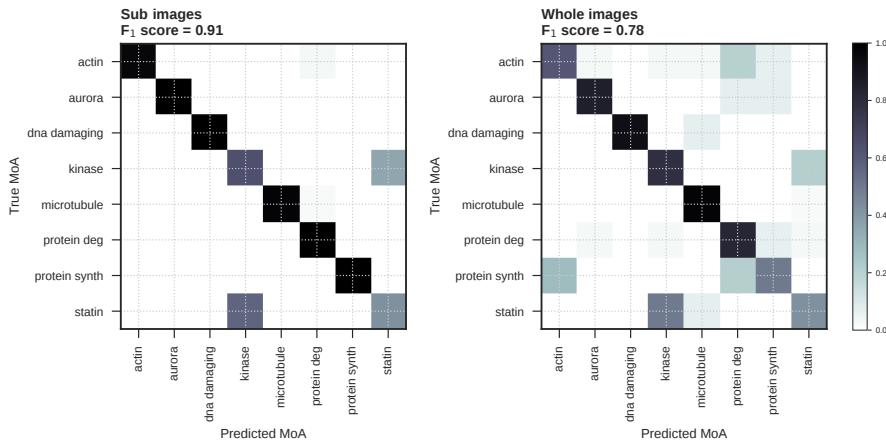
images. Using this consensus prediction, the sub-image validation classification accuracy increased from 0.847 to 0.912. Looking at confusion matrices calculated for both sub-image and whole images revealed that neither approach had difficulties at predicting a particular MoA class (figure 3.6).

Following these results the rest of the work involving CNNs used sub-images during training and prediction. Whilst sub-images improved model training and classification accuracy, it also introduces more complexity as images have to pre-processed to indentify cells and crop to a bounding box. It also introduces another parameter in terms of image size which has to be considered and optimised. While here I chose  $300 \times 300$  pixel images corresponding to  $97.5 \mu\text{m}^2$ , this was chosen pragmatically to fully capture a single cell and a portion of any adjacent cells. This value could be optimised by running several models with differently sized cropped images, although this value is largely dependent on cell line characteristics, magnification and image binning.

### 3.2.2 More complex CNN architectures outperform simpler AlexNet

As CNNs can be constructed with a wide variety of architectures, and the field is still rapidly developing, I remained closed to well established architectures in the literature. However, as most images are digitally represented in three colour channels (red, green, blue (RGB)), the vast majority of CNN models are constructed in a way that input is restricted to three colour channels, therefore it is necessary to adapt these architectures to work with the differently shaped inputs and additional parameters generated by the 5 channel images generated with the ImageXpress.

The two different CNN architectures were tested based on the hypothesis that a deeper, more



**Figure 3.6:** Confusion matrices comparing sub-image and whole image classification accuracy on 8 mechanistic classes of compounds.

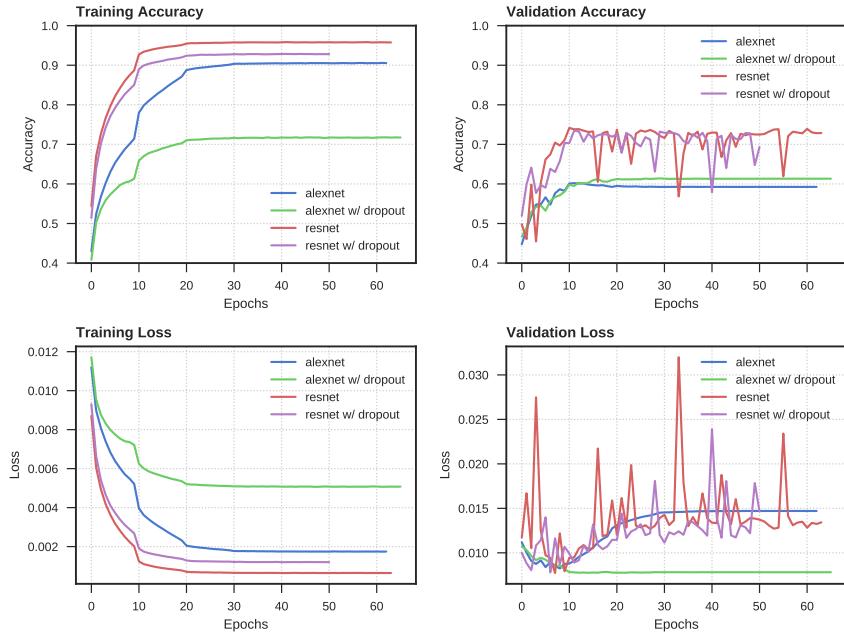
complex architecture (ResNet18<sup>61</sup>) will be capable of learning more subtle features, although more complex models with greater numbers of internal parameters are more prone to overfitting when training data is limited. On the other hand, a more simple model such as AlexNet<sup>62</sup> which contains fewer convolutional layers will be less able to perform complex transformations of the data, and therefore theoretically limit the subtle features which can be extracted and learned from an image. While this might theoretically reduce accuracy, in the absence of large amount of training data it may reduce overfitting due to the fewer number of parameters.

In an effort to reduce over-fitting, both models were evaluated with and without dropout in their dense layers during training. Dropout is a form of regularisation and works by randomly ignoring a fixed proportion of neurons during the training phase, with the theory that this prevents the model becoming too dependent on the output of particular neuron and leads to more robust features used for classification.

Four models in total were trained on sub-images of all eight cell-lines pooled into a single dataset. The models were ResNet18, ResNet18 with dropout, AlexNet and AlexNet with dropout. During training the two ResNet18 models outperformed the AlexNets in both training and validation accuracy (figure (3.7)). AlexNet with dropout layers did outperform the other three approaches when it came to validation loss, as loss did not increase even after many epochs this model demonstrated it is less liable to overfit data. However, the ResNet18 models showed a substantial increase in classification accuracy, and if training is limited to fewer than 10 epochs they do not show worse over-fitting compared to the AlexNet models. Additional dropout layers does not seem to reduce ResNet18's liability to overfit beyond 10 epochs, this is not too surprising as principle behind ResNet18's residual architecture is to limit overfitting, and adding additional dropout to the final fully-connected layers is a crude approach.

### 3.2.3 Standardising image intensity does not improve CNN model convergence

When training CNN models it is common practice to standardise image intensities. This pre-processing step consists of subtracting the mean of the image (or image batch) from each pixel and



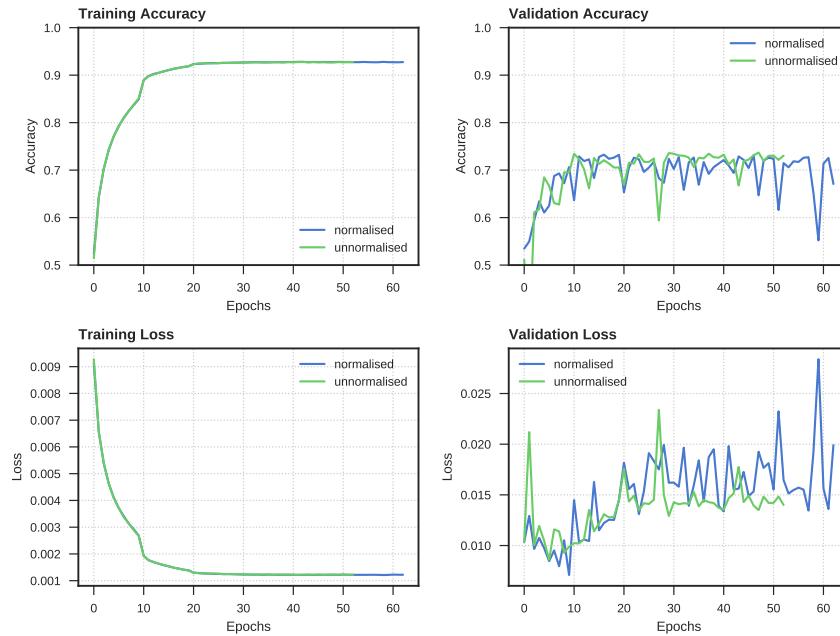
**Figure 3.7:** Comparison of CNN architectures. A comparison of AlexNet and ResNet18 architectures with and without dropout training and predicting on 5 channel  $244 \times 244$  pixel 5 channel images of all eight cell lines. Loss was calculated using cross entropy on 8 mechanistic classes of compounds.

dividing the result by the standard deviation. The theory is this reduces training time and helps CNN models converge faster by ensuring the weights calculated during training are all on a similar scale which in turn restrains the gradients used in backpropagation. This pre-processing makes sense in the classical and traditional academic use of CNNs which are often trained on images or photographs from many different sources with inconsistent lighting and colours. However, the images used in this high-content screening dataset are all from a single microscope with a carefully controlled light source, in addition the intensities of the different channels carry a biological information relating to the abundance of different proteins or cellular structures. Therefore I wanted to assess if standardising image intensities per image channel improved model convergence and classification accuracy compared to un-normalised intensity values<sup>i</sup>.

Two models based on the ResNet18 architecture were trained on chopped  $300 \times 300$  pixel images of a pooled dataset of all eight cell lines, one of the models was fed images standardised per channel, the other raw image intensities. After 48 hours of training (54 and 64 epochs for unnormalised and normalised models respectively<sup>ii</sup>) both models demonstrated identical training curves for training accuracy and loss, while validation accuracy and loss curves showed no striking difference in the performance between the two methods, although the normalisation pre-processing step appears to cause sudden drops in model performance indicated by decreased accuracy and increased loss

<sup>i</sup>Although un-normalised, intensity values were converted from 16 bit unsigned integers (65536 grayscale values) to 8 bit unsigned integers (256 grayscale values). This reduces training time and storage size at the expense of intensity accuracy.

<sup>ii</sup>The number of epochs per 48 hours does not indicate how fast a model converges, but rather the affect of availability of compute resources used for image loading.



**Figure 3.8:** Effect of image intensity normalisation on CNN training. ResNet18 models training and predicting on eight pooled cell-lines with and without standardising image intensities per image per channel.

(figure 3.8).

There is the possibility that training a model on disparate imaging datasets – from either different microscopes with different illumination settings, or different concentrations of reagents – then image standardisation may play a more important role. However, as intensity standardisation did not improve model performance in this case I chose to continue CNN work using un-standardised images, as there is an argument that standardisation may remove biologically relevant information for no benefit.

### 3.2.4 Single cell/Image aggregates improve classification accuracies with decision trees.

TODO, delete as appropriate when results come in.

### 3.2.5 Principal component analysis does (not) improve classification accuracy with decision trees.

TODO, delete as appropriate when results come in.

### 3.2.6 RF/CNN outperforms CNN/RF when using a single cell-line

TODO, delete as appropriate when results come in.

### 3.2.7 Data from additional cell lines does (not) improve model performance

TODO, delete as appropriate when results come in.

### 3.2.8 On the transferrability of models to new unseen cell lines

TODO

## 3.3 Discussion

TODO.

## 3.4 Methods

### 3.4.1 Accuracy

Validation accuracy during training was measured using the Jaccard similarity score of the  $i$ th samples with true label set  $y_i$  and predicted label set  $\hat{y}_i$ :

$$J(y_i, \hat{y}_i) = \frac{|y_i \cap \hat{y}_i|}{|y_i \cup \hat{y}_i|} \quad (3.1)$$

The  $F_1$  score was used post training to determine classification accuracy. The  $F_1$  score is the harmonic mean of both the precision and recall. So given true positives (tp), false positives (fp) and false negatives (fn)

$$\text{precision} = \frac{\text{tp}}{\text{tp} + \text{fp}} \quad (3.2)$$

$$\text{recall} = \frac{\text{tp}}{\text{tp} + \text{fn}} \quad (3.3)$$

$$F_1 = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}} \quad (3.4)$$

### 3.4.2 Ensemble of decision trees

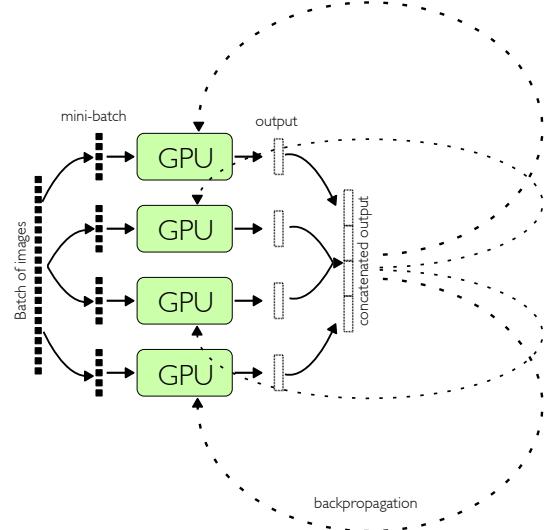
Models were created using scikit-learn version 0.19 in python 3.6.2.

### 3.4.3 Convolutional neural networks

All code related to neural networks was written in pytorch v0.3 for python 3.5, and all ANN models were trained on nvidia K80 GPUs.

#### Data parallelism

As training CNNs is computationally expensive and time consuming, data parallelism was used to share batches of images across multiple GPUs trained in parallel. This technique replicates the CNN model on each device, which processes a portion of the input data, the updated weights for all devices are then averaged and model replicates are updated synchronously after each batch (figure 3.9). This speeds up model training approximately linearly with the number of GPUs and allows use of larger batch sizes.



**Figure 3.9:** Increased training speed by data parallelism. Models are replicated across an array of GPUs, the input batch is split evenly among the devices, with each device processing a portion in parallel. During backpropagation the updated weights for all replicas are averaged and models weights are updated synchronously.

## Architecture

### Training parameters

Image intensities were standardised on an individual image and channel basis by taking each image in the form of a [width  $\times$  height  $\times$  channel] array and subtracting the mean of each channel from each pixel value in that channel, and dividing the pixel value by the standard deviation of the original channel.

### Image preparation

# 4

# MEASURING DISTINCT PHENOTYPIC RESPONSE

Note: this chapter is based on previously published work: "Development of the Theta Comparative Cell Scoring Method to Quantify Diverse Phenotypic Responses Between Distinct Cell Types", S Warchal, J Dawson, N.O Carragher. *ASSAY and Drug Development Technologies*, pages 395-406, 7:14, 2016. and "High-Dimensional Profiling: The Theta Comparative Cell Scoring Method", *Phenotypic Screening. Methods in Molecular Biology* 1787, 171-181.

## 4.1 Introduction

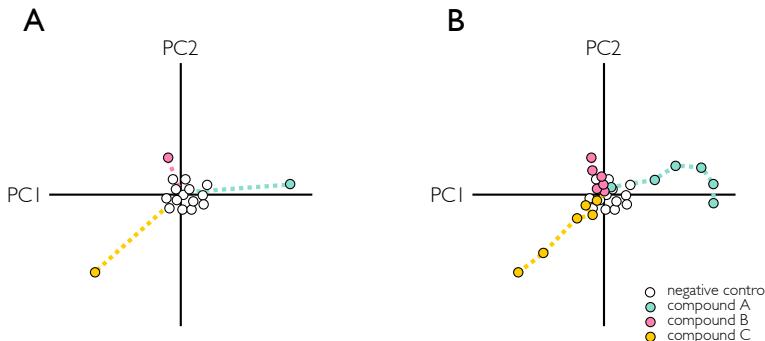
### 4.1.1 Comparing response to small molecules across a panel of cell lines

Comparative analysis of cell line panels treated with compounds are routinely used in pharmacogenomic studies and drug sensitivity profiling. These studies often use large numbers of cell lines and simple measures of compound response such as growth inhibition or cell death, allowing researchers to interrogate sensitivity of various small molecule therapies in a number of genomic backgrounds representing different diseases, disease-subtypes or patient populations.

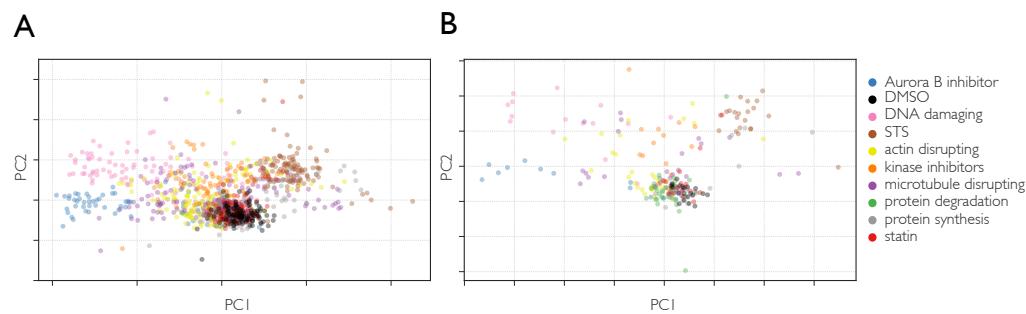
Using high-content imaging methods with cell line panels enables more complex cellular readouts than cell death resulting in a more detailed characterisation of compound effect. However, in order to apply multiparametric high-content data to pharmacogenomic studies, there needs to be a robust – and ideally univariate – measure of compound response to correlate drug sensitivity with genomic or proteomic datasets.

### 4.1.2 Quantifying compound response in high content screens

A simple but effective method to quantify the magnitude of compound response from multiparametric data is to calculate the distance from the negative control to the compound induced phenotype in feature space. This idea was first demonstrated by Tanaka *et al.* using PCA to reduce the dimensionality of a high content screening dataset to 3 principal components, and taking the distance from the centroid of the negative control replicates to the compound co-ordinates.<sup>63</sup> The distance from the negative control in PCA space is an effective metric for detecting phenotypically active compounds. In addition, distance measurements can be repeated for multiple concentrations of a compound to produce a concentration – phenotypic-distance response curve (see figure 4.1) and EC<sub>50</sub> values. However, one issue in calculating the distance-from-negative-control metric of compound activity is that it disregards much of the information relating to the position in feature space, as depicted in figure 4.1, two compounds may have similar distances yet those distances may be produced by very different morphological changes. In order to discern between two such compounds there needs to be a measure of directionality.



**Figure 4.1:** Diagram illustrating measuring magnitude of compound response by distance from the negative control centroid in principal component space. **(A)** Phenotypic distance to three different compounds. Compound A and B show phenotypic activity as they are distanced from the negative control cluster, whereas compound B shows little activity. Note that compound A and compound C have similar distances from the negative control centroid, yet have very different values in principal component space. **(B)** A titration series for each of the three compounds, showing how increasing concentrations of compounds A and C show increasing distance from the negative control, whereas weakly active compound C does not increase in distance.



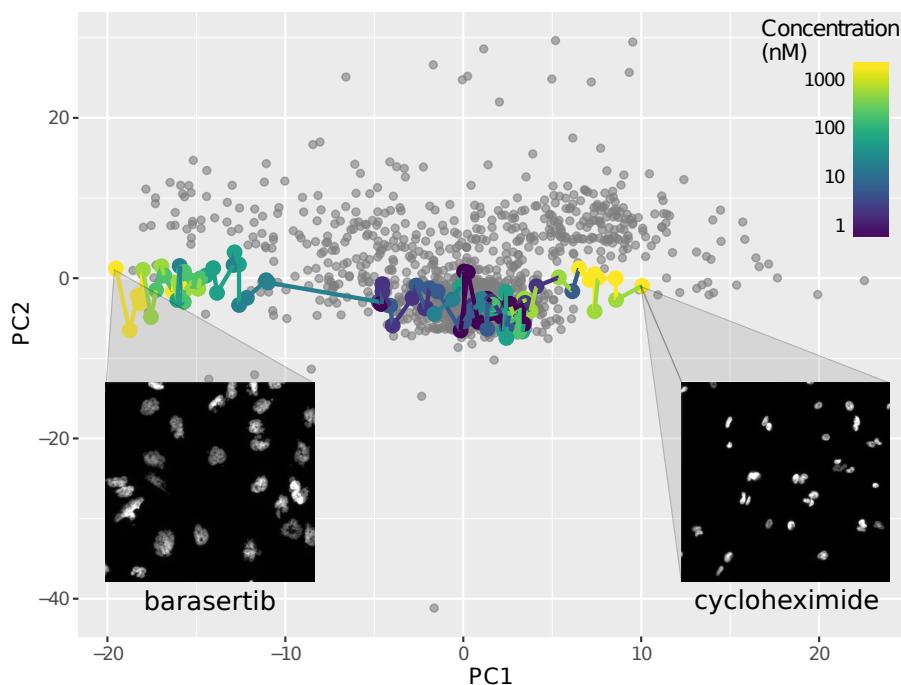
**Figure 4.2:** MoA clustering of compounds based on PCA of their morphological features. Principal components calculated from morphological features of 24 compounds grouped into 8 mechanistic classes. **(A)** Principal components calculated from an image average of individual cell measurements. **(B)** Each point represents a well average from individual cell measurements as each well contains 9 image sites. STS: staurosporine.

## 4.2 Results

### 4.2.1 Compound titrations produce a phenotypic ‘direction’

Visualising high-content imaging data from compound screens in principal component space reveals a number of patterns and produces a representation of the overall structure of the data. Performing PCA on morphological feature data from 24 compounds representing 9 mechanistic classes and plotting the first 2 principal components reveals compounds with the same MoA tend to cluster with one another in PCA space (figure 4.2).

When taking concentrations of compounds into account, is it possible to visualise the effect of increasing concentrations of a compound and how the distance from the negative control and inactive compounds increases. Figure 4.3 shows two highlighted compounds from the same data as in figure 4.2, we can see as compound concentration increases morphologies become increasingly distant



**Figure 4.3:** Principal components of Cellprofiler features calculated from a 24 compound high content screen in MDA-MB-231 cells. Barasertib (left) and cycloheximide (right) titrations are highlighted to show two active compounds with distinct phenotypes heading in different directions in phenotypic space with increasing concentration. Images shown next to points are from the Hoechst stain labelling nuclei morphology produced by  $1 \mu\text{M}$  of each compound.

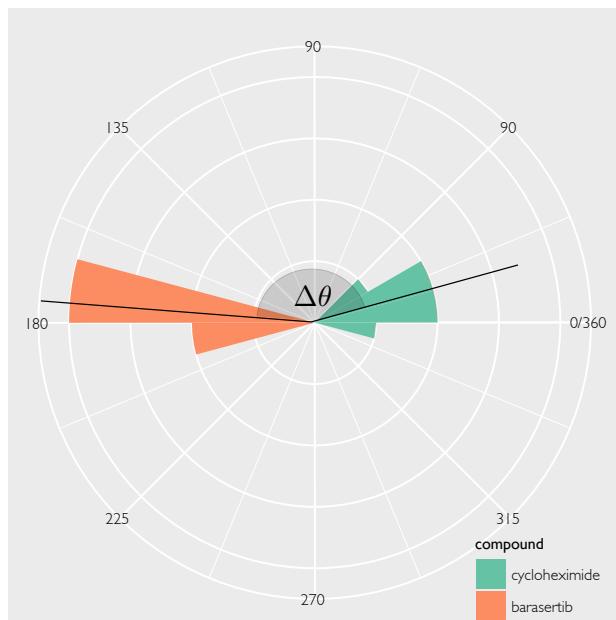
from the untreated negative control cluster positioned centrally, with the two different compounds producing opposite directions. Mirroring the differences in direction, the morphologies produced by barasertib and cycloheximide are also very different from one another, with barasertib – an Aurora B kinase – inhibitor producing large irregular nuclei, and cycloheximide creating small bright nuclei. This direction in PCA space can be thought of as a phenotypic direction, which can be measured and quantified independent from potency<sup>i</sup>.

#### 4.2.2 Difference in phenotypic direction can be used to quantify distinct phenotypes

Using direction in addition to distance it is now possible to distinguish between equally phenotypically potent compounds with distinct morphological effects. By calculating an angle ( $\theta$ ) between phenotypic directions as a function of cosine dissimilarity, a univariate value can be used to quantify phenotypic distance between either different compounds, or cell-lines treated with the same compound to detect distinct phenotypic response. By calculating  $\theta$  against a fixed reference vector, the difference in  $\theta$  ( $\Delta\theta$ ) between two treatments can be quantified and visualised in polar co-ordinates as histograms or rose plots (figure 4.4). Compounds with the same phenotypic direction will have a small  $\Delta\theta$  and compounds with dissimilar phenotypes having a large  $\Delta\theta$ , when expressed in degrees the values are constrained between  $0^\circ$  and  $180^\circ$ .

Although the data in figures 4.3 & 4.2 show the negative control points clustered near the origin

<sup>i</sup>as measured by distance from the negative control cluster centroid

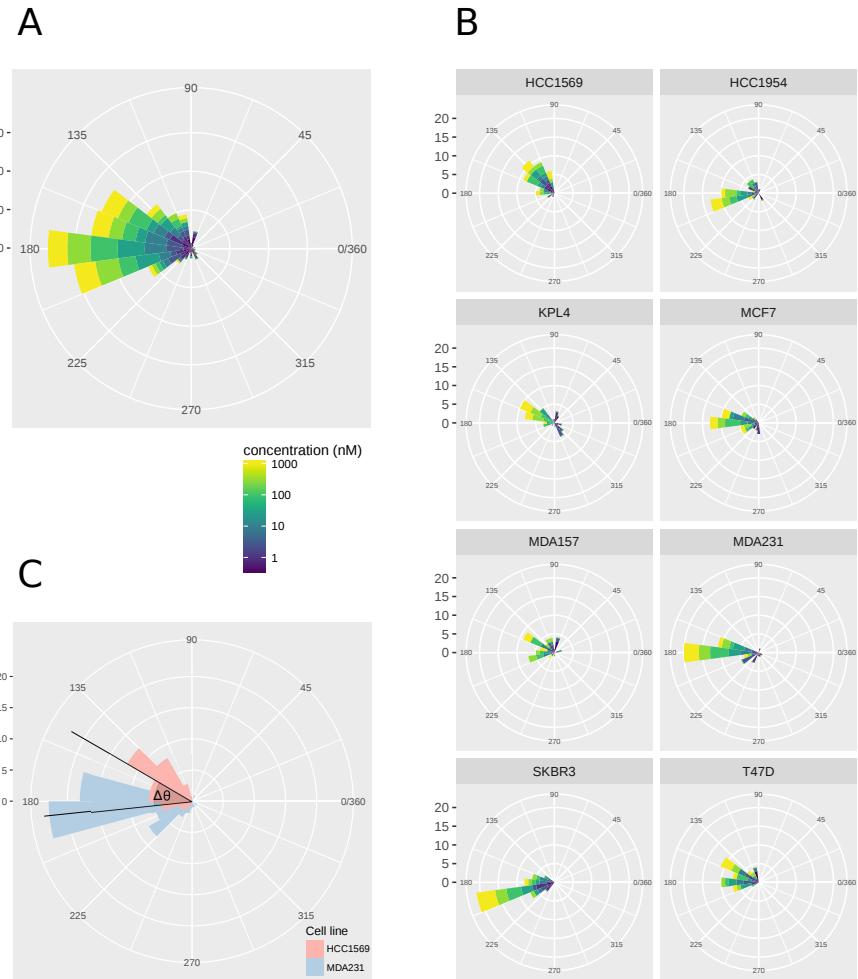


**Figure 4.4:** Visualisation of  $\Delta\theta$  to quantify the difference in phenotypic direction between two compounds. Histograms in polar co-ordinates show the  $\theta$  values of treatments against a fixed reference vector, with  $\Delta\theta$  calculated as the difference between the average  $\theta$  (black lines) of each compound.

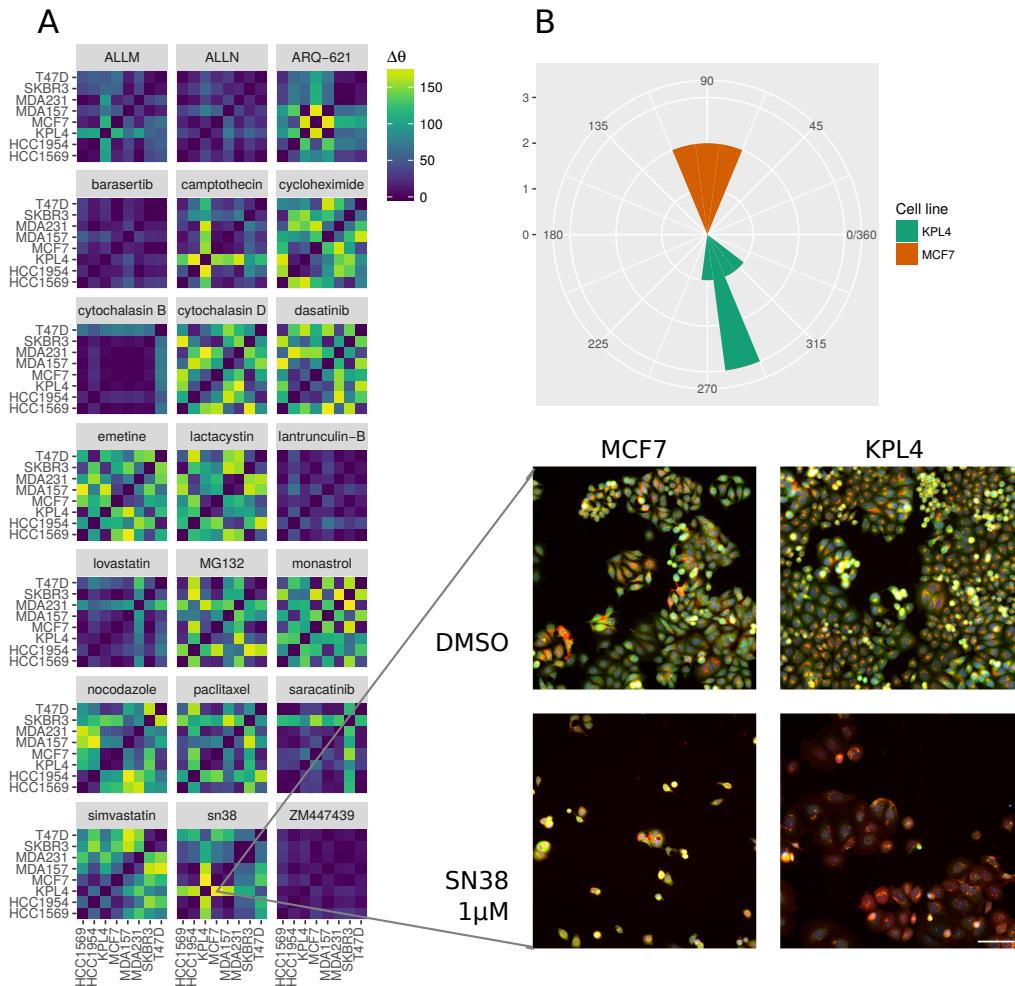
(0, 0) in principal component co-ordinates this is not guaranteed and should not be relied upon, so it is necessary to translate the principal components co-ordinates so that the negative control centroid is positioned over the median. In addition, inactive compounds will be positioned in proximity to the negative control points and calculated  $\theta$  values will be misleading, therefore removing inactive compounds based on distance from the negative control is an important pre-processing step.

#### 4.2.3 SN38 elicits a distinct phenotypic response between cell lines

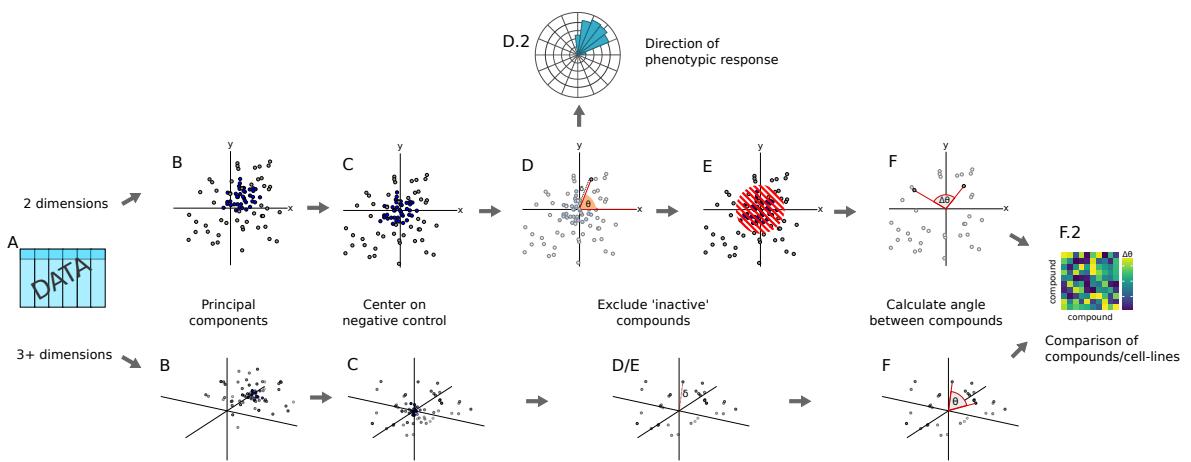
Instead of calculating  $\Delta\theta$  between compounds it is also possible to calculate  $\Delta\theta$  between cell lines per compound. To identify and quantify differential phenotypic responses,  $\Delta\theta$  was calculated between pairs of 8 breast cancer cell lines treated with 24 small molecules at the three highest concentrations (0.1  $\mu$ M, 0.3  $\mu$ M, 1  $\mu$ M). 21 out of the 24 compounds were found to be sufficiently active across the 8 cell lines to proceed, and the difference in phenotypic direction was calculated for all pairs of cell lines for each compound. Figure 4.6 shows a heatmap of the calculated  $\Delta\theta$  values. Some compounds such as the Aurora B inhibitors ZM447439 and barasertib showed very little difference in phenotypic response between the breast cancer cell lines, whereas compounds such as the topoisomerase I inhibitor SN38 demonstrated a single cell-line (KPL4) having a distinct response compared to the 7 others. Particularly striking is the difference between the MCF7 and KPL4 cell lines with a  $\Delta\theta$  of 179°, indicated near opposite phenotypic responses between the pair of cell lines to the topoisomerase I inhibitor.



**Figure 4.5:** Visualisation  $\Delta\theta$  to quantify the difference in phenotypic response between cell lines when treated with barasertib. **(A)** Circular histogram of  $\theta$  values of barasertib calculated for eight cell lines. **(B)** Phenotypic direction of cell lines treated with barasertib stratified by cell line. **(C)** Representation of  $\Delta\theta$  for the difference between HCC1569 and MDA-MB-231 cell lines. Note that in this case  $\Delta\theta$  is relatively small.



**Figure 4.6:** Heatmap of  $\Delta\theta$  values between pairs of cell lines for separate compounds. **(A)**  $\Delta\theta$  calculated between pairs of cell lines treated with 21 compounds as 1  $\mu\text{M}$  concentration. Images show differential response between KPL4 and MCF7 cell lines treated with 1  $\mu\text{M}$  SN38. MCF7 cells are observed to decrease in cell area with bright staining for the endoplasmic reticulum, whereas KPL4 cells produce a ‘fried egg’ morphology with large spread cells and weak endoplasmic reticulum staining. Channels used are as follows: *Red* - MitoTracker DeepRed (mitochondria); *Green* - Concanavalin A (endoplasmic reticulum); *Blue* - Hoechst33342 (nuclei). Scale bar: 100  $\mu\text{m}$ . **(B)** Histogram of  $\theta$  values calculated for MCF7 and KPL4 cells treated with 1  $\mu\text{M}$  SN38.  $\Delta\theta = 179^\circ$



**Figure 4.7:** Theta comparative cell scoring (TCCS) workflow. **(A)** Normalised and standardised numerical data. **(B)** Principal component analysis, negative control values coloured in blue. **(C)** Centering of principal component values to the negative control centroid. **(D)** Calculation of distance from the origin to each data point, an activity cutoff is derived from the standard deviation of the distance to the negative control values. **(D.2)** In two-dimensional space, a directional histogram can be created by the angle of each vector against a reference vector. **(E)** Inactive compounds excluded based on distance from the origin. **(F)** Determining the angle between compounds/cell-lines. **(F.2)** Visualisation or clustering of compounds based on  $\theta$  values.

### 4.3 Discussion

A number of methods exist to classify drug MoA and profile drug response in the context of high-content imaging studies, most of these have only been applied to a single cell type. The method described in this chapter, named as theta comparative cell scoring (TCCS), was developed to provide a pragmatic way to perform comparative high-content imaging studies across genetically and morphologically distinct cell lines. TCCS should be viewed as an extension to the common distance-in-PCA approach taking directionality into consideration in addition to distance from controls. The benefits of TCCS over previous methods are as follows: (1) the use of distance from the negative control to remove inactive compounds as one of the first steps prevents spurious differences that would be present in measures such as correlation or simple cosine similarity; (2) The comparison of each data point to a common reference vector enables visualisation of a phenotypic direction.

When comparing compound response between cell lines the most critical step, regardless of subsequent methods, is to account for the inherent morphological differences between untreated cell lines. Without this normalisation step morphologically distinct cell lines are not directly comparable as their large scale morphological differences will mask any difference in morphological response to a compound.

The TCCS method removes compounds which are deemed to be inactive if they are not sufficiently distant from the negative control (see figure 4.7). While this increases the robustness of the calculation by removing spurious differences in direction, it also introduces a new problem when compounds elicit large differences in potency between cell lines. This would result in the removal of

such compounds from the analysis despite producing a genuine, and potentially biologically interesting, differential response between cell lines. This can be rectified by identifying these compounds when computing compound distances from the negative control in principal component space – any compounds that show large differences in this distance between cell lines can be flagged for further analysis before removal.

When using high-content imaging data with a lot of morphological feature measurements, using the first two principal components as depicted in this chapter may only account for a small proportion of variation in the data. This may lead to potentially missing interesting differences which are only evident in later principal components.

Fortunately, as part of the TCCS algorithm the cosine similarity equation uses the dot product of the two vectors reducing any two equal length vectors to a single number, enabling the use of 3 or more principal components. Therefore the proportion of variance to keep in the data can be specified beforehand, and the dimensionality of the data reduced in a way to suit the statistical properties of different datasets.

An interesting prospect of ‘phenotypic direction’ is relating directions back to combinations of morphological features to provide more interpretability to the results. This is possible with PCA by using the feature loadings describe the contributions of original features used to construct each principal component. However, as PCA uses arbitrary positive and negative weights for these feature loadings, other dimensional reductions techniques might be better suited for generating more interpretable results. One example is non-negative matrix factorisation which would return only positive weights for the morphological features, making the contribution of morphological features to the phenotypic direction more interpretable.

Multiple concentrations are not often used in high throughput cell based screening assays despite providing useful information to detect off-target effects as well as reducing false negatives by screening at incorrect concentrations. A potential improvement of the TCCS method is to incorporate data from compound titrations as in figure 4.3 and fitting a linear model to the data points providing information relating to goodness of fit. This could potentially be used to identify compounds with off-target effects at higher concentrations if they do not fit a linear model well which indicates the data points going off at a tangent at higher concentrations towards phenotypic space indicative of cell death (e.g figure 4.1 B compound A).

In conclusion, the TCCS method presents an alternative to (dis)similarity measures such as correlation and cosine distance with important prior steps to account for peculiarities in high-content screening data, enabling high-content screening studies for quantifying distinct phenotypic response between morphologically diverse cell types.

## 4.4 Methods

### 4.4.1 Data pre-processing

Tabular data from Cellprofiler measuring 309 morphological features for each cell was aggregated to an image median. To remove batch effects and to remove inherent cell-line specific morphologies

data was normalised by dividing each morphological feature by the median negative control value for that feature per plate. Each feature was then standardised to a mean of zero and unit variance on the pooled data.

#### 4.4.2 Principal component analysis

Principal components were calculated using the `prcomp` function in R v3.2, with no centering or scaling as this was performed manually beforehand.

#### 4.4.3 Selecting the number of principal components

The number of principal components to used in the analysis can be determined by specifying beforehand the proportion of variance in the data that should be kept, and then finding the minimum number of principal components that account for that proportion of variance in the dataset.

E.g in R:

```

1 threshold = 0.8
2 pca_output = prcomp(data)
3 pc_variance = pca_output$stdev^2
4 cumulative_prop_variance = cumsum(pc_variance) / sum(pc_variance)
5 n_components = min(which(cumulative_prop_variance >= threshold))

```

where `data` is numeric dataframe of morphological features.

#### 4.4.4 Centering the data on the negative control

In order to centre the principal component data so that the mediod of the negative control was positioned on the origin, the median value for each feature columns for the negative control data was calculated. Then finding how much this differs from the origin for each feature, all principal component values were adjusted by this difference.

1. Calculate the median value  $m$  for each principal component for the negative control data (medioids).
2. Subtract each medioid from 0 in order to find the difference from the origin to  $\delta m_i$ , where  $i$  is the  $i^{th}$  principal component.
3. Add  $\delta m_i$  to each value in the  $i^{th}$  principal component.

For example in R, given a dataframe `data` containing a metadata column "compound\_name" of compound names, with "DMSO" as a negative control, and `feature_cols` as a list of non-metadata column names:

```

1 medioids = apply(data[data[, "compound_name"] == "DMSO"], 2, median)
2 delta_m = 0 - medioids # δm
3 for (i in seq_along(feature_cols)) {
4   feature = feature_cols[i]
5   # feature_column_i := feature_column_i + δm_i
6   data[, feature] = data[, feature] + delta_m[i]
7 }

```

#### 4.4.5 Identifying inactive compounds

Inactive compounds were identified by determining a minimum cut-off distance to the negative control centroid in principal component space. This was calculated by first finding the  $l_1$  norm<sup>ii</sup> from each compound at all concentrations to the negative control centroid. The standard deviation of all these distances was calculated and any compound which was within 2 standard deviations of the negative control centroid at 1  $\mu\text{M}$  was deemed inactive, if a compound was found to be inactive in any one of the eight cell lines it was removed from the analysis.

#### 4.4.6 Calculating $\theta$ and $\Delta\theta$

$\theta$  was calculated by taking cosine dissimilarity between two vectors ( $u$  and  $v$ ) in principal component space and converting into degrees.

$$\theta = \cos^{-1} \left( \frac{\mathbf{u} \cdot \mathbf{v}}{\|\mathbf{u}\| \|\mathbf{v}\|} \right) \cdot \frac{180}{\pi} \quad (4.1)$$

When  $v$  is a common fixed reference vector,  $\Delta\theta = |\theta_i - \theta_j|$  where  $\theta_i$  and  $\theta_j$  are theta values for 2 vectors. As opposite phenotypic directions are at  $180^\circ$ ,  $\Delta\theta$  values greater than  $180^\circ$  should be thought as converging towards similar phenotypes. Therefore  $\Delta\theta$  values were constrained to a maximum value of  $180^\circ$  by subtracting any value greater than  $180^\circ$  from  $360^\circ$ .

$$\theta = \begin{cases} 360 - \theta & \text{if } \theta > 180 \\ \theta & \text{otherwise} \end{cases} \quad (4.2)$$

---

<sup>ii</sup>A.K.A Manhattan or city-block distance

# 5

## LARGE COMPOUND SCREEN ACROSS 8 BREAST CANCER CELL LINES

### 5.1 Section name



# 6 | CHEMINFORMATICS

## 6.1 Section name



# 7 | DISCUSSION AND CONCLUSION

## 7.1 Section name



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